

FORM PTO-1390  
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1768

U.S. APPLICATION NO (If known, see 37 CFR §1.5)

**09/646778**

INTERNATIONAL APPLICATION NO

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/DE99/01087

7 APRIL 1999

9 APRIL 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.



**Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:**

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
  - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☒ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

**Items 11. to 16. below concern document(s) or information included:**

11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
  - ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☐ Other items or information:

U.S. APPLICATION NO. (if known, see 37 CFR §1.5) <b>09/646778</b>		INTERNATIONAL APPLICATION NO. <b>PCT/DE99/01087</b>		ATTORNEY'S DOCKET NUMBER <b>SCH 1768</b>	
17. <input checked="" type="checkbox"/> The following fees are submitted:				<b>CALCULATIONS</b> PTO USE ONLY	
<b>BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)):</b>					
Search Report has been prepared by the EPO or JPO.....				\$840.00	
International preliminary examination fee paid to USPTO (37 CFR §1.482).....				\$670.00	
No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2)).....				\$760.00	
Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO.....				\$970.00	
International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4).....				\$96.00	
<b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				<b>\$840.00</b>	
Surcharge of <b>\$130.00</b> for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	41 - 20 =	21	x \$ 18.00		\$378.00
Independent claims	7 - 3 =	4	x \$ 78.00		\$312.00
MULTIPLE DEPENDENT CLAIM(S) (if applicable)				+ \$ 260.00	
<b>TOTAL OF ABOVE CALCULATIONS =</b>				<b>\$1,530.00</b>	
Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				<b>\$1,530.00</b>	
Processing fee of <b>\$130.00</b> for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				<b>\$1,530.00</b>	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				<b>\$1,530.00</b>	
				Amount to be refunded	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,530.00</u> to cover the above fees is enclosed.					
b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed.					
c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO:					
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.					
Arlington Courthouse Plaza I					
2200 Clarendon Boulevard, Suite 1400					
Arlington, Virginia 22201					
(703) 243-6333					
Filed: 22 SEPTEMBER 2000					
AJZ:jmm					
				SIGNATURE	
				NAME	
				27,969	
				REGISTRATION NUMBER	

**IN THE UNITED STATES DESIGNATED/ELECTED OFFICE**

International Application No. : PCT/DE99/01087  
International Filing Date : 7 APRIL 1999  
Priority Date(s) Claimed : 9 APRIL 1998  
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.  
Title: HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

**IN THE CLAIMS:**

Claim 5, line 3, after "258-273" insert --of Claim 3--;  
Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;  
Claim 7, line 1, delete "claims 1 to 4" and insert --Claim 3--;  
Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;  
Claim 10, line 1, delete "claims 1 to 7" and insert --Claim 3--;  
Claim 11, lines 1 and 2, delete "one of claims 1 to 10" and insert --Claim 3--;  
Claim 12, line 2, delete "one of claims 1 to 10" and insert --Claim 3--;  
Claim 14, lines 1 and 2, delete "one of claims 12 and 13" and insert --Claim 12--;  
Claim 15, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;  
Claim 17, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;  
Claim 19, line 1, delete "one of claims 17 or 18" and insert --Claim 17--;  
Claim 20, line 2, delete "claims 17 to 19" and insert --Claim 17--;

Claim 31, line 2, after "258-273" insert --of Claim 3--;  
Claim 32, line 2, after "258-273" insert --of Claim 3--;  
Claim 33, line 2, after "agents" insert --of Claim 35--;  
Claim 34, line 2, after "agent" insert --of Claim 35--;  
Claim 36, line 1, delete "claims 1 to 10" and insert --Claim 3--;  
Claim 37, line 1, delete "claims 1 to 10" and insert --Claim 3;  
Claim 38, line 4, after "258-273" insert --of Claim 3--;  
Claim 41, line 1, delete "claims 1 to 7" and insert --Claim 3--.

8. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in [claims 1 to 6] claim 3, in such a sufficient amount that they hybridize with the sequences according to [claims 1 to 7] claim 3 or a sequence having 90% homology thereto.

#### REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,

Anthony J. Zelano, Reg. No. 27,969  
Attorney for Applicants  
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
Arlington Courthouse Plaza 1  
2200 Clarendon Boulevard, Suite 1400  
Arlington, VA 22201  
Direct Dial: 703-812-5311  
Facsimile: 703-243-6410  
Email: zelano@mwzb.com

AJZ:jmm



**Human Nucleic Acid Sequences from Ovarian Tumor Tissue**

The invention relates to human nucleic acid sequences from ovarian tumor tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main cancer causes of death in women is ovarian cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which play a role as candidate genes in ovarian cancer, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which are expressed elevated in ovarian tumor tissue.

The invention also relates to nucleic acid sequences Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108, and 112, which are expressed elevated in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 124-257 and 274-307.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 124-257 and 274-307 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The invention also relates to phage-display phages, which are directed against a polypeptide or a fragment and which are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273 according to the invention.

The polypeptides of sequences Seq. ID Nos. 124-257 and 274-305 according to the invention can also be used as tools for finding active ingredients against ovarian cancer, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides, which can be used as tools for finding active ingredients against ovarian cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 124-257 and 274-305 as pharmaceutical agents in the gene therapy for treatment of ovarian cancer or for the production of a pharmaceutical agent for treatment of ovarian cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-305.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-123 and 258-273 for use as vehicles for gene transfer.



## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for tumor-related candidate genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the ovarian tumor tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

**Example 2****Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 68 was found which occurs 6.08 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 68

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0141	0.0244	0.5758	1.7366
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0126	0.0082	1.5299	0.6536
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0847	0.1300	7.6946
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0153	0.0043	3.5827	0.2791
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0136	0.5611	1.7821
Uterus-myometrium	0.0153	0.0000	undef	0.0000
Uterus-general	0.0384			
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.0147			
White blood cells	0.0426			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0259
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0479
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

**2.1.2**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 86 was found which occurs 7.82 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

00  
01  
02  
03  
04  
05  
06  
07  
08  
09  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99



Electronic Northern for SEQ. ID NO.: 86

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0128	0.9153	1.0926
Breast	0.0090	0.0169	0.5293	1.8893
Small intestine	0.0092	0.0331	0.2781	3.5964
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0204	0.0426	0.4795	2.0856
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0274	0.0195	1.4020	0.7133
Hematopoietic	0.0107	0.1136	0.0941	10.6267
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0307	0.0137	2.2358	0.4473
Testicles	0.0115	0.0819	0.1406	7.1142
Lung	0.0104	0.0286	0.3629	2.7557
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0342	0.4758	2.1016
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0270	0.5277	0.0512	19.5264
Uterus-myometrium	0.0229	0.0408	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0095			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0696	Ovary_n	0.0090
Brain	0.0167	Ovary_t	0.0000
Hematopoietic	0.0626	Endocrine tissue	0.0245
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0285	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0303	Nerves	0.0010
Prostate	0.0997	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0155
		Uterus_n	0.0000

**2.1.3**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 114 was found which occurs 6.94 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

03  
02  
07  
06  
04  
04  
00  
02  
03  
00  
00  
00

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0083	0.0102	0.8129	1.2302
Lung	0.0193	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0136	0.0000	undef	0.0000
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0065	0.0064	1.0236	0.9769
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0305	0.0000	undef	0.0000
Uterus-myometrium	0.0032	0.0000	undef	undef
Uterus-general	0.0089			
Breast hyperplasia	0.0445			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.1418
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0047
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0154
Kidney		Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

In an analogous procedure, the following Northern were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0179	0.0075	2.3818	0.4196
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0059	0.0103	0.5760	1.7362
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0052	0.0164	0.3175	3.1494
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels		Hematopoietic	0.0057
Lung	0.0142	Skin-muscle	0.0032
Suprarenal gland	0.0145	Testicles	0.0154
Kidney	0.0254	Lung	0.0164
Placenta	0.0000	Nerves	0.0141
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0025
Gastrointestinal	0.0000
Hematopoietic	0.0171
Skin-muscle	0.0194
Testicles	0.0000
Lung	0.0082
Nerves	0.0020
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0064	0.0019	3.4026	0.2939
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0044	0.0000	undef	0.0000
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.1908	0.0267	37.4714
Uterus-general	0.0096			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0065
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0051	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0572	0.0000	undef
Gastrointestinal	0.0034	0.0075	0.4529	2.2083
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0022	0.0021	1.0799	0.9260
Skin	0.0013	0.0379	0.0353	28.3379
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0041	2.5402	0.3937
Muscle-skeleton	0.0017	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0128	0.0000		
Prostate hyperplasia	0.0000	0.0000		
Seminal vesicle	0.0089	0.0000		
Sensory organs	0.0000	0.0000		
White blood cells	0.0035	0.0000		
Cervix	0.0106	0.0000		

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0142	Skin-muscle	0.0065
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0062	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0208
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 5

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



## Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0075	1.8715	0.5343
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0390	0.3070	3.2573
Endocrine tissue	0.0290	0.0376	0.7698	1.2990
Gastrointestinal	0.0211	0.0324	0.6508	1.5365
Brain	0.0126	0.0144	0.8742	1.1439
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0218	0.0204	1.0669	0.9373
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0190	0.0205	0.9252	1.0808
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0408	0.3741	2.6732
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0217			
Cervix	0.0319			

FETUS  
% frequency

Development	
Gastrointestinal	0.0557
Brain	0.0167
Hematopoietic	0.0063
Skin	0.0079
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0213
Suprarenal gland	0.0181
Kidney	0.0254
Placenta	0.0185
Prostate	0.0121
Sensory organs	0.0000
	0.0251

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0476
Ovary_n	0.3190
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0151
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0000
Testicles	0.0309
Lung	0.0082
Nerves	0.0010
Prostate	0.0000
Sensory Organs	0.0310
Uterus_n	0.0458

Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0113	0.2268	4.4083
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0030	0.0010	2.8798	0.3472
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0062	0.0123	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0163	0.0205	0.7930	1.2610
Kidney	0.0017	0.0055	0.2951	3.3428
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast
Gastrointestinal		Ovary_n
Brain	0.0000	Ovary_t
Hematopoietic	0.0000	Endocrine tissue
Skin	0.0000	Fetal
Hepatic	0.0000	Gastrointestinal
Heart-blood vessels	0.0000	Hematopoietic
Lung	0.0000	Skin-muscle
Suprarenal gland	0.0000	Testicles
Kidney	0.0000	Lung
Placenta	0.0000	Nerves
Prostate	0.0000	Prostate
Sensory organs	0.0000	Sensory Organs
		Uterus_n

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0064	0.0038	1.7013 0.5878	
Small intestine	0.0031	0.0000	undef 0.0000	
Ovary	0.0000	0.0156	0.0000 undef	
Endocrine tissue	0.0068	0.0125	0.5434 1.8403	
Gastrointestinal	0.0000	0.0046	0.0000 undef	
Brain	0.0037	0.0000	undef 0.0000	
Hematopoietic	0.0027	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0065	0.0000 undef	
Heart	0.0042	0.0137	0.3084 3.2426	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0031	0.0000	undef 0.0000	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0000	0.0060	0.0000 undef	
Kidney	0.0054	0.0068	0.7930 1.2610	
Pancreas	0.0050	0.0000	undef 0.0000	
Penis	0.0120	0.0000	undef 0.0000	
Prostate	0.0022	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	0.0000 undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0089			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0026			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0333
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0034	0.0201	0.1698	5.8889
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0081	0.0072	1.1314	0.8839
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0068	0.1583	0.0427	23.4317
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0096	0.0000	undef	0.0000
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0039
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0032
Suprarenal gland	Testicles	0.0309
Kidney	Lung	0.0000
Placenta	Nerves	0.0100
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0077
	Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0170	0.0201	0.8491	1.1778
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0126	0.0072	1.7485	0.5719
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0093	0.0061	1.5241	0.6561
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0137	0.0180	0.7615	1.3133
Kidney	0.0054	0.0479	0.1133	8.8268
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast 0.0000
Gastrointestinal	0.0139	Ovary_n 0.0000
Brain	0.0083	Ovary_t 0.0000
Hematopoietic	0.0063	Endocrine tissue 0.0082
Skin	0.0118	Fetal 0.0000
Hepatic	0.0000	Gastrointestinal 0.0057
Heart-blood vessels	0.0000	Hematopoietic 0.0259
Lung	0.0107	Skin-muscle 0.0154
Suprarenal gland	0.0072	Testicles 0.0082
Kidney	0.0000	Lung 0.0040
Placenta	0.0247	Nerves 0.0205
Prostate	0.0182	Prostate 0.0000
Sensory organs	0.0249	Sensory Organs 0.0042
	0.0000	Uterus_n

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0019	1.3611	0.7347
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	0.0000
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0120	0.7139	1.4008
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0035			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0061	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



## Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0179	0.6538	1.5296
Breast	0.0307	0.0226	1.3611	0.7347
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0074	0.0133	0.5538	1.8057
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0148	0.0137	1.0794	0.9265
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0353	0.0164	2.1591	0.4631
Stomach-esophagus	0.0387	0.0077	5.0421	0.1983
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0163	0.0274	0.5948	1.6813
Pancreas	0.0198	0.0166	1.1966	0.8357
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0064	3.0709	0.3256
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0182			
Cervix	0.0426			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0249	Hematopoietic	0.0114
Lung	0.0181	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0061		0.0164
Placenta	0.0499	Lung	0.0110
Prostate	0.0126	Nerves	0.0274
Sensory organs		Prostate	0.0000
		Sensory Organs	0.0458
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0044	0.0021	2.1599	0.4630
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0104	0.0041	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0083	0.0000	undef	undef
Penis	0.0060	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0096	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0118	0.0000	undef	undef
Seminal vesicle	0.0017	0.0000	undef	undef
Sensory organs	0.0319	0.0000	undef	undef
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0259
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0062	Testicles	0.0164
Kidney	0.0000	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0251	Prostate	0.0000
Sensory organs		Sensory Organs	0.0333
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0032	0.0137	0.2313	4.3235
Heart	0.0000	0.0000	undef	undef
Testicles	0.0073	0.0020	3.5562	0.2812
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0050	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0068	0.0000	undef	0.0000
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0061			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	0.0000
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		
Gastrointestinal	0.0000	Breast 0.0000
Brain	0.0000	Ovary_n 0.0000
Hematopoietic	0.0000	Ovary_t 0.0000
Skin	0.0000	Endocrine tissue 0.0000
Hepatic	0.0000	Fetal 0.0000
Heart-blood vessels	0.0000	Gastrointestinal 0.0000
Lung	0.0000	Hematopoietic 0.0000
Suprarenal gland	0.0000	Skin-muscle 0.0000
Kidney	0.0000	Testicles 0.0000
Placenta	0.0000	Lung 0.0000
Prostate	0.0000	Nerves 0.0000
Sensory organs	0.0000	Prostate 0.0000
		Sensory Organs 0.0000
		Uterus_n

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0096	0.0093	1.0354	0.9658
Brain	0.0059	0.0021	2.8798	0.3472
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064	0.0000	undef	undef
Prostate hyperplasia	0.0059	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0017	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

FETUS  
% frequency

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0157
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0121
Placenta	0.0249
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.0060
Ovary_t	0.0203
Endocrine tissue	0.0245
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0171
Skin-muscle	0.0097
Testicles	0.0000
Lung	0.0246
Nerves	0.0060
Prostate	0.0205
Sensory Organs	0.0387
Uterus_n	0.0250



## Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0263	0.5347	1.8702
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0090	0.0312	0.2878	3.4745
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0222	0.0113	1.9635	0.5093
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0135	0.0123	1.1007	0.9085
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0205	0.7930	1.2610
Pancreas	0.0083	0.0221	0.3739	2.6743
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Breast hyperplasia	0.0102	0.0954	0.1067	9.3678
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0119			
Sensory organs	0.0089			
White blood cells	0.0235			
Cervix	0.0087			
	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0203
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0058
Hepatic	Gastrointestinal 0.0488
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0154
Kidney	Lung 0.0164
Placenta	Nerves 0.0060
Prostate	Prostate 0.0068
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0083

## Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0204	1.1441	0.8741
Breast	0.0192	0.0470	0.4083	2.4491
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0546	0.1645	6.0803
Endocrine tissue	0.0204	0.0079	2.7170	0.3691
Gastrointestinal	0.0268	0.0416	0.6443	1.5522
Brain	0.0037	0.0154	0.2400	4.1669
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0476	0.0259	1.8382	0.5440
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0166	0.0184	0.9032	1.1072
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0069	0.0300	0.2284	4.3775
Kidney	0.0543	0.0411	1.3217	0.7566
Pancreas	0.0363	0.0110	3.2906	0.3039
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0218	0.0128	1.7060	0.5862
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0535			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0078			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0204
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0017
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0040
Placenta	Nerves	0.0137
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0083
	Uterus_n	

## Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0074	0.0051	1.4399	0.6945
Hematopoietic	0.0027	0.0379	0.0706	14.1689
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0128	0.1706	5.8615
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n



Electronic Northern for SEQ. ID NO.: 29

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0021	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0009			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0038	0.0113	0.3403	2.9389
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0702	0.0426	23.4526
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0556	0.0278	2.0018	0.4995
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0062	0.0082	0.7621	1.3122
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0110	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0255	0.2559	3.9077
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0192			
Uterus-general	0.0357			
Breast hyperplasia	0.0890			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0123	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0061	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0118			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus_n	



## Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0663	0.0741	0.8942	1.1183
Small intestine	0.0640	0.0846	0.7561	1.3225
Ovary	0.1104	0.0165	6.6733	0.1499
Endocrine tissue	0.0958	0.1951	0.4912	2.0358
Gastrointestinal	0.0511	0.0426	1.1987	0.8343
Brain	0.1188	0.1527	0.7781	1.2851
Hematopoietic	0.0584	0.0863	0.6771	1.4769
Skin	0.1016	0.1136	0.8940	1.1186
Hepatic	0.0698	0.0000	undef	0.0000
Heart	0.0048	0.0776	0.0613	16.3199
Testicles	0.1304	0.0000	undef	0.0000
Lung	0.0230	0.0819	0.2811	3.5571
Stomach-esophagus	0.1620	0.1227	1.3209	0.7571
Muscle-skeleton	0.0580	0.1073	0.5402	1.8511
Kidney	0.1045	0.0480	2.1773	0.4593
Pancreas	0.0516	0.0959	0.5381	1.8583
Penis	0.0529	0.1491	0.3545	2.8205
Prostate	0.0749	0.0800	0.9360	1.0684
Uterus-endometrium	0.0632	0.0426	1.4843	0.6737
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.1067	0.2309	0.4621	2.1640
Breast hyperplasia	0.1528	0.0000	undef	0.0000
Prostate hyperplasia	0.0480			
Seminal vesicle	0.0476			
Sensory organs	0.0534			
White blood cells	0.0235			
Cervix	0.1309			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0333	Ovary_n	0.1595
Brain	0.0626	Ovary_t	0.0152
Hematopoietic	0.0590	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0391	Hematopoietic	0.0000
Lung	0.0650	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0432	Lung	0.0573
Placenta	0.0424	Nerves	0.0181
Prostate	0.0249	Prostate	0.0342
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 34

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0598	0.0501	19.9782
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0000	undef	undef
Skin	0.0048	0.0000	undef	0.0000
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0299	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0106			
Sensory organs				
White blood cells				
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

	NORMAL	TUMOR	Ratios
	% frequency	% frequency	N/T
Bladder	0.0000	0.0026	0.0000 undef
Breast	0.0000	0.0038	0.0000 undef
Small intestine	0.0061	0.0000	undef 0.0000
Ovary	0.0030	0.0234	0.1279 7.8175
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0192	0.0185	1.0354 0.9658
Brain	0.0015	0.0062	0.2400 4.1669
Hematopoietic	0.0013	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0052	0.0061	0.8467 1.1810
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0060	0.0000 undef
Muscle-skeleton	0.0027	0.0000	undef 0.0000
Kidney	0.0000	0.0110	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus-endometrium	0.0000	0.0000	undef undef
Uterus-myometrium	0.0000		
Uterus-general	0.0030		
Breast hyperplasia	0.0000		
Prostate hyperplasia	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		
White blood cells			
Cervix			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0139	0.0000	undef
Hematopoietic	0.0022	0.0000	undef	0.0000
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0137	0.0000	undef
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0068	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0023
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000



## Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0286	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0072	0.4114	2.4307
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0058	0.0117	0.4920	2.0326
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0137	0.3965	2.5219
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0068	0.0000	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0059			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0043			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0291
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 40

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0051	0.0056	0.9074	1.1021
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0102	0.0025	4.0755	0.2454
Brain	0.0115	0.0093	1.2425	0.8048
Hematopoietic	0.0044	0.0062	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0062	0.0061	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0120	0.1428	7.0040
Pancreas	0.0027	0.0068	0.3965	2.5219
Penis	0.0000	0.0000	undef	undef
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0021	3.0709	0.3256
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0035			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0071	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0247	Lung	0.0164
Placenta	0.0061	Nerves	0.0070
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 41

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 42

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Heart	0.0038	0.0000	undef	0.0000
Testicles	0.0052	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0059	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0023
Hepatic	0.0000	Hematopoietic	0.0114
Heart-blood vessels	0.0000	Skin-muscle	0.0000
Lung	0.0000	Testicles	0.0000
Suprarenal gland	0.0000	Lung	0.0164
Kidney	0.0000	Nerves	0.0010
Placenta	0.0000	Prostate	0.0000
Prostate	0.0499	Sensory Organs	0.0000
Sensory organs	0.0000	Uterus_n	0.0042

## Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.3130	0.3000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 44

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0260	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 45

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder			0.0000	undef
Breast	0.0000	0.0102	0.0056	1.5879 0.6298
Small intestine	0.0090	0.0056	undef	0.0000
Ovary	0.0031	0.0000	0.1535	6.5146
Endocrine tissue	0.0060	0.0390	1.3585	0.7361
Gastrointestinal	0.0034	0.0025	0.0628	12.0723
Brain	0.0019	0.0231	0.0000	undef
Hematopoietic	0.0000	0.0031	0.0000	undef
Skin	0.0060	0.0000	0.0433	23.0839
Hepatic	0.0037	0.0847	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	0.0000	undef
Lung	0.0021	0.0117	0.2032	4.9209
Stomach-esophagus	0.0000	0.0102	0.0077	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0000	0.0000	undef	0.0000
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	3.3668	0.2970
Uterus-myometrium	0.0229	0.0068	undef	undef
Uterus-general	0.0000	0.0000		
Breast hyperplasia	0.0009			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0491
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0125
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 46

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0090	0.0263	0.3403	2.9389
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0170	0.0050	3.3962	0.2944
Gastrointestinal	0.0172	0.0046	3.7275	0.2683
Brain	0.0081	0.0216	0.3771	2.6517
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0140	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0020	4.0643	0.2460
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0121	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 47

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0090	0.0019	4.7637	0.2099
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5060
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0059	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0118	0.0000	undef	undef
Sensory organs	0.0017	0.0000	undef	undef
White blood cells	0.0106	0.0000	undef	undef
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0152
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0032
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0020
Placenta	Nerves 0.0000
Prostate	Prostate 0.0077
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0179	0.0169	1.0586	0.9446
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0286	0.2093	4.7774
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0287	0.0278	1.0354	0.9658
Brain	0.0229	0.0164	1.3949	0.7169
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0350	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0239	0.0225	1.0623	0.9414
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0262	0.0085	3.0709	0.3256
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0208			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0167	Ovary_n	0.1595
Brain	0.0188	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0320	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0124	Lung	0.0164
Placenta	0.0182	Nerves	0.0221
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 49

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0275	0.1542	6.4853
Heart	0.0115	0.0000	undef	0.0000
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0109	0.0137	0.7930	1.2610
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0064	0.6824	1.4654
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0208			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0036			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0039
Hepatic	0.0000
Heart-blood vessels	0.0260
Lung	0.0000
Suprarenal gland	0.0036
Kidney	0.0000
Placenta	0.0000
Prostate	0.0061
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0020
Nerves	0.0205
Prostate	0.0000
Sensory Organs	0.0042
Uterus_n	



Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0179	0.4358	2.2944
Breast	0.0064	0.0094	0.6805	1.4694
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0073	0.0102	0.7112	1.4060
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0272	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0194
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0100
Placenta	Nerves	0.0000
Prostate	Prostate	0.0077
Sensory organs	Sensory Organs	
	Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 51

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0072	0.5143	1.9446
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0061	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0198	0.0060	3.1411	0.3184
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0153	0.0106	1.4331	0.6978
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0178			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0026			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0213	Hematopoietic	0.0456
Lung	0.0072	Skin-muscle	0.0065
Suprarenal gland	0.1014	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0179	0.0038	4.7637	0.2099
Small intestine	0.0092	0.0496	0.1854	5.3946
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0153	0.0251	0.6113	1.6358
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0155	0.0103	1.5119	0.6614
Hematopoietic	0.0040	0.0758	0.0529	18.8919
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0388	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0177	0.0143	1.2338	0.8105
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0109	0.0274	0.3965	2.5219
Pancreas	0.0231	0.0221	1.0470	0.9551
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0095			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0142	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0060
Placenta	0.0061	Nerves	0.0068
Prostate	0.0499	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 53

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0153	1.5254	0.6555
Breast	0.0115	0.0113	1.0208	0.9796
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0090	0.0286	0.3140	3.1849
Endocrine tissue	0.0102	0.0125	0.8151	1.2268
Gastrointestinal	0.0230	0.0278	0.8283	1.2072
Brain	0.0148	0.0144	1.0285	0.9723
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0106	0.0065	0.0000	undef
Heart	0.0058	0.0000	0.3855	2.5941
Testicles	0.0125	0.0123	1.0161	0.9842
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0137	0.0120	1.1422	0.8755
Muscle-skeleton	0.0136	0.0274	0.4956	2.0176
Kidney	0.0099	0.0110	0.8974	1.1143
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0109	0.0152	0.5687	1.7585
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0136	0.5611	1.7821
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0087			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0034	Endocrine tissue	0.0017
Skin	0.0000	Fetal	0.0000
Hepatic	0.0520	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0181	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0371	Lung	0.0020
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 54

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0032	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0031	0.0020	1.5241	0.6561
Lung	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0017	0.0060	0.2856	3.5020
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0221	0.0748	13.3713
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0043	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0032	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells	0.0000	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0060
Placenta	0.0121	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 55

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0061	0.0496	0.1236	8.0920
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0140	0.0185	0.7600	1.3159
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0294	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0412	0.3341	2.9932
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0139			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0304
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0260	Gastrointestinal	0.0488
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0303	Nerves	0.0090
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 56

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0077	0.0132	0.5833	1.7144
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0072	0.3086	3.2409
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0000	0.0469	0.0000	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0085	0.7677	1.3026
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0182			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0246
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0128	0.0150	0.8507	1.1756
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0051	0.0226	0.2264	4.4166
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0074	0.0103	0.7200	1.3890
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0102	0.6096	1.6403
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0139			
Cervix	0.0106			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Skin-muscle	0.0077
Kidney	0.0124	Testicles	0.0082
Placenta	0.0000	Lung	0.0120
Prostate	0.0000	Nerves	0.0274
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus_n	



## Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0585	0.0332	1.7601	0.5681
Breast	0.0230	0.0132	1.7499	0.5715
Small intestine	0.0153	0.0827	0.1854	5.3946
Ovary	0.0150	0.0546	0.2741	3.6482
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0416	0.4602	2.1730
Brain	0.0163	0.0277	0.5866	1.7046
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0404	0.0847	0.4765	2.0985
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0297	0.0412	0.7196	1.3897
Testicles	0.0863	0.1169	0.7380	1.3551
Lung	0.0364	0.0266	1.3678	0.7311
Stomach-esophagus	0.0290	0.0767	0.3782	2.6444
Muscle-skeleton	0.0411	0.0360	1.1422	0.8755
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0132	0.0497	0.2659	3.7607
Penis	0.0359	0.0800	0.4493	2.2259
Prostate	0.0262	0.0128	2.0473	0.4885
Uterus-endometrium	0.0338	0.0528	0.6402	1.5621
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0251			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0528	Ovary_n	0.0000
Brain	0.1198	Ovary_t	0.0000
Hematopoietic	0.0275	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0366
Hepatic	0.0520	Gastrointestinal	0.0057
Heart-blood vessels	0.0818	Hematopoietic	0.0389
Lung	0.0253	Skin-muscle	0.0154
Suprarenal gland	0.0254	Testicles	0.0491
Kidney	0.0371	Lung	0.0120
Placenta	0.0424	Nerves	0.0068
Prostate	0.0499	Prostate	0.0077
Sensory organs	0.0251	Sensory Organs	0.0250
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0039	0.0036	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0102	0.0251	0.4075	2.4537
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0140	0.0082	1.7099	0.5848
Hematopoietic	0.0053	0.1515	0.0353	28.3379
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0104	0.0184	0.5645	1.7715
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0835	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0375	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0182
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0182	Nerves	0.0241
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0000	0.0150	0.0000	undef
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0153	0.0139	1.1045	0.9054
Brain	0.0022	0.0154	0.1440	6.9448
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	6.3239	0.7179	8.8087	0.1135
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0089			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0106			
Sensory organs				
White blood cells				
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.2721	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.2685
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 65

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0245	0.0165	1.4830	0.6743
Ovary	0.0090	0.0520	0.1727	5.7908
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0044	0.0123	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0381	0.0970	0.3922	2.5500
Heart	0.0074	0.0137	0.5397	1.8529
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0082	0.6350	1.5747
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0163	0.0616	0.2643	3.7829
Pancreas	0.0396	0.0055	7.1795	0.1393
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0153	0.2863	0.0534	18.7357
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0043			
White blood cells	0.0249			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0242	Nerves	0.0010
Prostate	0.0049	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0250
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0026	0.0169	0.1512	6.6125
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0057	0.0185	0.3106	3.2193
Brain	0.0044	0.0062	0.7200	1.3890
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0272
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0169
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0171
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0328
Placenta	Nerves	0.0080
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0125
	Uterus_n	

## Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0288	0.0000	undef	0.0000
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0102	0.0954	0.1067	9.3678
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0342
Lung	0.0108	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 70

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0324	0.0075	4.3019	0.2325
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0135	0.0102	1.3209	0.7571
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096	0.0000	undef	undef
Prostate hyperplasia	0.0149	0.0089	1.6800	0.5952
Seminal vesicle	0.0118	0.0130	0.9077	1.1011
Sensory organs	0.0130	0.0106	1.2264	0.8155
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0182	Nerves	0.0070
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.0895	1.1768	0.8498
Breast	0.0652	0.0846	0.7713	1.2966
Small intestine	0.1073	0.0992	1.0813	0.9248
Ovary	0.0629	0.1353	0.4649	2.1509
Endocrine tissue	0.0579	0.0451	1.2830	0.7794
Gastrointestinal	0.1379	0.2220	0.6213	1.6096
Brain	0.0702	0.0534	1.3153	0.7603
Hematopoietic	0.1056	0.1136	0.9293	1.0761
Skin	0.0587	0.0847	0.6931	1.4427
Hepatic	0.0285	0.1035	0.2757	3.6266
Heart	0.1293	0.0412	3.1353	0.3189
Testicles	0.3403	0.1754	0.2296	4.3556
Lung	0.0914	0.1063	0.8598	1.1631
Stomach-esophagus	0.0387	0.1840	0.2101	4.7599
Muscle-skeleton	0.0548	0.1260	0.4351	2.2982
Kidney	0.0814	0.1438	0.5665	1.7654
Pancreas	0.0363	0.1878	0.1936	5.1662
Penis	0.1138	0.0800	1.4227	0.7029
Prostate	0.0697	0.0958	0.7279	1.3738
Uterus-endometrium	0.1824	0.0000	undef	0.0000
Uterus-myometrium	0.0838	0.0951	0.8818	1.1341
Uterus-general	0.1171	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0922			
Seminal vesicle	0.0712			
Sensory organs	0.0706			
White blood cells	0.1448			
Cervix	0.1810			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0557	Breast	0.0340
Gastrointestinal	0.1083	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0253
Hematopoietic	0.0944	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0163
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0712	Hematopoietic	0.0000
Lung	0.1409	Skin-muscle	0.0292
Suprarenal gland	0.0507	Testicles	0.0077
Kidney	0.1297	Lung	0.0246
Placenta	0.0545	Nerves	0.0090
Prostate	0.0499	Prostate	0.0274
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0042



## Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0895	0.7409	1.3497
Breast	0.0371	0.0489	0.7591	1.3174
Small intestine	0.0766	0.0000	undef	0.0000
Ovary	0.0270	0.0754	0.3573	2.7989
Endocrine tissue	0.0170	0.0326	0.5225	1.9139
Gastrointestinal	0.0805	0.0833	0.9664	1.0348
Brain	0.0177	0.0390	0.4547	2.1992
Hematopoietic	0.0896	0.0758	1.1822	0.8459
Skin	0.0551	0.1695	0.3249	3.0775
Hepatic	0.0238	0.0776	0.3064	3.2640
Heart	0.0604	0.1237	0.4883	2.0480
Testicles	0.0288	0.0702	0.4100	2.4391
Lung	0.0519	0.0429	1.2096	0.8267
Stomach-esophagus	0.0676	0.0843	0.8022	1.2466
Muscle-skeleton	0.0223	0.0240	0.9280	1.0775
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0132	0.0773	0.1709	5.8500
Penis	0.0838	0.0533	1.5724	0.6360
Prostate	0.0567	0.0255	2.2179	0.4509
Uterus-endometrium	0.0946	0.0000	undef	0.0000
Uterus-myometrium	0.0762	0.0679	1.1223	0.8911
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0772			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0272
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.1468
Hematopoietic	0.0393	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0105
Hepatic	0.0260	Gastrointestinal	0.0366
Heart-blood vessels	0.0285	Hematopoietic	0.0057
Lung	0.0145	Skin-muscle	0.0292
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0679	Lung	0.0328
Placenta	0.0364	Nerves	0.0040
Prostate	0.0997	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 74

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0468	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0110	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0353	0.0164	2.1591	0.4631
Lung	0.1836	0.1227	1.4969	0.6681
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0050	0.0221	0.2244	4.4571
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0128	0.1706	5.8615
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.1246			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 76

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0301	0.0851	11.7556
Small intestine	0.0000	0.0331	0.0000	undef
Ovary	0.0030	0.0728	0.0411	24.3213
Endocrine tissue	0.0000	0.0100	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0510	0.0596	0.8565	1.1675
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.1695	0.0217	46.1678
Hepatic	0.0523	0.1747	0.2996	3.3382
Heart	0.0138	0.0137	1.0023	0.9977
Testicles	0.0000	0.0935	0.0000	undef
Lung	0.0000	0.0818	0.0889	11.2478
Stomach-esophagus	0.0240	0.0230	0.0000	undef
Muscle-skeleton	0.3910	0.2760	0.0869	11.5066
Kidney	0.1123	0.4108	0.9516	11.0508
Pancreas	0.0030	0.0387	2.9060	0.3441
Penis	0.0000	0.0000	undef	0.0000
Prostate	0.0068	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.2111	0.0320	31.2422
Uterus-myometrium	0.0051	0.0000	undef	undef
Uterus-general	0.0064	0.1908	0.0267	37.4714
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.1838			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0696	Breast	0.0000
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0107	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0254	Skin-muscle	0.0032
Suprarenal gland	0.0062	Testicles	0.0000
Kidney	0.2302	Lung	0.0164
Placenta	0.0000	Nerves	0.0231
Prostate	0.1632	Prostate	0.0068
Sensory organs		Sensory Organs	0.0310
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 78

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0153	1.0170	0.9833
Breast	0.0090	0.0244	0.3664	2.7290
Small intestine	0.0123	0.0496	0.2472	4.0460
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0172	0.0324	0.5325	1.8779
Brain	0.0044	0.0216	0.2057	4.8614
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0190	0.0068	2.7756	0.3603
Pancreas	0.0063	0.0110	0.7479	1.3371
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0106	1.2284	0.8141
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0113			
Sensory organs	0.0113			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0256
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0309
Kidney	Lung	0.0164
Placenta	Nerves	0.0100
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.1084
	Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 79

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0273	0.0332	0.8214	1.2174
Breast	0.0230	0.0188	1.2250	0.8164
Small intestine	0.0276	0.0331	0.8342	1.1988
Ovary	0.0210	0.0650	0.3224	3.1022
Endocrine tissue	0.0238	0.0276	0.8645	1.1567
Gastrointestinal	0.0172	0.0463	0.3728	2.6827
Brain	0.0118	0.0144	0.8228	1.2153
Hematopoietic	0.0214	0.0379	0.5646	1.7711
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1338	5.4400
Heart	0.0540	0.0550	0.9830	1.0173
Testicles	0.0173	0.0585	0.2952	3.3877
Lung	0.0322	0.0450	0.7159	1.3969
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0240	0.0600	0.3998	2.5014
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0165	0.0221	0.7479	1.3371
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0240	0.4005	0.5926	1.6874
Uterus-endometrium	0.0270	0.1055	0.2561	3.9053
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0534			
Sensory organs	0.0588			
White blood cells	0.0234			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0557	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0663	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0256
Hepatic	0.0142	Gastrointestinal	0.0122
Heart-blood vessels	0.0253	Hematopoietic	0.0000
Lung	0.0507	Skin-muscle	0.0583
Suprarenal gland	0.0432	Testicles	0.0231
Kidney	0.0303	Lung	0.0491
Placenta	0.1247	Nerves	0.0221
Prostate	0.0251	Lung	0.0821
Sensory organs		Nerves	0.0000
		Prostate	0.0000
		Sensory Organs	0.0416
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 80

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0139	0.0000	undef
Brain	0.0044	0.0041	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0000	0.0000	undef
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0044	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0093
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0114
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0082
Kidney	Lung	0.0060
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 81

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0129	0.3051	3.2777
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0090	0.0416	0.2159	4.6326
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0126	0.0031	4.0798	0.2451
Hematopoietic	0.0080	0.1136	0.0706	14.1689
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0104	0.0164	0.6350	1.5747
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0119	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0104	0.0000	undef	undef
Sensory organs	0.0000	0.0000	undef	undef
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0152
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0070
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0065
Suprarenal gland	Testicles 0.0231
Kidney	Lung 0.0082
Placenta	Nerves 0.0191
Prostate	Nerves 0.0068
Sensory organs	Prostate 0.0155
	Sensory Organs 0.0250
	Uterus_n

Electronic Northern for SEQ. ID NO.: 82

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0435	0.8076	1.2383
Small intestine	0.0576	0.0489	1.1778	0.8490
Ovary	0.0337	0.0165	2.0391	0.4904
Endocrine tissue	0.0659	0.1353	0.4871	2.0531
Gastrointestinal	0.0801	0.0878	0.9121	1.0963
Brain	0.0441	0.1203	0.3664	2.7294
Hematopoietic	0.1072	0.0298	3.5998	0.2778
Skin	0.0201	0.1515	0.1323	7.5568
Hepatic	0.0661	0.0000	undef	0.0000
Heart	0.0428	0.0582	0.7353	1.3600
Testicles	0.0572	0.0687	0.8327	1.2010
Lung	0.0460	0.1988	0.2315	4.3193
Stomach-esophagus	0.0416	0.0634	0.6555	1.5255
Muscle-skeleton	0.0290	0.0613	0.4727	2.1155
Kidney	0.0360	0.0180	1.9989	0.5003
Pancreas	0.0489	0.0411	1.1896	0.8406
Penis	0.1371	0.0552	2.4829	0.4028
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0741	0.0426	1.7402	0.5747
Uterus-myometrium	0.0203	0.0000	undef	0.0000
Uterus-general	0.0534	0.0475	1.1223	0.8911
Breast hyperplasia	0.0407	0.0000	undef	0.0000
Prostate hyperplasia	0.0639			
Seminal vesicle	0.0476			
Sensory organs	0.0623			
White blood cells	0.0588			
Cervix	0.0546			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0696	Breast	0.0068
Gastrointestinal	0.1971	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0304
Hematopoietic	0.0551	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0262
Hepatic	0.1040	Gastrointestinal	0.1220
Heart-blood vessels	0.0427	Hematopoietic	0.0285
Lung	0.1120	Skin-muscle	0.0356
Suprarenal gland	0.1521	Testicles	0.0309
Kidney	0.0309	Lung	0.2211
Placenta	0.1212	Nerves	0.0502
Prostate	0.0748	Prostate	0.0615
Sensory organs	0.0628	Sensory Organs	0.1471
		Uterus_n	0.0125



## Electronic Northern for SEQ. ID NO.: 83

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0156	0.0077	2.0339	0.4917
Small intestine	0.0307	0.0169	1.8147	0.5510
Ovary	0.0123	0.0165	0.7415	1.3487
Endocrine tissue	0.0120	0.0416	0.2878	3.4745
Gastrointestinal	0.0273	0.0176	1.5526	0.6441
Brain	0.0153	0.0324	0.4733	2.1127
Hematopoietic	0.0192	0.0154	1.2479	0.8013
Skin	0.0147	0.0379	0.3882	2.5762
Hepatic	0.0220	0.0000	undef	0.0000
Heart	0.0238	0.0065	3.6765	0.2720
Testicles	0.0170	0.0137	1.2336	0.8107
Lung	0.0230	0.0234	0.9839	1.0163
Stomach-esophagus	0.0177	0.0204	0.8637	1.1579
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0154	0.0060	2.5700	0.3891
Pancreas	0.0190	0.0000	undef	0.0000
Penis	0.0132	0.0166	0.7977	1.2536
Prostate	0.0240	0.0000	undef	0.0000
Uterus-endometrium	0.0109	0.0106	1.0236	0.9769
Uterus-myometrium	0.0338	0.0000	undef	0.0000
Uterus-general	0.0305	0.0000	undef	0.0000
Breast hyperplasia	0.0204	0.0000	undef	0.0000
Prostate hyperplasia	0.0416			
Seminal vesicle	0.0208			
Sensory organs	0.0178			
White blood cells	0.0235			
Cervix	0.0087			
	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.1595
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0111
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0097
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0491
Placenta	Nerves	0.0231
Prostate	Prostate	0.0342
Sensory organs	Sensory Organs	0.0083
	Uterus_n	

Electronic Northern for SEQ. ID NO.: 84

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0153	2.0339	0.4917
Breast	0.0192	0.0320	0.6005	1.6654
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0060	0.0416	0.1439	6.9489
Endocrine tissue	0.0273	0.0451	0.6038	1.6562
Gastrointestinal	0.0230	0.0093	2.4850	0.4024
Brain	0.0177	0.0164	1.0799	0.9260
Hematopoietic	0.0174	0.0379	0.4587	2.1798
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0381	0.0055	5.8924	0.1700
Heart	0.0159	0.0000	undef	0.0000
Testicles	0.0115	0.0351	0.3280	3.0489
Lung	0.0187	0.0123	1.5241	0.6561
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0109	0.0205	0.5287	1.8915
Pancreas	0.0083	0.0166	0.4986	2.0057
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0405	0.0528	0.7682	1.3018
Uterus-myometrium	0.0305	0.0204	1.4964	0.6683
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0327			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0165			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0272
Gastrointestinal	0.0557	Ovary_n	0.0000
Brain	0.0222	Ovary_t	0.0152
Hematopoietic	0.0250	Endocrine tissue	0.0000
Skin	0.0118	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0249	Skin-muscle	0.0259
Suprarenal gland	0.0181	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0062	Nerves	0.0341
Prostate	0.0242	Prostate	0.0274
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 85

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0102	0.0000 undef	
Small intestine	0.0051	0.0395	0.1296 7.7146	
Ovary	0.0092	0.0165	0.5561 1.7982	
Endocrine tissue	0.0030	0.0312	0.0959 10.4234	
Gastrointestinal	0.0000	0.0050	0.0000 undef	
Brain	0.0038	0.0139	0.2761 3.6217	
Hematopoietic	0.0081	0.0113	0.7200 1.3890	
Skin	0.0027	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0074	0.0000	undef 0.0000	
Testicles	0.0000	0.0117	0.0000 undef	
Lung	0.0062	0.0020	3.0482 0.3281	
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933	
Muscle-skeleton	0.0034	0.0120	0.2856 3.5020	
Kidney	0.0027	0.0000	undef 0.0000	
Pancreas	0.0033	0.0000	undef 0.0000	
Penis	0.0030	0.1066	0.0281 35.6140	
Prostate	0.0044	0.0043	1.0236 0.9769	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0076	0.0000	undef 0.0000	
Uterus-general	0.0153	0.0000	undef 0.0000	
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0087
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0486	0.4014	2.4911
Breast	0.0064	0.0338	0.1890	5.2900
Small intestine	0.0153	0.0165	0.9268	1.0789
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0052	0.0123	0.4200	2.3811
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0184	0.0847	0.2166	4.6168
Hepatic	0.0048	0.0388	0.1225	8.1599
Heart	0.0074	0.0962	0.0771	12.9706
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0665	0.0573	1.1612	0.8612
Stomach-esophagus	0.0193	0.0383	0.5042	1.9833
Muscle-skeleton	0.0788	0.0300	2.6271	0.3807
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0116	0.0166	0.6980	1.4326
Penis	0.0000	0.0000	0.0000	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0954	0.0000	undef
Uterus-general	0.0128			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.1682			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0557
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0064
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0032
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0125
	Uterus_n

## Electronic Northern for SEQ. ID NO.: 89

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0153	0.0038	4.0832	0.2449
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0068	0.0025	0.0000	undef
Endocrine tissue	0.0077	0.0046	2.7170	0.3681
Gastrointestinal	0.0052	0.0021	1.6567	0.6036
Brain	0.0174	0.0000	2.5199	0.3968
Hematopoietic	0.0844	0.0000	undef	0.0000
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0201	0.0275	0.7324	1.3653
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0156	0.0061	2.5402	0.3937
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0034	0.0060	0.5711	1.7510
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0050	0.0055	0.8974	1.1143
Pancreas	0.0329	0.1066	0.3089	3.2376
Penis	0.0022	0.0021	1.0236	0.9769
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0076	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0121			
White blood cells	0.0852			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0136
Gastrointestinal		Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0028	Endocrine tissue	0.0000
Skin	0.0063	Fetal	0.0087
Hepatic	0.0079	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0154
Suprarenal gland	0.0107	Testicles	0.0164
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0169	0.2268	4.4083
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0326	0.1567	6.3796
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0067	0.0062	1.0799	0.9260
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0143	0.5806	1.7223
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0059	0.0000	undef	undef
Seminal vesicle	0.0356	0.0000	undef	undef
Sensory organs	0.0118	0.0000	undef	undef
White blood cells	0.0052	0.0000	undef	undef
Cervix	0.0000	0.0000	undef	undef

FETUS  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0111
Hematopoietic	0.0125
Skin	0.0118
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0107
Suprarenal gland	0.0181
Kidney	0.0000
Placenta	0.0124
Prostate	0.0061
Sensory organs	0.0000
	0.0126

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0130
Testicles	0.0231
Lung	0.0164
Nerves	0.0060
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 91

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0081	0.0082	0.9899	1.0102
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0073	0.0307	0.2371	4.2179
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0000	0.0106	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0106			

	FETUS	STANDARDIZED/SUBTRACTED
	% frequency	LIBRARIES % frequency
Development	0.0139	Breast 0.0000
Gastrointestinal	0.0028	Ovary_n 0.0000
Brain	0.0063	Ovary_t 0.0000
Hematopoietic	0.0079	Endocrine tissue 0.0000
Skin	0.0000	Fetal 0.0064
Hepatic	0.0000	Gastrointestinal 0.0122
Heart-blood vessels	0.0071	Hematopoietic 0.0057
Lung	0.0000	Skin-muscle 0.0130
Suprarenal gland	0.0000	Testicles 0.0000
Kidney	0.0121	Lung 0.0329
Placenta	0.0000	Nerves 0.0040
Prostate	0.0000	Prostate 0.0274
Sensory organs	0.0000	Sensory Organs 0.0000
		Uterus_n 0.0083

## Electronic Northern for SEQ. ID NO.: 92

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0132	0.2917	3.4287
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0000	0.0000	undef	undef
Lung	0.0145	0.0061	2.3708	0.4218
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0139			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0153	0.0000 undef	
Breast	0.3077	0.0113	0.6805 1.4694	
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0030	0.0286	0.1047 9.5548	
Endocrine tissue	0.0034	0.0075	0.4528 2.2083	
Gastrointestinal	0.0019	0.0093	0.2071 4.8289	
Brain	0.0059	0.0082	0.7200 1.3890	
Hematopoietic	0.0067	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0042	0.0000	undef 0.0000	
Testicles	0.0113	0.0234	0.4920 2.0326	
Lung	0.0021	0.0061	0.3387 2.9526	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0051	0.0000	undef 0.0000	
Kidney	0.0054	0.0068	0.7930 1.2610	
Pancreas	0.0017	0.0331	0.0495 20.0570	
Pituitary	0.0090	0.0267	0.3369 2.9678	
Penis	0.0044	0.0021	2.0473 0.4885	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0051	0.0000	undef 0.0000	
Uterus-general	0.0032	0.0000	undef 0.0000	
Breast hyperplasia	0.0000	0.0000	undef undef	
Prostate hyperplasia	0.0000	0.0000	undef undef	
Seminal vesicle	0.0009	0.0000	undef 0.0000	
Sensory organs	0.0000	0.0000	undef undef	
White blood cells	0.0000	0.0000	undef undef	
Cervix	0.0000	0.0000	undef undef	

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast 0.0000
Gastrointestinal	0.0000	Ovary_n 0.0000
Brain	0.0028	Ovary_t 0.0000
Hematopoietic	0.0063	Endocrine tissue 0.0245
Skin	0.0039	Fetal 0.0116
Hepatic	0.0000	Gastrointestinal 0.0122
Heart-blood vessels	0.0000	Hematopoietic 0.0114
Lung	0.0036	Skin-muscle 0.0000
Suprarenal gland	0.0000	Testicles 0.0082
Kidney	0.0062	Lung 0.0070
Placenta	0.0000	Nerves 0.0068
Prostate	0.0000	Prostate 0.0000
Sensory organs	0.0000	Sensory Organs 0.0125
		Uterus_n

## Electronic Northern for SEQ. ID NO.: 94

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000 undef	
Breast	0.0115	0.0132	0.8750 1.1429	
Small intestine	0.0337	0.0496	0.6797 1.4713	
Ovary	0.0030	0.0390	0.0768 13.0292	
Endocrine tissue	0.0085	0.0251	0.3396 2.9444	
Gastrointestinal	0.0747	0.0879	0.8501 1.1763	
Brain	0.0007	0.0000	undef 0.0000	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0037	0.0000	undef 0.0000	
Hepatic	0.0048	0.0194	0.2451 4.0800	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0351	0.0000 undef	
Lung	0.0042	0.0143	0.2903 3.4446	
Stomach-esophagus	0.0483	0.0077	6.3027 0.1587	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0163	0.0137	1.1896 0.8406	
Pancreas	0.0231	0.0166	1.3960 0.7163	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0065	0.0106	0.6142 1.6282	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0119	0.0089		
Prostate hyperplasia	0.0089	0.0000		
Seminal vesicle	0.0000	0.0000		
Sensory organs	0.0000	0.0106		
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Suprarenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0246
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 95

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1092	0.0460	2.3729	0.4214
Breast	0.0627	0.0865	0.7249	1.3795
Small intestine	0.1012	0.1158	0.8739	1.1443
Ovary	0.0599	0.1509	0.3970	2.5190
Endocrine tissue	0.0852	0.2984	0.2854	3.5039
Gastrointestinal	0.0900	0.0925	0.9733	1.0274
Brain	0.1811	0.0637	2.8450	0.3515
Hematopoietic	0.0521	0.1136	0.4587	2.1798
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0809	0.0582	1.3889	0.7200
Heart	0.1092	0.0962	1.1344	0.8815
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0634	0.1104	0.5739	1.7425
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0463	0.0420	1.1014	0.9079
Kidney	0.0706	0.1369	0.5155	1.9400
Pancreas	0.0743	0.1049	0.7085	1.4114
Penis	0.1467	0.0800	1.8345	0.5451
Prostate	0.0567	0.0873	0.6491	1.5405
Uterus-endometrium	0.0811	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.1155	0.9242	1.0820
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.1407			
Prostate hyperplasia	0.0713			
Seminal vesicle	0.0534			
Sensory organs	0.0353			
White blood cells	0.0390			
Cervix	0.0532			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.1113	Breast	0.0068
Gastrointestinal	0.0694	Ovary_n	0.0000
Brain	0.0938	Ovary_t	0.0253
Hematopoietic	0.0590	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.1281	Hematopoietic	0.0000
Lung	0.0397	Skin-muscle	0.0454
Suprarenal gland	0.0507	Testicles	0.0077
Kidney	0.0432	Lung	0.0246
Placenta	0.0485	Nerves	0.0753
Prostate	0.0499	Prostate	0.0205
Sensory organs	0.1381	Sensory Organs	0.0077
		Uterus_n	0.0500

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0135	0.0000	undef	0.0000
Prostate	0.0000	0.0136	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0016
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

00010770-070000

Electronic Northern for SEQ. ID NO.: 97

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0077	0.0075	1.0208	0.9796
Small intestine	0.0061	0.0331	0.1854	5.3946
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0044	0.0154	0.2880	3.4724
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0970	0.0980	10.1999
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0789	0.0532	1.4850	0.6734
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0021	7.1654	0.1396
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0096			
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0445			
Seminal vesicle	0.1411			
Sensory organs	0.0026			
White blood cells	0.1917			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0061	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 98

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0013	0.0056	0.2268 4.4083	
Small intestine	0.0052	0.0000	undef 0.0000	
Ovary	0.0000	0.0130	0.0000 undef	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0000	0.0093	0.0000 undef	
Brain	0.0007	0.0021	0.3600 2.7779	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0095	0.0000	undef 0.0000	
Heart	0.0011	0.0000	undef 0.0000	
Testicles	0.0000	0.0234	0.0000 undef	
Lung	0.0021	0.0020	1.0161 0.9842	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0027	0.0000	undef 0.0000	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0735
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 99

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0090	0.0056	1.5879	0.6298
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0051	0.0025	2.0377	0.4907
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0015	0.0041	0.3600	2.7779
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0031	0.0000	undef	0.0000
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0103	0.0060	1.7133	0.5837
Pancreas	0.0081	0.0068	1.1896	0.8406
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0064	0.6824	1.4654
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0204
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0134
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0097
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0100
Prostate	0.0424	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0312	0.0179	1.7434	0.5736
Small intestine	0.0205	0.0244	0.8376	1.1939
Ovary	0.0675	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0442	0.1354	7.3822
Gastrointestinal	0.0051	0.0025	2.0377	0.4907
Brain	0.0862	0.0463	1.8638	0.5365
Hematopoietic	0.0067	0.0133	0.4984	2.0063
Skin	0.0120	0.0000	undef	0.0000
Hepatic	0.0477	0.0000	undef	0.0000
Heart	0.0143	0.0388	0.3676	2.7200
Testicles	0.0212	0.0412	0.5140	1.9456
Lung	0.0230	0.0234	0.9839	1.0163
Stomach-esophagus	0.0374	0.0450	0.8313	1.2029
Muscle-skeleton	0.0290	0.0000	undef	0.0000
Kidney	0.0137	0.0600	0.2284	4.3775
Pancreas	0.0054	0.0274	0.1983	5.0439
Penis	0.0066	0.0442	0.1496	6.6857
Prostate	0.0449	0.0267	1.6847	0.5936
Uterus-endometrium	0.0240	0.0234	1.0236	0.9769
Uterus-myometrium	0.0068	0.0000	undef	0.0000
Uterus-general	0.0229	0.0136	1.6834	0.5940
Breast hyperplasia	0.0255	0.0000	undef	0.0000
Prostate hyperplasia	0.0384			
Seminal vesicle	0.0238			
Sensory organs	0.0534			
White blood cells	0.0235			
Cervix	0.0303			
	0.0319			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0304
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0000	Lung	0.0164
Placenta	0.0182	Nerves	0.0020
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042



Electronic Northern for SEQ. ID NO.: 101

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0000	0.0188	0.0000	undef
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0120	0.0442	0.2709	3.6916
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0134	0.0185	0.7248	1.3797
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0321	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0478	0.0450	1.0623	0.9414
Stomach-esophagus	0.0676	0.0690	0.9804	1.0200
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0116	0.0055	2.0940	0.4775
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.1101			
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 102

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0588	0.3979	2.5129
Breast	0.0179	0.0507	0.3529	2.8339
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0180	0.0546	0.3289	3.0402
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0364	0.0786	0.4629	2.1603
Brain	0.0067	0.0216	0.3086	3.2409
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0323	0.1471	6.7999
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0270	0.0225	1.2008	0.8328
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0616	0.5287	1.8915
Pancreas	0.0132	0.0607	0.2176	4.5964
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0069			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0136
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0253
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0169
Hepatic	Gastrointestinal 0.0498
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0231
Kidney	Lung 0.0164
Placenta	Nerves 0.0100
Prostate	Prostate 0.0205
Sensory organs	Sensory Organs 0.0077
	Uterus_n 0.0083

Electronic Northern for SEQ. ID NO.: 103

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0351	0.0256	1.3729	0.7284
Small intestine	0.0077	0.0094	0.8166	1.2245
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0211	0.0463	0.4556	2.1950
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0204	0.6096	1.6403
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5631
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0178			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0272
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0410
Kidney	0.0062	Lung	0.0010
Placenta	0.0242	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0230	1.3559	0.7375
Breast	0.0435	0.0320	1.3611	0.7347
Small intestine	0.0429	0.0165	2.5952	0.3853
Ovary	0.0210	0.0676	0.3100	3.2263
Endocrine tissue	0.0341	0.0752	0.4528	2.2083
Gastrointestinal	0.0230	0.0185	1.2425	0.8048
Brain	0.0525	0.0554	0.9466	1.0564
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0329	0.0962	0.3414	2.9288
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0166	0.0327	0.5080	1.9684
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0343	0.0240	1.4278	0.7004
Kidney	0.0624	0.0822	0.7600	1.3158
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0419	0.0000	undef	0.0000
Prostate	0.0174	0.0405	0.4310	2.3202
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0381	0.0136	2.8057	0.3564
Uterus-general	0.0662	0.0954	0.6939	1.4412
Breast hyperplasia	0.0608			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0235			
White blood cells	0.0035			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0101
Hematopoietic	0.0876	Endocrine tissue	0.0490
Skin	0.0039	Petal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0142	Skin-muscle	0.0356
Suprarenal gland	0.0434	Testicles	0.0154
Kidney	0.0000	Lung	0.0410
Placenta	0.0556	Nerves	0.0402
Prostate	0.0364	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
	0.1130	Uterus_n	0.0375

## Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0639	0.3051	3.2777
Breast	0.0333	0.0470	0.7077	1.4129
Small intestine	0.0399	0.1819	0.2191	4.5647
Ovary	0.0150	0.0702	0.2132	4.6905
Endocrine tissue	0.0238	0.0903	0.2642	3.7857
Gastrointestinal	0.0900	0.1110	0.8111	1.2329
Brain	0.0067	0.0267	0.2492	4.0126
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0011	0.0962	0.0110	90.7941
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0184	0.3387	2.9526
Stomach-esophagus	0.0483	0.3527	0.1370	7.2985
Muscle-skeleton	0.0000	0.0360	0.0000	undef
Kidney	0.0733	0.1575	0.4655	2.1483
Pancreas	0.0694	0.0276	2.5128	0.3980
Penis	0.0090	0.0533	0.1685	5.9357
Prostate	0.0109	0.0255	0.4265	2.3446
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0000	0.4771	0.0000	undef
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.1068			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0319			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	Breast	0.0136
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0122
Hepatic	Gastrointestinal	0.4149
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0154
Kidney	Lung	0.0573
Placenta	Nerves	0.0040
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

## Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0102	0.0132	0.7777	1.2858
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0119	0.0075	1.5849	0.6309
Brain	0.0307	0.0093	3.3124	0.3018
Hematopoietic	0.0111	0.0144	0.7714	1.2964
Skin	0.0094	0.0379	0.2470	4.0483
Hepatic	0.0441	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0170	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0229	0.0245	0.9314	1.0737
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0034	0.0120	0.2856	3.5020
Pancreas	0.0190	0.0205	0.9252	1.0808
Penis	0.0083	0.0110	0.7479	1.3371
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0105	0.6142	1.6282
Uterus-myometrium	0.0405	0.0000	undef	0.0000
Uterus-general	0.0000	0.0272	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0191			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0068
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0097
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0185	Nerves	0.0131
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 108

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0051	0.0000 undef	
Small intestine	0.0051	0.0132	0.3889 2.5715	
Ovary	0.0061	0.0000	undef 0.0000	
Endocrine tissue	0.0000	0.0156	0.0000 undef	
Gastrointestinal	0.0034	0.0125	0.2717 3.6805	
Brain	0.0077	0.0000	undef 0.0000	
Hematopoietic	0.0037	0.0062	0.6000 1.6668	
Skin	0.0080	0.0000	undef 0.0000	
Hepatic	0.0037	0.0000	undef 0.0000	
Heart	0.0048	0.0129	0.3676 2.7200	
Testicles	0.0032	0.0000	undef 0.0000	
Lung	0.0058	0.0000	undef 0.0000	
Stomach-esophagus	0.0093	0.0123	0.7621 1.3122	
Muscle-skeleton	0.0097	0.0153	0.6303 1.5866	
Kidney	0.0034	0.0000	undef 0.0000	
Pancreas	0.0027	0.0068	0.3965 2.5219	
Penis	0.0017	0.0055	0.2991 3.3428	
Prostate	0.0090	0.0267	0.3369 2.9678	
Uterus-endometrium	0.0392	0.0213	1.8425 0.5427	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0051	0.0000	undef 0.0000	
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0104			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0285
Lung	0.0072	Skin-muscle	0.0324
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0247	Lung	0.0246
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0410
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

	NORMAL	TUMOR	Ratios
	% frequency	% frequency	N/T
Bladder			
Breast	0.0078	0.0102	0.7627 1.3111
Small intestine	0.0166	0.0282	0.5896 1.6955
Ovary	0.0031	0.0000	undef 0.0000
Endocrine tissue	0.0060	0.0390	0.1535 6.5146
Gastrointestinal	0.0392	0.0527	0.7439 1.3442
Brain	0.0153	0.0370	0.4142 2.4145
Hematopoietic	0.0059	0.0072	0.8228 1.2153
Skin	0.0080	0.0000	undef 0.0000
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0000	0.0129	0.0000 undef
Testicles	0.0064	0.0687	0.0925 10.8088
Lung	0.0058	0.0000	undef 0.0000
Stomach-esophagus	0.0239	0.0470	0.5080 1.9684
Muscle-skeleton	0.0000	0.0077	0.0000 undef
Kidney	0.0120	0.0120	0.9994 1.0006
Pancreas	0.0299	0.0000	undef 0.0000
Penis	0.0182	0.0110	1.6453 0.6078
Prostate	0.0210	0.0000	undef 0.0000
Uterus-endometrium	0.0305	0.0106	2.8662 0.3489
Uterus-myometrium	0.0203	0.1055	0.1920 5.2070
Uterus-general	0.0076	0.0136	0.5611 1.7821
Breast hyperplasia	0.0102	0.0000	undef 0.0000
Prostate hyperplasia	0.0352		
Seminal vesicle	0.0446		
Sensory organs	0.0267		
White blood cells	0.0353		
Cervix	0.0147		
	0.0106		

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	
Gastrointestinal	0.0000
Brain	0.0222
Hematopoietic	0.0000
Skin	0.0197
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0178
Suprarenal gland	0.0145
Kidney	0.0000
Placenta	0.0185
Prostate	0.0000
Sensory organs	0.0000

Breast	
Ovary_n	0.0058
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0000
Gastrointestinal	0.0365
Hematopoietic	0.0000
Skin-muscle	0.0259
Testicles	0.0000
Lung	0.0410
Nerves	0.0151
Prostate	0.0342
Sensory Organs	0.0155
Uterus_n	0.0125



Electronic Northern for SEQ. ID NO.: 111

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0460	0.2542	3.5333
Breast	0.0192	0.0376	0.5104	1.9593
Small intestine	0.0000	0.0496	0.0000	undef
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0102	0.6096	1.6403
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0271	0.0137	1.9826	0.5044
Pancreas	0.0132	0.0221	0.5983	1.6714
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0240	0.0298	0.8043	1.2434
Uterus-endometrium	0.0000	0.0328	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0408
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0608
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 112

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0051	0.0207	0.2475	4.0410
Ovary	0.0123	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0338	0.0886	11.2920
Gastrointestinal	0.0017	0.0025	0.6792	1.4722
Brain	0.0038	0.0185	0.2071	4.8289
Hematopoietic	0.0022	0.0092	0.2400	4.1669
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0847	0.0433	23.0839
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0275	0.1927	5.1882
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0109	0.0000	undef	0.0000
Penis	0.0033	0.0055	0.5983	1.6714
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	0.0000
Uterus-myometrium	0.0135	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	0.0000
Seminal vesicle	0.0118	0.0000	undef	undef
Sensory organs	0.0009	0.0000	undef	undef
White blood cells	0.0213	0.0000	undef	0.0000
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0354
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0062	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs	0.0249	Sensory Organs	0.0375
	0.0251	Uterus_n	

## Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0409	0.2860	3.4963
Breast	0.0256	0.0376	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0090	0.0390	0.2303	4.3431
Endocrine tissue	0.0477	0.0702	0.6792	1.4722
Gastrointestinal	0.0479	0.0231	2.0708	0.4829
Brain	0.0229	0.0349	0.6564	1.5234
Hematopoietic	0.0281	0.0000	undef	0.0000
Skin	0.0624	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0519	0.0000	undef	0.0000
Testicles	0.0230	0.0468	0.4920	2.0326
Lung	0.0270	0.0491	0.5504	1.8170
Stomach-esophagus	0.0387	0.0230	1.6807	0.5950
Muscle-skeleton	0.0377	0.0840	0.4487	2.2286
Kidney	0.0462	0.0411	1.1235	0.8901
Pancreas	0.0116	0.0276	0.4188	2.3877
Penis	0.0150	0.0533	0.2808	3.5624
Prostate	0.0283	0.0490	0.5786	1.7284
Uterus-endometrium	0.0541	0.0528	1.0243	0.9763
Uterus-myometrium	0.0305	0.0272	1.1223	0.8911
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0312			
Cervix	0.0213			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0611	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0320	Hematopoietic	0.0000
Lung	0.0397	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0164
Kidney	0.0247	Lung	0.0050
Placenta	0.0303	Nerves	0.0068
Prostate	0.1247	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	

## Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0702	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0052	0.0020	2.5402	0.3937
Lung	0.0193	0.0230	0.8404	1.1900
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0110	0.1496	6.6857
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0954	0.0000	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0118			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 116

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0102	0.0025	4.0755	0.2454
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0073	0.0123	0.5927	1.6872
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0081	0.0068	1.1896	0.8406
Kidney	0.0017	0.0055	0.2991	3.3428
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0021	3.0709	0.3256
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0078			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0032
Lung	0.0036	Skin-muscle	0.0154
Suprarenal gland	0.0254	Testicles	0.0082
Kidney	0.0124	Lung	0.0060
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 117

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0517	0.0879	0.5886	1.6991
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0381	0.0518	0.7353	1.3600
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0164	0.0635	15.7470
Lung	0.0290	0.0230	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0033	0.0110	0.2991	3.3428
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0043	0.5118	1.9538
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	0.0000
Prostate hyperplasia	0.0000	0.0000	undef	0.0000
Seminal vesicle	0.0000	0.0000	undef	0.0000
Sensory organs	0.0000	0.0000	undef	0.0000
White blood cells	0.0000	0.0000	undef	0.0000
Cervix	0.0000	0.0000	undef	0.0000

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

## Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0056	0.2268	4.4083
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0019	0.0046	0.4142	2.4145
Gastrointestinal	0.0022	0.0031	0.7200	1.3890
Brain	0.0040	0.0000	undef	0.0000
Hematopoietic	0.0073	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0000	undef	0.0000
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0010	0.0061	0.1593	5.9051
Lung	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0027	0.0068	0.3965	2.5219
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0022	0.0021	1.0236	0.9769
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0043			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 121

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0153	0.7627	1.3111
Small intestine	0.0026	0.0132	0.1944	5.1431
Ovary	0.0031	0.0165	0.1854	5.3946
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0030	0.0062	0.4800	2.0835
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.1760	0.0518	3.4008	0.2941
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0010	0.0082	0.1270	7.8735
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0188	0.0060	3.1411	0.3184
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0174	0.0277	0.6299	1.5875
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0030	0.0954	0.0000	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0009			
cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	



## Electronic Northern for SEQ. ID NO.: 122

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.1125	0.9361	1.0683
Breast	0.1164	0.1015	1.1468	0.8720
Small intestine	0.0491	0.0662	0.7415	1.3487
Ovary	0.0479	0.1015	0.4723	2.1173
Endocrine tissue	0.0562	0.0251	2.2415	0.4461
Gastrointestinal	0.1015	0.1758	0.5777	1.7311
Brain	0.0296	0.1273	0.2322	4.3058
Hematopoietic	0.0535	0.0000	undef	0.0000
Skin	0.2166	0.0000	undef	0.0000
Hepatic	0.0809	0.1035	0.7813	1.2800
Heart	0.4133	0.2612	1.5825	0.6319
Testicles	0.0748	0.0468	1.5989	0.6254
Lung	0.1506	0.1227	1.2278	0.8145
Stomach-esophagus	0.2126	0.1073	1.9808	0.5048
Muscle-skeleton	0.0805	0.1680	0.4793	2.0863
Kidney	0.0543	0.0890	0.6100	1.6393
Pancreas	0.0562	0.1712	0.3281	3.0479
Penis	0.1497	0.2399	0.6240	1.6026
Prostate	0.0850	0.0362	2.3483	0.4258
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.1019	0.4489	2.2276
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0991			
Prostate hyperplasia	0.0832			
Seminal vesicle	0.0801			
Sensory organs	0.1059			
White blood cells	0.0720			
Cervix	0.0639			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0835	Breast	0.0544
Gastrointestinal	0.0361	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0433	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0466
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0961	Hematopoietic	0.0421
Lung	0.0867	Skin-muscle	0.0000
Suprarenal gland	0.0761	Testicles	0.1474
Kidney	0.0309	Lung	0.0110
Placenta	0.1151	Nerves	0.0205
Prostate	0.5984	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0075	0.2264	4.4166
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0069	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0134
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0130
Lung	0.0254	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0030
Kidney	0.0182	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0125
Sensory organs		Sensory Organs	
		Uterus_n	

Electronic Northern for Seq. ID: 258

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0047	0.0000 undef
Breast	0.0018	0.0014	1.2524 0.7585
Large intestine	0.0019	0.0000	undef 0.0000
Small intestine	0.0027	0.0213	0.1288 7.7625
Ovary	0.0000	0.0167	0.0000 undef
Endocrine tissue	0.0064	0.0000	undef 0.0000
Brain	0.0012	0.0010	1.1605 0.8617
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0051	0.0000	undef undef
Testicles	0.0050	0.0118	0.4786 1.4737
Lung	0.0029	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0037	0.0000 undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0019	0.0000	undef 0.0000
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0040		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0098
Lungs_n	0.0000
Lungs_t	0.0030
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0121
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 259

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0000	0.0000	undef undef
Large intestine	0.0117	0.0023	4.9785 0.2009
Small intestine	0.0070	0.0014	5.0097 0.1996
Ovary	0.0000	0.0057	0.0000 undef
Endocrine tissue	0.0082	0.0000	undef 0.0000
Brain	0.0000	0.0119	0.0000 undef
Skin	0.0032	0.0089	0.3621 2.7613
Hepatic	0.0006	0.0000	undef 0.0000
Heart	0.0037	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0081	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0019	0.0000	undef 0.0000
Kidney	0.0145	0.0000	undef 0.0000
Pancreas	0.0000	0.0037	0.0000 undef
Prostate	0.0022	0.0000	undef 0.0000
T lymphoma	0.0017	0.0000	undef 0.0000
Uterus	0.0019	0.0000	undef 0.0000
White blood cells	0.0025	0.0075	0.3381 2.9576
Hematopoietic	0.0059	0.0138	0.4284 2.3344
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0027		
Sensory organs	0.0080		
	0.0141		
	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0011
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles n	0.0084
Testicles t	0.0000
Lungs n	0.0195
Lungs t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 260

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0062	0.0000	undef 0.0000
Large intestine	0.0019	0.0085	0.2243 4.4591
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0529	0.0000 undef
Endocrine tissue	0.0032	0.0071	0.4527 2.2091
Brain	0.0023	0.0020	1.1605 0.8617
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0051	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lung	0.0088	0.0037	2.3680 0.4223
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0022	0.0000	undef 0.0000
Pancreas	0.0083	0.0000	undef 0.0000
Prostate	0.0028	0.0013	2.1706 0.4607
T lymphoma	0.0051	0.0224	0.2254 4.4364
Uterus	0.0015	0.0000	undef 0.0000
White blood cells	0.0027	0.0304	0.0902 11.0896
Hematopoietic	0.0013		
Penis	0.0000		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles n	0.0000
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0060
Nerves	0.0000
Kidney t	0.0113
Ovary Uterus	0.0000
Prostate n	0.0000
Sensory Organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 261

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0025	0.0000	undef 0.0000
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0009	0.0014	0.6262 1.5969
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0027	0.0000	undef 0.0000
Brain	0.0000	0.0191	0.0000 undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0006	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0010	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0055	0.0000 undef
T lymphoma	0.0019	0.0000	undef undef
Uterus	0.0051	0.0000	undef 0.0000
White blood cells	0.0015	0.0000	undef 0.0000
Hematopoietic	0.0034	0.0000	undef 0.0000
Penis	0.0013		
Seminal vesicle	0.0000		
Sensory organs	0.0070		
	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0023
Ovary Uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 262		
	NORMAL % freq.	TUMOR % freq.
B lymphoma		RATIOS N/T T/N
Bladder	0.0150	undef 0.0000
Breast	0.0156	6.6380 0.1506
Large intestine	0.0158	2.8179 0.3549
Small intestine	0.0038	1.1456 0.7432
Ovary	0.0110	0.3435 2.5109
Endocrine tissue	0.0178	0.5333 1.8752
Brain	0.0064	0.3018 3.3116
Skin	0.0081	1.3539 0.7386
Hepatic	0.0110	undef 0.0000
Heart	0.0139	0.7324 1.3653
Testicles	0.0193	undef 0.0000
Lung	0.0080	0.5786 1.7137
Stomach-esophagus	0.0175	1.3531 0.7390
Muscle-skeleton	0.0000	0.0000 undef
Kidney	0.0077	0.1546 1.4671
Pancreas	0.0045	0.4642 2.1540
Prostate	0.0132	undef 0.0000
T lymphoma	0.0104	1.1370 0.8795
Uterus	0.0101	0.8762 1.7888
White blood cells	0.0192	0.8353 1.1971
Hematopoietic	0.0055	0.1803 5.5448
Penis	0.0067	
Seminal vesicle	0.0080	
Sensory organs	0.0070	
	0.0118	

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0162
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0484
Testicles n	0.0123
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0100
Nerves	0.0000
Kidney t	0.0293
Ovary Uterus	0.0000
Prostate n	0.0000
Sensory Organs	0.0000
White blood cells	

## Electronic Northern for Seq. ID: 263

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0136	0.9198 1.0872
Breast	0.0039	0.0188	0.2075 4.8204
Large intestine	0.0114	0.0281	0.4070 2.4568
Small intestine	0.0211	0.0342	1.4801 0.6756
Ovary	0.0082	0.0000	undef 0.0000
Endocrine tissue	0.0089	0.0286	0.3111 3.2147
Brain	0.0161	0.0151	1.0599 0.9435
Skin	0.0211	0.0110	1.9204 0.5199
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0046	0.0127	0.3662 2.7307
Testicles	0.0162	0.0000	undef 0.0000
Lung	0.0080	0.0178	0.4523 2.2108
Stomach-esophagus	0.0136	0.0111	1.2278 0.8145
Muscle-skeleton	0.0072	0.0128	0.5666 1.7648
Kidney	0.0188	0.0185	1.0206 0.9799
Pancreas	0.0157	0.0145	1.0831 0.9232
Prostate	0.0083	0.0221	0.3739 2.6743
T lymphoma	0.0123	0.0039	3.1352 0.3190
Uterus	0.0000	0.0149	0.0000 undef
White blood cells	0.0077	0.0230	0.3368 2.9684
Hematopoietic	0.0082	0.0000	undef 0.0000
Penis	0.0094		
Seminal vesicle	0.0107		
Sensory organs	0.0070		
	0.0235		

PETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary n	0.1595
Ovary t	0.0203
Endocrine tissue	0.0000
Fetal	0.0069
Gastrointestinal	0.0488
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles n	0.0167
Testicles-t	0.0000
Lungs n	0.0195
Lungs t	0.0000
Nerves	0.0060
Kidney t	0.0060
Ovary Uterus	0.0158
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000



## Electronic Northern for Seq. ID: 264

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0150	0.0136	1.1037 0.9060
Large intestine	0.0273	0.0211	1.2907 0.7748
Small intestine	0.0229	0.0632	0.3618 2.7639
Ovary	0.0268	0.0256	1.0466 0.9555
Endocrine tissue	0.0192	0.0000	undef 0.0000
Brain	0.0089	0.0501	0.1778 5.6255
Skin	0.0193	0.0142	1.3580 0.7364
Hepatic	0.0041	0.0160	0.2539 3.9391
Heart	0.0073	0.0000	undef 0.0000
Testicles	0.0465	0.0254	1.8311 0.5461
Lung	0.0091	0.0412	0.2215 4.5144
Stomach-esophagus	0.0120	0.0000	undef 0.0000
Muscle-skeleton	0.0204	0.0185	1.1050 0.9049
Kidney	0.0290	0.0384	0.7557 1.3233
Pancreas	0.0069	0.0185	0.3711 2.6946
Prostate	0.0537	0.0189	1.8570 0.5385
T lymphoma	0.0380	0.0110	3.4403 0.2907
Uterus	0.0330	0.0130	2.5323 0.3949
White blood cells	0.0051	0.0075	0.6762 1.4788
Hematopoietic	0.0148	0.0138	1.0709 0.9338
Penis	0.0075	0.0000	undef 0.0000
Seminal vesicle	0.0147		
Sensory organs	0.0054		
	0.0000		
	0.0235		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0204
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0040
Nerves	0.0000
Kidney t	0.0090
Ovary uterus	0.0121
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

## Electronic Northern for Seq. ID: 265

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0000	0.0272	0.0000 undef
Large intestine	0.0117	0.0023	4.9785 0.2009
Small intestine	0.0141	0.0155	0.9109 1.0979
Ovary	0.0920	0.0968	0.9488 1.0528
Endocrine tissue	0.0247	0.0000	undef 0.0000
Brain	0.0208	0.0882	0.2354 4.2478
Skin	0.0016	0.0000	undef 0.0000
Hepatic	0.0050	0.0010	0.0000 undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0444	0.0000 undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0165	0.0111	1.4909 0.6707
Kidney	0.0362	0.0128	2.8338 0.3529
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0166	0.0000 undef
T lymphoma	0.0207	0.0352	0.5895 1.6963
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0027	0.0000	
Seminal vesicle	0.0000		
Sensory organs	0.0915	0.0118	

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0278
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary uterus	0.0113
Prostate_n	0.0182
Sensory Organs	0.0000
White blood cells	0.0000

Breast	0.0068
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary Uterus	0.0000
Prostate	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 267

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0050	0.0000	
Large intestine	0.0000	0.0070	undef 0.0000
Small intestine	0.0026	0.0014	0.0000 undef
Ovary	0.0000	0.0000	1.9786 0.5323
Endocrine tissue	0.0055	0.0000	undef undef
Brain	0.0000	0.0000	undef 0.0000
Skin	0.0000	0.0000	0.0000 undef
Hepatic	0.0029	0.0010	undef undef
Heart	0.0000	0.0000	2.9013 0.3447
Testicles	0.0000	0.0394	0.0000 undef
Lung	0.0030	0.0000	undef undef
Stomach-esophagus	0.0040	0.0000	undef 0.0000
Muscle-skeleton	0.0049	0.0000	undef 0.0000
Kidney	0.0000	0.0000	undef 0.0000
Pancreas	0.0034	0.0000	undef undef
Prostate	0.0000	0.0048	undef undef
T lymphoma	0.0000	0.0000	0.0000 undef
Uterus	0.0028	0.0000	undef undef
White blood cells	0.0000	0.0000	undef 0.0000
Hematopoietic	0.0007	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0034	0.0000	undef 0.0000
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0035
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles t	0.0000
Testicles n	0.0042
Lungs n	0.0000
Lungs t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 268

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0094	1.2446 0.8035
Breast	0.0088	0.0253	0.3479 2.8744
Large intestine	0.0192	0.0028	6.7278 0.1486
Small intestine	0.0192	0.0213	0.9018 1.1089
Ovary	0.0030	0.0143	0.2074 4.8219
Endocrine tissue	0.0193	0.0035	5.4321 0.1841
Brain	0.0081	0.0249	0.3249 3.0774
Skin	0.0184	0.0000	undef 0.0000
Hepatic	0.0093	0.0063	1.4649 0.6826
Heart	0.0112	0.0000	undef 0.0000
Testicles	0.0040	0.0118	0.3393 2.9475
Lung	0.0126	0.0037	3.4204 0.2924
Stomach-esophagus	0.0072	0.0000	undef 0.0000
Muscle-skeleton	0.0120	0.0037	3.2472 0.3080
Kidney	0.0157	0.0048	3.2497 0.3077
Pancreas	0.0050	0.0110	0.4487 2.2285
Prostate	0.0104	0.0052	1.9897 0.5026
T lymphoma	0.0051	0.0000	undef 0.0000
Uterus	0.0163	0.0092	1.7670 0.5659
White blood cells	0.0110	0.0000	undef 0.0000
Hematopoietic	0.0027		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0139
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0036
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0124
Kidney	0.0121
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast_t	0.0000
Large_intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0151
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0257
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0010
Nerves	0.0000
Kidney_t	0.0000
Ovary Uterus	0.0023
Prostate_n	0.0243
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 269

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0025	0.0000	undef 0.0000
Large intestine	0.0156	0.0047	3.3190 0.3013
Small intestine	0.0079	0.0014	5.6359 0.1774
Ovary	0.0096	0.0057	1.6820 0.5945
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0030	0.0191	0.1553 6.4291
Skin	0.0064	0.0018	3.6214 0.2761
Hepatic	0.0058	0.0060	0.9671 1.0340
Heart	0.0037	0.0000	undef 0.0000
Testicles	0.0000	0.0127	0.0000 undef
Lung	0.0091	0.0000	undef 0.0000
Stomach-esophagus	0.0080	0.0000	undef 0.0000
Muscle-skeleton	0.0068	0.0037	1.8417 0.5430
Kidney	0.0030	0.0064	0.0000 undef
Pancreas	0.0034	0.0111	0.3093 3.2335
Prostate	0.0045	0.0000	undef 0.0000
T lymphoma	0.0083	0.0110	0.7479 1.1371
Uterus	0.0057	0.0117	0.4823 2.0732
White blood cells	0.0025	0.0000	undef 0.0000
Hematopoietic	0.0044	0.0092	0.4819 2.0750
Penis	0.0034	0.0000	undef 0.0000
Seminal vesicle	0.0027		
Sensory organs	0.0188		
	0.0141		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary n	0.0000
Ovary t	0.0152
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0032
Skin-muscle	0.0000
Testicles n	0.0000
Testicles_t	0.0000
Lungs n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0077
Prostate n	0.0000
Sensory organs	
White blood cells	

Electronic Northern for Seq. ID: 270

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0075	0.0000	undef 0.0000
Breast	0.0156	0.0047	3.3190 0.3013
Large intestine	0.0167	0.0197	0.8499 1.1767
Small intestine	0.0307	0.0199	1.5378 0.6503
Ovary	0.0082	0.0213	0.3865 2.5875
Endocrine tissue	0.0059	0.0334	0.1778 5.6285
Brain	0.0321	0.0248	1.2934 0.7732
Skin	0.0365	0.0170	2.1504 0.4650
Hepatic	0.0257	0.0000	undef 0.0000
Heart	0.0000	0.0127	0.0000 undef
Testicles	0.0426	0.0000	undef 0.0000
Lung	0.0161	0.0118	1.3571 0.7369
Stomach-esophagus	0.0272	0.0222	1.2278 0.8144
Muscle-skeleton	0.0072	0.0000	undef 0.0000
Kidney	0.0137	0.0074	1.8555 0.5389
Pancreas	0.0246	0.0145	1.7022 0.5875
Prostate	0.0050	0.0000	undef 0.0000
T lymphoma	0.0179	0.0065	2.7494 0.3637
Uterus	0.0177	0.0612	0.2630 3.8026
White blood cells	0.0118	0.0046	2.5703 0.3891
Hematopoietic	0.0219	0.0000	undef 0.0000
Penis	0.0147		
Seminal vesicle	0.0188		
Sensory organs	0.0281		
	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0108
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0110
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0281
Nerves	0.0000
Kidney_t	0.0068
Ovary uterus	0.0061
Prostate_n	0.0232
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 271

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0407	0.3066 3.2617
Breast	0.0117	0.0164	0.7112 1.4061
Large intestine	0.0123	0.0098	1.2524 0.7985
Small intestine	0.0057	0.0057	1.0092 0.9909
Ovary	0.0165	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0143	0.2074 4.8219
Brain	0.0096	0.0195	0.4938 2.0250
Skin	0.0122	0.0070	1.7408 0.5745
Hepatic	0.0130	0.0000	undef 0.0000
Heart	0.0093	0.0000	undef 0.0000
Testicles	0.0071	0.0137	0.5169 1.9347
Lung	0.0201	0.0059	3.3828 0.2947
Stomach-esophagus	0.0117	0.0148	0.7893 1.2669
Muscle-skeleton	0.0072	0.0320	0.2267 4.4110
Kidney	0.0086	0.0000	undef 0.0000
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0017	0.0055	0.2992 3.3427
T lymphoma	0.0065	0.0117	0.5627 1.7770
Uterus	0.0126	0.0149	0.8453 1.1830
White blood cells	0.0059	0.0322	0.1836 5.4469
Hematopoietic	0.0062	0.0304	0.2029 4.9287
Penis	0.0107		
Seminal vesicle	0.0000		
Sensory organs	0.0141		
	0.0235		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0250
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0211
Nerves	0.0000
Kidney_t	0.0248
Ovary Uterus	0.0000
Prostate_n	0.0232
Sensory Organs	0.0000
White blood cells	



## Electronic Northern for Seq. ID: 272

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0136	0.1840 5.4361
Breast	0.0039	0.0117	0.3319 3.0130
Large intestine	0.0246	0.0070	3.5068 0.2852
Small intestine	0.0287	0.0399	0.7208 1.3873
Ovary	0.0082	0.0426	0.1932 5.1750
Endocrine tissue	0.0148	0.0381	0.3889 2.5717
Brain	0.0161	0.0266	0.6016 1.6568
Skin	0.0220	0.0130	1.6961 0.5896
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0000	0.0381	0.0000 undef
Testicles	0.0132	0.0000	undef 0.0000
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0214	0.0129	1.6538 0.6047
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0069	0.0000	undef 0.0000
Pancreas	0.0134	0.0193	0.6964 1.4360
Prostate	0.0264	0.0276	0.9573 1.0446
T lymphoma	0.0075	0.0104	0.7235 1.3821
Uterus	0.0227	0.0373	0.6086 1.6431
White blood cells	0.0059	0.0138	0.4284 2.3344
Hematopoietic	0.0082	0.0607	0.1353 7.3931
Penis	0.0053		
Seminal vesicle	0.0161		
Sensory organs	0.0141		
	0.0000		

FETUS  
% freq.

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0375
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0061
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0136
Breast t	0.0000
Large Intestine t	0.0000
Ovary n	0.0000
Ovary t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles n	0.0000
Testicles t	0.0195
Lungs n	0.0000
Lungs t	0.0121
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0061
Prostate n	0.0000
Sensory Organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 273

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0078	0.0188	0.4149 2.4104
Large intestine	0.0079	0.0112	0.7045 1.4195
Small intestine	0.0019	0.0057	0.3364 2.9727
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0215	0.1383 7.2328
Brain	0.0080	0.0053	1.5089 0.6627
Skin	0.0041	0.0070	0.5803 1.7234
Hepatic	0.0147	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0203	0.0000	undef 0.0000
Lung	0.0000	0.0355	0.0000 undef
Stomach-esophagus	0.0039	0.0111	0.3508 2.8506
Muscle-skeleton	0.0145	0.0128	1.1335 0.8822
Kidney	0.0120	0.0074	1.6236 0.6159
Pancreas	0.0000	0.0048	0.0000 undef
Prostate	0.0000	0.0276	0.0000 undef
T lymphoma	0.0085	0.0065	1.3023 0.7679
Uterus	0.0303	0.0149	2.0287 0.4929
White blood cells	0.0133	0.0092	1.4458 0.6917
Hematopoietic	0.0205	0.0000	undef 0.0000
Penis	0.0027		
Seminal vesicle	0.0054		
Sensory organs	0.0000		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0152
Fetal	0.0245
Gastrointestinal	0.0023
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0098
Kidney_t	0.0000
Ovary Uterus	0.0090
Prostate_n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## 2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

The consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from ovarian tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

**Example 4****Mapping of nucleic acid sequences on the human genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

#### **Example 5**

##### **Obtaining genomic DNA sequences (BAC clones)**

The genomic BAC clones that contain the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well." In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq. ID No.

Identified BACs

4	195/N/3	206/P/3	384/I/3	323/G/9	
5	222/B/10	404/E/10	526/F/20	565/P/11	279/F/14
9	501/L/21				
11	490/P/4	321/I/23	410/F/5	443/N/20	
19	311/A/19	505/F/17	216/D/8	219/C/22	
29	382/N/10	539/L/7			
31	530/D/11				
35	503/N/10				
37	547/D/16	215/P/16	439/K/6		
39	216/L/9	512/F/5	203/J/15		
45	205/K/7	250/H/22	283/C/17	528/B/20	402/L/11
80	371/A/20	470/L/3	495/L/3		
92	254/M/9	376/O/12	421/L/18	429/J/19	
112	243/O/14	520/K/15	565/J/17	565/J/24	

**TABLE I**

Col. 1 - Seq. ID No.  
Col. 2 - Expression  
Col. 3 - Function  
Col. 4 - Modules  
Col. 5 - Cytogenetic localization  
Col. 6 - Nearest marker



TABLE I

Seq. ID No.	Expression	Function
1	Overexpressed in ovarian tumor tissue	Unknown
2	Overexpressed in ovarian tumor tissue	Unknown
3	Overexpressed in ovarian tumor tissue	Unknown
4	Overexpressed in ovarian tumor tissue	P52r1PK
5	Overexpressed in ovarian tumor tissue	Unknown
6	Overexpressed in ovarian tumor tissue	Unknown
7	Overexpressed in ovarian tumor tissue	Unknown
8	Overexpressed in ovarian tumor tissue	Unknown
9	Overexpressed in ovarian tumor tissue	Unknown
10	Overexpressed in ovarian tumor tissue	Unknown
12	Overexpressed in ovarian tumor tissue	Unknown
13	Overexpressed in ovarian tumor tissue	Unknown
15	Overexpressed in ovarian tumor tissue	Unknown
16	Overexpressed in ovarian tumor tissue	Unknown
18	Overexpressed in ovarian tumor tissue	Unknown
19	Overexpressed in ovarian tumor tissue	Unknown

TABELLE I

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
1	in Ovariumorgewebe überexprimiert	unbekannt		1p31.1-p34.1	SHGC-2542-2540,2456; D1S448-D1S500; WI-6555; D1S198-D1S462
2	in Ovariumorgewebe überexprimiert	unbekannt		2p22.3-p23.3	SGC32173; D2S174-D2S390; TIGR-A00H24/D2S392-D2S390
3	in Ovariumorgewebe überexprimiert	unbekannt		4p15.1	WI-15951 (D4S1043-SHGC-16179)
4	in Ovariumorgewebe überexprimiert	P52/IPK		11q13.5-q14.1	SHGC-31396 (SHGC-32287, D11S4681)
5	in Ovariumorgewebe überexprimiert	unbekannt		1q22	SHGC-31641
6	in Ovariumorgewebe überexprimiert	unbekannt		13q33.1-q34	AFM310yds
7	in Ovariumorgewebe überexprimiert	unbekannt		8q11.23-q12.1	SHGC-32002; D8S1828-D8S507
8	in Ovariumorgewebe überexprimiert	unbekannt		4q24	SHGC-36699
9	in Ovariumorgewebe überexprimiert	unbekannt	PRO_RICH	2q35	SHGH-32531 (D2S1297, SHGC-35276)
10	in Ovariumorgewebe überexprimiert	unbekannt	PHD		
12	in Ovariumorgewebe überexprimiert	unbekannt		5q23.3-q31.1	AFM200yag=D5S414
13	in Ovariumorgewebe überexprimiert	unbekannt		3p23	WI-6841,D3S1569-D3S1563
15	in Ovariumorgewebe überexprimiert	unbekannt		6q22.1-q24.3	SHGC-33316; D6S453-D6S311
16	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	10p15.3	Cbat1h03; D10S533-D10S594, SHGC-11812; D10S556-D10S591
18	in Ovariumorgewebe überexprimiert	unbekannt	Ribosomal_L24e	15q21.3-q22.1	Cda17g12; D15S209-D15S198
19	in Ovariumorgewebe überexprimiert	unbekannt		11q14.3	SHGC-36010 (D11S1979, D11S1687)

Seq. ID No.	Expression	Function
20	Overexpressed in ovarian tumor tissue	Unknown
21	Overexpressed in ovarian tumor tissue	Unknown
22	Overexpressed in ovarian tumor tissue	Unknown
23	Overexpressed in ovarian tumor tissue	Unknown
24	OverExpressed in ovarian tumor tissue	Unknown
25	Overexpressed in ovarian tumor tissue	Branchio-oto-renal syndrome candidate gene
26	Overexpressed in ovarian tumor tissue	Unknown
27	Overexpressed in ovarian tumor tissue	Unknown
28	Overexpressed in ovarian tumor tissue	Unknown
29	Overexpressed in ovarian tumor tissue	Unknown
30	Overexpressed in ovarian tumor tissue	Unknown
31	Overexpressed in ovarian tumor tissue	Unknown
32	Overexpressed in ovarian tumor tissue	Partially homologous to R. norvegicus calpain
33	Overexpressed in ovarian tumor tissue	Partially homologous to human mRNA for fungal sterol-C5-desaturase homolog
34	Overexpressed in ovarian tumor tissue	Partially homologous to human GPx-3 mRNA for plasma glutathione peroxidase
35	Overexpressed in ovarian tumor tissue	Partially homologous to homo sapiens CHD2 mRNA

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
20	in Ovariumorgewebe überexprimiert	unbekannt		3q22.2-3q22.3	SHGC-34629 (SHGC-30855, SG C32794)
21	in Ovariumorgewebe überexprimiert	unbekannt		3q26.33-q29	AFM308y11 (D3S2363, D3S3669)
22	in Ovariumorgewebe überexprimiert	unbekannt		7q11.23	SHGC-37054
23	in Ovariumorgewebe überexprimiert	unbekannt			
24	in Ovariumorgewebe überexprimiert	unbekannt		4q28.1-q31.1	WI-30941; SGC30941; D4S1580-D4S427
25	in Ovariumorgewebe überexprimiert	Branchio-otico-renal syndrome candidate gene		7q32.3-q33	AFMc024we9
26	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	17q23.3	SHGC-64257
27	in Ovariumorgewebe überexprimiert	unbekannt		17p12-p13.2	SHGC-31370 (SHGC-35547-SHGC-35513)
28	in Ovariumorgewebe überexprimiert	unbekannt		10q22.3	Cla00w11, TIGR-A001X23,D10S607-D10S201
29	in Ovariumorgewebe überexprimiert	unbekannt		11q13.2-q13.5	WI-14303; D11S1436-D11S1314; TIGR-A005001; D11S913-D11S1314/RH-SHGC-14407
30	in Ovariumorgewebe überexprimiert	unbekannt		7p21.3	SHGC-14339
31	in Ovariumorgewebe überexprimiert	unbekannt		12p12.3	AFMb320va9
32	in Ovariumorgewebe überexprimiert	Partielles Homolog zu R. norvegicus calpain		11q41	SHGC-3992 (D1S2550-D1S2568)
33	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Human mRNA for fungal sterol-C5-desaturase homolog	Thymosin	11q23.3	WI-19895; D11S924-D11S925
34	in Ovariumorgewebe überexprimiert	Partiell homolog zu Human GPx-3 mRNA for plasma glutathione peroxidase	GSHPx	5q33.1	SHGC-10972
35	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Homo sapiens CHD2 mRNA		19q13.13-q13.2	AFMb018wh1

Seq. ID No.	Expression	Function
36	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus formin binding protein 21
38	Overexpressed in ovarian tumor tissue	Human homolog to Tribolium castaneum zinc finger protein
39	Overexpressed in ovarian tumor tissue	Human homolog to S. cerevisiae chromosome II sequence for ORF YBR1725
40	Overexpressed in ovarian tumor tissue	Human homolog to Rattus norvegicus rsly 1p
41	Overexpressed in ovarian tumor tissue	Human homolog to PEC-60=gastrointestinal peptide, swine
42	Overexpressed in ovarian tumor tissue	Human homolog to Mus musculus mCAF1 protein
43	Overexpressed in ovarian tumor tissue	Human homolog to Mouse mitochondrial genome; unidentified reading frame
44	Overexpressed in ovarian tumor tissue	Human homolog to Mouse kidney androgen-regulated protein (KAP)
45	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus Tera
46	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
47	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
48	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid K11H12
49	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid C43E11

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
No.					
36	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus formin binding protein 21	WW_rsp5_WWP		sISG31094; D2S292-D2S145
38	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Tribolium castaneum zinc finger protein		2p13.1-p16.1;RH; 2p13.1-p13.3	
39	in Ovariumorgewebe überexprimiert	Humanes Homolog zu S. cerevisiae chromosome II sequence for ORF YBR1725		19q12	AFM205y10 (D19S1080, D19S550)
40	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Rattus norvegicus rsly1p	Sec1	17	
41	in Ovariumorgewebe überexprimiert	Humanes Homolog zu PEC-60-gastrointestinal peptide, swine	kazal		
42	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mus musculus mCAF1 protein		9p22-p23.3	BDa16111; D8S549-D8S1733 bzw. S280
43	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse mitochondrial genome, Unidentified reading frame	oxidored_q1_N		
44	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse kidney androgen-regulated protein (KAP)		1p36.31-p36.13	SHGC-11461 (D1S2565, SGC32561)
45	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus Tera		12p11.21-p11.23	SHGC-1349 (D12S1621/D12S1805)
46	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7		19q13.33-qter	SHGC-30173; D19S418-qTEL
47	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7	PRO_RICH	2p11.1-p11.2	D2S388-D2S2181
48	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid K11H12	UPF0005	10q23.1	SHGC-167-SHGC-11466; D10S551-D10S532
49	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C43E11	PRO_RICH	Xq22.3-Xq25	sISG2963; DXS1055-DXS1047

Seq. ID No.	Expression	Function
50	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid C40H1
51	Overexpressed in ovarian tumor tissue	Human homolog to <i>C. elegans</i> cosmid K02D10
52	Overexpressed in ovarian tumor tissue	Human homolog to bovine inorganic pyrophosphatase
53	Overexpressed in ovarian tumor tissue	Human homolog to B. laurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex
54	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein or others
55	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein
56	Overexpressed in ovarian tumor tissue	Human homolog of R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence
57	Overexpressed in ovarian tumor tissue	Homologous to Bruton's tyrosine kinase
58	Overexpressed in ovarian tumor tissue	dbpB-like protein
59	Overexpressed in ovarian tumor tissue	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
63	Overexpressed in ovarian tumor tissue	Protease, serine, 2 (trypsin 2)
65	Overexpressed in ovarian tumor tissue	Human annexin IV
67	Overexpressed in ovarian tumor tissue	Human X2 box repressor

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
50	in Ovarialtumorgewebe überexprimiert	Humanes Homolog zu <i>Caenorhabditis elegans</i> cosmid C4011		1q22	WI-7155
51	in Ovarialtumorgewebe überexprimiert	Humanes Homolog zu Bovine cosmid K02D10		7p11.2-p12.3	Cda11c08; D7S506-D7S499; SHGC-17265+1581; D7S489-D7S2429
52	in Ovarialtumorgewebe überexprimiert	Inorganische pyrophosphatase	Pyrophosphatase	3q26.1	SHGC-9372
53	in Ovarialtumorgewebe überexprimiert	Humanes Homolog zu B. taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex		3q13.12-q13.2	D3S1310-D3S1575
54	in Ovarialtumorgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein aber anders		20q13.33	SHGC-11512
55	in Ovarialtumorgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein	PRO_RICH; MSP_DOMAIN	15q25.3-15q26.1	SHGC-69080 (D15S202/D15S1046, D15S1178)
56	in Ovarialtumorgewebe überexprimiert	Humanes Homolog des R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence	PRO_RICH	1p32.2-p31.2	SGC34409
57	in Ovarialtumorgewebe überexprimiert	Homolog zu Bruton's tyrosine kinase	rrm; PRO_RICH	10q21.1-q22.1	WI-11265; D10S581-D10S270
58	in Ovarialtumorgewebe überexprimiert	dbpB-like protein	CSD; PRO_RICH	15q25.3-15q26.1	AFM282wg5-D15S202 (D15S1046; D15S1187)
59	in Ovarialtumorgewebe überexprimiert	Tyrosine 3'-monooxygenase/tyrophan 5-monooxygenase activation protein	PRO_RICH	2p25.2-p25.1	
63	in Ovarialtumorgewebe überexprimiert	Protease, serine, 2 (trypsin 2)	lypsin	7q35	SHGC-16894
65	in Ovarialtumorgewebe überexprimiert	Humanes Annexin IV	annexin	2p13.1-p16.1	SHGC-9858
67	in Ovarialtumorgewebe überexprimiert	Human X2 box repressor		16q12.1-q22.1	WI-6174; D16S408-D16S3089; Cda01910; D16S419-D16S415



Seq. ID No.	Expression	Function
68	Overexpressed in ovarian tumor tissue	Human transcriptional coactivator PC4
69	Overexpressed in ovarian tumor tissue	Human tetratricopeptide repeat protein
70	Overexpressed in ovarian tumor tissue	Human tax1-binding protein TXBP151
72	Overexpressed in ovarian tumor tissue	Human prothymosin alpha
73	Overexpressed in ovarian tumor tissue	Human profilin
74	Overexpressed in ovarian tumor tissue	Human pepsinogen C
76	Overexpressed in ovarian tumor tissue	Human osteopontin
78	Overexpressed in ovarian tumor tissue	Human non-histone chromosomal protein
79	Overexpressed in ovarian tumor tissue	Human mRNA for protein disulfide isomerase-related protein P5
80	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0332
81	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0078
82	Overexpressed in ovarian tumor tissue	Human mRNA for 90-kDA heat-shock protein
83	Overexpressed in ovarian tumor tissue	Human major nuclear matrix protein
84	Overexpressed in ovarian tumor tissue	Human Ku (p70/p80) subunit
85	Overexpressed in ovarian tumor tissue	Human interferon-induced 17-kDa/15-kDa protein
86	Overexpressed in ovarian tumor tissue	Human hsc70 gene for 71 kd heat shock cognate protein
88	Overexpressed in ovarian tumor tissue	Human gamma-interferon-inducible protein (IP-30)

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
68	in Ovariumorgewebe überexprimiert	Human transcriptional coactivator PC4		5p15.1	SGC32812, D5S477-D5S851
69	in Ovariumorgewebe überexprimiert	Human tetrapeptide repeat protein		5q33.2-q33.3	TIGR-A002013; D5S412-D5S422
70	in Ovariumorgewebe überexprimiert	Human lax-binding protein TXBP151		7p14.1-p21.3	SGC31789; D7S516-D7S632
72	in Ovariumorgewebe überexprimiert	Human prothymosin alpha			
73	in Ovariumorgewebe überexprimiert	Human profilin	profilin	17p13.3	
74	in Ovariumorgewebe überexprimiert	Human pepsinogen C	asp	6p21.1	SGC35331; D6S426-D6S271
76	in Ovariumorgewebe überexprimiert	Human osteopontin	Osteopontin	4q13.3-q22.1	SHGC-9669; D4S1542-D4S1544
78	in Ovariumorgewebe überexprimiert	Human non-histone chromosomal protein	HMG14_17	21q22.3	
79	in Ovariumorgewebe überexprimiert	Human mRNA for protein disulfide isomerase-related protein P5	thiorel	2p23.3-p24.1	SGC31703; D2S287-D2S131; sISG1958; D2S162-D2S287
80	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0332		3p21.1	SHGC-14798 (D3S4210, SHGC-11985)
81	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0078	PRO_RICH		SHGC-9647; D7S651-D7S477; WI-1419; D8S289-D8S1799 +2 weitere auf Chr.8
82	in Ovariumorgewebe überexprimiert	Human mRNA for 90-kDa heat-shock protein	HSP90	4, 11, 1, 6	SHGC-11305
83	in Ovariumorgewebe überexprimiert	Human major nuclear matrix protein	RBD; ZF_MATRIN	5q31.1	SHGC-3183
84	in Ovariumorgewebe überexprimiert	Human Ku (p70/p80) subunit		2q34-q35	SHGC-11966; D2S2382-D2S164; WI-8140; D2S143-D2S164
85	in Ovariumorgewebe überexprimiert	Human interferon-induced 17-kDa15-kDa protein	ubiquitin	1p36.31-p36.32	
86	in Ovariumorgewebe überexprimiert	Human hsc70 gene for 71 kd heat shock cognate protein	HSP70	11q23.3-q25	D20S113-D20S97
88	in Ovariumorgewebe überexprimiert	Human gamma-interferon-inducible protein (IP-30)		19p13.13	SHGC-32638; D18S699-D18S407

Seq. ID No.	Expression	Function
89	Overexpressed in ovarian tumor tissue	Human fatty acid binding protein homolog (FA-FABF)
90	Overexpressed in ovarian tumor tissue	Human enhancer of rudimentary homolog
91	Overexpressed in ovarian tumor tissue	Human deleted in split hand/split foot 1 (DSS1)
92	Overexpressed in ovarian tumor tissue	Human decay-accelerating factor mRNA
93	Overexpressed in ovarian tumor tissue	Human chromosome segregation gene homolog CAS
94	Overexpressed in ovarian tumor tissue	Human carcinoma-associated antigen GA733-2, human epithelial glycoprotein (EGP)
95	Overexpressed in ovarian tumor tissue	Human calmodulin
96	Overexpressed in ovarian tumor tissue	Human Bax alpha
97	Overexpressed in ovarian tumor tissue	Human antileukoprotease (ALP)
98	Overexpressed in ovarian tumor tissue	Homo sapiens UDP-galactose-4-epimerase
99	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for putative progesterone binding protein
100	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for galectin-3
101	Overexpressed in ovarian tumor tissue	Homo sapiens monocyte/macrophage 1g-related receptor MIR-7 (MIR cl-7)
102	Overexpressed in ovarian tumor tissue	Homo sapiens Kunitz-type protease inhibitor
103	Overexpressed in ovarian tumor tissue	Homo sapiens hCPE-R mRNA for CPE-receptor
105	Overexpressed in ovarian tumor tissue	Homo sapiens DNA for amyloid precursor protein
106	Overexpressed in ovarian tumor tissue	Homo sapiens CD24 signal transducer

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
89	in Ovariumtumorgewebe überexprimiert	Human fatty acid binding protein homologue (PA-FABP)		17p11.2	SHGC-9883
90	in Ovariumtumorgewebe überexprimiert	Human enhancer of rudimentary homolog	ER	14q22.3-q24.2	WI-8921; D14S63-D14S251
91	in Ovariumtumorgewebe überexprimiert	Human deleted in split hand/split foot 1 (DSS1)		7q21.3-q22.1	D5S1977-D5S428 (Hs.85215)
92	in Ovariumtumorgewebe überexprimiert	Human decay-accelerating factor mRNA		1q32.2	SHGC-11228
93	in Ovariumtumorgewebe überexprimiert	Human chromosome segregation gene homolog CAS	IBN_NT	20q13	
94	in Ovariumtumorgewebe überexprimiert	Human carcinoma-associated antigen GAT33-2; Human epithelial glycoprotein (EGP)	thyroglobulin_1	2p15-p21	AA113218; D2S119-D2S337
95	in Ovariumtumorgewebe überexprimiert	Human calmodulin	EF_HAND_2	2p16.3-p21	WI-9106; D2S391-D2S123
96	in Ovariumtumorgewebe überexprimiert	Human Bax alpha	Bcl-2	19q13.3-q13.4	
97	in Ovariumtumorgewebe überexprimiert	Human antileukoprotease (ALP)	wap	20q13.3-q13.2	WI-6969 (D20S880; SGC34003)
98	in Ovariumtumorgewebe überexprimiert	Homo sapiens UDP-galactose 4-epimerase	3beta_HSD	1p36.11	SHGC-11459 (RH420-D1S3295)
99	in Ovariumtumorgewebe überexprimiert	Homo sapiens mRNA for putative progesterone binding protein		4q31.1	SHGC-4275
100	in Ovariumtumorgewebe überexprimiert	Homo sapiens mRNA for galectin-3	Gal-bind_lecln	14q12-q22.3	D14S276-D14S86
101	in Ovariumtumorgewebe überexprimiert	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7)	7m_1; G_PROTEIN_RECEPT OR_2; PRO_RICH	12q14.2-q14.3	SHGC-33073
102	in Ovariumtumorgewebe überexprimiert	Homo sapiens Kunitz-type protease inhibitor	Kunitz_BPT1	19q13.2	TIGR-A007F08; D19S421-D19S408
103	in Ovariumtumorgewebe überexprimiert	Homo sapiens hCPE-R mRNA for CPE-receptor	PRO_RICH	7q11.23	
105	in Ovariumtumorgewebe überexprimiert	Homo sapiens DNA for amyloid precursor protein	Kunitz_BPT	21q21.2-q22.11	WI-8902; D21S265-D21S260
106	in Ovariumtumorgewebe überexprimiert	Homo sapiens CD24 signal transducer		6p21	AFM115m12; SHGC-13709 - SHGC-32498

Seq. ID No.	Expression	Function
107	Overexpressed in ovarian tumor tissue	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)
108	Overexpressed in ovarian tumor tissue	Histone H2B
110	Overexpressed in ovarian tumor tissue	H. sapiens, gene for membrane cofactor protein
111	Overexpressed in ovarian tumor tissue	H. sapiens TROP-2 gene
112	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Icin protein
113	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for BiP protein
114	Overexpressed in ovarian tumor tissue	H. sapiens HE4 mRNA for extracellular proteinase inhibitor homolog
115	Overexpressed in ovarian tumor tissue	H. sapiens for neutrophil gelatinase associated lipocalin
116	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Sm protein G
117	Overexpressed in ovarian tumor tissue	H. sapiens for glutathione peroxidase-GI
120	Overexpressed in ovarian tumor tissue	CDC28 protein kinase 2
121	Overexpressed in ovarian tumor tissue	B-factor, properdin
122	Overexpressed in ovarian tumor tissue	Annexin II
123	Overexpressed in ovarian tumor tissue	ADP-ribosylation factor like 1
258	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 2
259	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 3

Seq ID	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
107	in Ovarialtumorgewebe überexprimiert	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)		1q31.1	SHGC-58249/D1S2602/WI-2775; WI-7265
108	in Ovarialtumorgewebe überexprimiert	Histone H2B	histone; Archaeal histone	6p21.2-p21.31	WI-11733; D6S276-D6S439
110	in Ovarialtumorgewebe überexprimiert	H.sapiens, gene for Membrane cofactor protein	sushi	1q32.1-q32.2	SHGC-12033; D1S456-D1S2891
111	in Ovarialtumorgewebe überexprimiert	H.sapiens TROP-2 gene	thyroglobulin_1	1p32.2-p32.3	SHGC-12661; D1S476-D1S220
112	in Ovarialtumorgewebe überexprimiert	H.sapiens mRNA for Icdn protein		11q14.1	SHGC-31540; D11S4179-D1S937;; SG31540; D11D911-D11S1352
113	in Ovarialtumorgewebe überexprimiert	H.sapiens mRNA for BIP protein	HSP70; PRO_RICH	9q33.3-q34.11	WI-6005; D9S282-D9S260
114	in Ovarialtumorgewebe überexprimiert	H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue	wap	20q13.2-q13.13	SGC30446; D20S119-D20S197;; WI-30446
115	in Ovarialtumorgewebe überexprimiert	H.sapiens for neutrophil gelatinase associated lipocalin	lipocalin	9q34	
116	in Ovarialtumorgewebe überexprimiert	H.sapiens mRNA for Sm protein G		18q21.1	SHGC-8871 D18S484; D18S851)
117	in Ovarialtumorgewebe überexprimiert	H.sapiens for glutathione peroxidase-G1	NLS_BP; GSHPx	14q24.1	
120	in Ovarialtumorgewebe überexprimiert	CDC28 protein kinase 2	GKS	9q21.31-q22.1	SHGC-11955; D8S1812-D8S283;; SGC31294; D8S153-D8S264
121	in Ovarialtumorgewebe überexprimiert	B-factor, propeptin	VWA DOMAIN; TRYPsin_CATAL; sushi; tyrosin		DXS255-DXS426
122	in Ovarialtumorgewebe überexprimiert	Annexin II	annexin	15q22.1-q22.31	WI-8600+WI-9161; D15S186-D15S159
123	in Ovarialtumorgewebe überexprimiert	ADP-ribosylation factor like 1	arf	12q22-q23.1	SHGC-12629; D12S1727-D12S78;; WI-7420; D12S346-D12S78
258	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No. 2			
259	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No. 3			

Seq. ID No.	Expression	Function
260	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 4
261	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 10
262	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 18
263	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 25
264	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 26
265	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 30
266	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 34
267	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 42
268	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 46
269	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 47
270	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 48
271	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 50
272	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 52
273	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 56

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
260	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 4			
261	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 10			
262	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 18			
263	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 25			
264	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 26			
265	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 30			
266	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 34			
267	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 42			
268	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 46			
269	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 47			
270	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 48			
271	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 50			
272	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 52			
273	in Ovarialtumorgewebe überexprimiert	Verlängerung zu Seq ID No: 56			



TABLE II

Seq. ID. No.

ORF Seq. ID. No.

1	124	125	126	127	128	129
2	130	131				
3	132					
4	133	134				
5	135					
6	136	137				
7	138	139				
8	140	141				
9	142	143				
10	144	145				
12	148	149				
13	150	151	152	153		
15	155	156	157			
16	158	159	160			
18	163	164				
19	165					
20	166	167				
21	168	169				
22	170	171	172			
23	173	174				
24	175	176				
25	177	178				
26	179					
27	180	181				
28	182	183	184			
29	185	186				
30	187	188				
31	189	190	191			
32	192	193	194	195	196	
33	197	198	199			
34	200	201				
35	202	203	204			
36	205	206	207	208		
38	210	211				
39	212	213	214	215		
40	216					
41	217	218				
42	219	220	221			
43	222	223	224	225		
44	226	227				
45	228	229	230	231	232	
46	233	234	235			
47	236	237	238			
48	239	240				
49	241	242				
50	243	244	245			
51	306	307				
52	246					
53	247	248	249			
54	250	251				

Seq. ID. No.

ORF Seq. ID. No.

---

55	252	253	254
56	255	256	
57	257		
258	274	275	
259	276	277	
260	278	279	
261	280	281	
262	282	283	
263	284	285	
264	286	287	
265	288	289	
266	290	291	
267	292	293	
268	294	295	
269	296	297	
270	298	299	
271	300	301	
272	302	303	
273	304	305	

The inventive nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 124-257 and 274-307 are described in the following sequence protocol.

**Sequence Protocol****(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

**(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Ovarian Tumor Tissue****(iii) Number of sequences: 284****(iv) COMPUTER READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

cgggatttta cccgggttttaa aaagcggaacc ttctcccgccg tacacccgaa ggtaccccaaa 60
tatgggtagg tccgggttttc caacttggcca aacgtatggg gaagcccggg gatggcttcc 120
ataaaatttc cagcgggatta tggcatttcc ttccaggaaat acccttgggt aaagccctgc 180
tgcgaataat gcatttccaa acttgaataa taggtgtgaa cagtggtgac cagttttaaag 240
ctttcacttc atttgtgttt tttaattaa gattagaag ttcccccaat tacaaaactgg 300
ttttasaata tggacatact ggttttaata cctgctttgc atattccacac atggctcaact 360
gggacatggt asaactttgat ttgcataatt ttatgctgtg tggataacta actatagtta 420
ttttacacta gtttttaatat ttctattttt ggggaaaaaat cttttttcac ttctcatgat 480
agcgtgtata tatataatgt aaatctttat atacagaaat atcagtacct gaacaaaattc 540
aaaagcacatt tggtttatta acccttgctc cttgcctggc tcatagggtt caaattataa 600
ctgatttaca ttctcagcta tatttacttt ttaaaatgct gagttttcca ttttaaaact 660
taaatagac atcttaattg gtgaaaatgg tttaaaactac ttattgttgg taggcacatc 720
gtgtcaagtg aagttagtttt ataggtaggg gttttttctc ccccttcacc aggggtgggtg 780
gaataaagtg atttggccaa tgtgtaatat ttaaaactgt ctgtaaaata agtgtctggc 840
catttgggat gatttctgtg tgtgaaaggt cccaaaaatca aaatgggtaca tccataatca 900
gccaccattt aaccccttct tgttctaaaa caaaaaacc aaaggcgctgg ttgtaggggt 960
gaggtggggg agtatttttaa tttttggaat ttgggagaaca gacagcttta ctttgaagg1020
ttggaaacgc agcactatac atgaaatata aacaaaaaac ctttactgtt tctaaaattc1080
ctagatgtct attatttgggt tgaagtgtga gtattccaca gaaagtggta attatcttt1140
ctctctctct ccactagaaa attaggtaaa taatggatc ctataaatggg agcactaccal1200
cttctaaaaa cacaacatga atgataaatt aaaaaagttt tctaggattg tctttattc1260
tgcgccattt attgataaac agtgaaggaa attttcaaaa atttttaaga atgtttgtc1320
acgtcatttt tagaaaatgt ctactcgtat atgttaatgt ccagttttaa aatattggal1380
catcttcaat cttaaacatt tctatttagc tgaattgttc tccatatact ttccaaaaga1440
aaacttttag ttataaagat tactttttgg atataagttt ttaactcga taacttacta1500
ttctgcattt taggaagga ggtaatttgt tttaatgat gatataacttg tgcgtgtgt1560
ttggatctta tgaagctgag catgttctgc actggtgcta atgtctata taattttata1620
tttccacaca tgaagcttac ccagagatta atttagtcca tatgaactat tgacccattg1680
ttcattgaga cagcaacata cgcactccta aatcagtggt tttagacttt tcaagtatct1740
aaactcattt cacaacatgta ccatgtttta taaacctctt gatttccagc aacatactat1800
agaaaacacc tgcactcaca aacacaactt ccagtgta tccattgctg tctgagagaga1860
caaacatgca atacttggta tgttgcaagc ttccaagata gccctgaactt aaaaagtgtg1920
tgcatttagt gtaactgatg gatataaatt tgcctcctag ttcaattgtt gccaagact1980
aaaactgtga accataactt ctctatttgg tgggtataaa ctgaaaaata agattttatt2040
tcatgtcacc ttctaaaag tctaaaaaac aatcaaatag gatcatgttt attgtcatgt2100
gtttctgggt ttctgacctg tgtgcacacc cctgtgtgtt tataattttt aaattgaa2160
ttatatgggt tttttatttg tctaaaaaca ggcgtgtgaa tccatttttg gaagggact2220
tatcttaagt actaatgact taattgggaa agttgaaatc ttgtaaaaa caaaactcaa2280
ggactcttgg gattttaatc taattgtcac tctgtaggc agatgcact ttgtgataa2340
tggaaagtta agcataccga atgctacttt tgggtgacaa acgggcttaa tagtccgggg2400

```

## (2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 798 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

gcctatatgt gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaaaag 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa tagggagactt tagcacactt cactgttttc tagaagtcca gaattttggal80
cctccacgtg aaagaactgt tcttacctct gaactggggg ctcccataag ggataatttt240
cctcagagta gcaaaagtctt tcttattaga gaaatcttgt gactcagatg aagtcaggga300
tagaagaccc ttggaccttg caggttaatg ctgattatct ctggcccttt cccttgatt360
tatgcaagga aggatatact gagctgatac tcttccaagc ctacaacttc aagttttatc420
atttgaactc aagtactcttt gctgctgagg aatggaatca aaagaacgta gtctcctggt480
gaccacctca gatctctatt attaggctag atgtatagcc tctactcccc cagcttcttg540
ctcttgacct tgactgttaa gtggcccttc tattagcagc caaggaaaag ggaaacatga600
gcttatccag aacgggtggca gagtctcctt ggcaatcaac caacgttgtc atgaaatatg660
cctcacactg tatagtctcat tataggacgt caggtttgtt gaaaaaagtg ggcaagacat720
gattaatgaa tcagaatcct gtttcatttg tgactttgat aaagactttt taatttttaa780
aaaaaaaaaa aaaaaaaaaa

```

798

## (2) INFORMATION ON SEQ ID NO. 3:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 882 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

attccaaaca tggcggtccc actagggggt atgttttctg ggcagccacc cggccccct 60
caggccccgc cgggccttcc gggccaagct togttttctc aggcagctcc aggcgctcct120
agaccttcca gcagtacttt ggtggacgag ttggagtcac ctttcgaggc ttgctttgcal80
tctctgggtga gtcaggacta tgtcaatggc accgatcagg aagaaattcg aaccggtgtt240
gatcagtgta tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttacaa300
aaaagattgc agttatctgt ccagaaacca gagcaagtta tcaaagagga tgtgtcagaa360
ctaaaggaatg aattacacgg gaaagatgca ctagtccaga agcacttgac aaagctgagg420
cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagccccg cgacatccct480

cagggctcct tggcctacct ggagcaggca tctgccaaaca tccctgcacc tctgaagcca540
acgtgagcaa agggcagagg cagtggcct atgagtgggc tgatgcgtga ggttggccac600
acattctctc ctgtggactt gacatttttg aagaactctt tgccagataa tgagttcat660
ttagtcttta gctccattg aaaaattttc cactattttt ataagctgtt aattttctga720
gtactctata acatgtctgt agcttggata aaccaagtaa gtattttttt tttgtcttta780
gcaaaagtta gactgtgaat atgatgacac agattctttt ttatgggtggc tttgtctgt840
ttaaattttt gcatgacttt taaaaaaaaa aaaaaaaaaa aa 882

```

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2901 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

acrtgagttaa gatgaaatca ggacactgaa acagaaaaaa attgatgaaa ctctctgagca 60
ggaacaaaaa cataaagaaa ccaacaatat caatgctcag aaccocagcg aagaagaggg 120
tgaaggggcaa gatagggaca ttctacctct aacccttgaa gagaaggaaa acaaaagata 180
ccraaaatct ctatttgaaa tcttgattct gatgggaaa caaaacatac ctctggatgg 240
acatgaggct gatgaaatcc cagaaggtct ctctactcca gataacttcc aggcactgct 300
ggagtgtcgg atcaattctg gtgaagaggt tctgagaaa cggtttgaga caacagcagt 360
taacaacgttg tttgttcaa aaacacagca gaggcagatg ctagagatct tggagtatgt 420
tattcgagaa gaaactctca ggggaagtga agactcacac ttcttttcca ttactactga 480
cgatgtagtg gacatagcag ggggaagaga cctacctgtg ttggcgaggt ttgttgatga 540
attctataac ctaagagagg aatttatagg ctctctgctt tatgaagcgg atgcagaaat 600
tttggtgtg aaatttcaca ctatgataac tgagaagtgg ggattaaata tggagtattg 660
tcgtggccag gcttacattg tctctagtgg attttcttcc aaatgaagag ttgtgtcttc 720
tagactttta gagaaatata cccaagctat ctacacactc tgccttctct gtgccttaaa 780
tatgtggttg gcaaaatcag tacctgttat gggagtatct gttgcattag gaacaattga 840
ggaagtttgt tcttttttcc atcgatcacc acaactgctt ttagaacttg acaacgtaat 900
tgctgttctt tttcagaaca gtaaaagaaa gggtaagaaa ctgaaggaaa tctgccattc 960
tcagtggaca ggcagggcat atgcttttga aattttatgt gaaactcctg aagcacttgt 1020
tttatgttta gatggtataa atagtgcac aaatattaga ttgaataact atatagctgg 1080
ccgagctatt tgaactctga gtgcagtgtc agattttgat tctacttgta ctattgtgtt 1140
tcttaaaatg gtccctattt ttacaagagc ctttgggaaa aacctccagg ggcaaacctc 1200
tgatgtcttc ttgtggccgg gtatgctgac tgcagtactc cattcactca acgaaatgag 1260
tggaaaaatg tgaagtttat catgaatttt ggtttgagga agccacaaat ttggcaaccal 1320
aaacttgata tcaaatgaaa ctccctggga aattcccgag ggttaacttg 1380
aatctcagct aacctctgag agttactata aagaaacctt aagtgtccca acagttagg 1440
acattctata gaaacttaaa gatataatt ccaagacaga cctcaaaagt cttataagct 1500

tatctctggt aacctcagtc atgggacaa ccaaaattcaa tacgtcggag gaacacctg 1560
ctgacagtga tagaagtga ctaccacaa ctgacacgct gtcagctgag ctctattgt 1620
ggagaatcaa atggaaacac agggggaaag atatagagct tccgtccacc atctatgaa 1680
ccctccacat gccgcacatc aagtttttcc ctaatgtgta tgcattgctg aaggtcctgt 1740
gtattcttcc tgtgatgaag gttgagaatg agcggtatga aaatggacga aagcgtctta 1800
aagacttttt gaggaaacct ttgacagacc aaaggtcaag taacttggct ttgcttaaca 1860
taaaatttga tataaaacac gacctggatt taatggtgga cacatatatt aaactctata 1920
caagttaagtc agagtcttat acagataatt ccgaaactgt ggaaaaatcc taagagactt 1980
ttaaaaaatg atgtctctat atttgatatt tggaaagaaa agccgtaagg tttatgtaga 2040
acccttaac ctaaaatatt ttgctctata ggactccatt gaatacatta gccattgata 2100
ctcactcgt taaatggcc cctgtttgaa ctctcaagct ttgaagacct acctgtctt 2160
ccaagagaga agcttgaagg tgcattgttt ccttttgcgt gatctctgtt gatggcactc 2220
tggatttgtt tcaagttaag cattttagac atagcattta ttactactgt ggaactctac 2280
ttgttgggtg ttatgaaatc ttgaaagaaa tatattttga agagggtggg gaggaaagga 2340
tacattttat aaaaatttgt agtgaagccc acaattgacc ttgtactaat aggagtttta 2400
agtatgttaa aaactataac tggacagtta caagaaatta ccggagaaaa gcttgtgagc 2460
tcaccaaaaa aggatttcag tgtagatttt gtctttcttg aacttaaaag acaaaatgac 2520
aaaagtgtga tggaaaaagc tgcctgttgt aggtatatgt tgcgtgttta cattctcttg 2580
tggagccrac atcttcttaa gcttttttgc acaactgatt tgcctgtttt ttttctctgt 2700
tggagacaga atcagaggcc atggtactga tcttgattta taagcaaaac ctgaaaaacc 2760
ctttttccat gactctata tactgctcta tcttgattta aaatatggaa atatttgctg 2820
tgaagaaatc caattttgta tagtttattt caatctaaat aaaaatgtga 2880
aaaaaasaaa aaaaaaaaaa a
2901

```

## (2) INFORMATION ON SEQ ID NO. 5:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

aaagaagaagag aaagaagaagaa aagaagattg tagctagggg gagagtaggt gaaaagatga 60
acaacatgac cggaagatt tcctaattct accacagcct ggctctacct taagtctttal20
ataaaagctt gactgaaggt accaaggtgt gctgaagtgg aagcaagatt ctccaagctc180
cagcatggta gacatcagtg gtggttaacca aggcagagacc ccaaggcaag gtgaacctca240
aaaatgggaa ctcaagtcct tgcatgccag ctgccctccc caccagaaag tccttggtcc300
agcccaacat cagtgcctct gagtgtgttt actagaaca aaggaagaat ttcttgtaa360

aaatatagac agagtgtcc ctggctttct cctcttgacg gaaggatgga ttctccatt420
ccataaccatc ttctcccccac actggcccca gaataactta attcaactat gtgaaaataa480
agattgtttt tggtttgagg gcatagggat ccattatccc ttattcttta tgaggcacta540
sattagcttt gtatgttatt aaatgtgtct cgtcaatgc 579

```

## (2) INFORMATION ON SEQ ID NO. 6:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2809 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gaggggccc  gtgcggttg  cataaatagg  tttctcact  cttcttttt  tcccttttt  60
atccctcact  cctcccccct  aacctcgctt  cagcacaaat  gacttaattc  agcattctga  120
tcataaggcc  cctcattttc  ctaatgtgtt  tcaaggaaac  tttttaggaa  aaatatccag  180
attattcacc  cacttttttt  agtatctact  acaactcctt  tttttctct  agagagttaa  240
gaggaacag  gtgtccttg  tctggagtca  agctaaacac  atgatttgtt  ttatcagcag  300
ctggagcaga  agtgaanaat  gtctttctgt  gagacagtaa  ttgtctactg  aagctttatg  360
gctgttttgc  actgattact  ccaggatcca  aaaacttgg  gaaagtcact  gaaacactca  420
aggcaaatca  ctttacagcc  ctgagtgctt  gtcaccatag  ttgtcataat  gaatatgaat  480
ccactagtgt  tgtggttag  gaaatcctgt  agttgtattt  tcttgaactg  aaatatttga  540
ctcaaaataa  ttaagactca  ttgtcatttt  tcactctggc  attattgtgg  acaagtgtac  600
atattaact  tctttgcttt  ctgttaagct  tagcttttaa  aatgcatttt  cctctgtcct  660
gtctttaact  agtatatact  gcttataatt  atagtgggtt  tcacagacta  taaaattgaa  720
tgtatgaact  ttttatttat  atcagtgttt  ttaataatga  agatattttt  ggagttaagg  780
tgctgtcttg  taagcaggtt  ttaactatag  taagattttt  ttctcttcat  ttgctttttt  840
tgttttcatt  taacaatttt  ttttttacac  ggacacaaac  ctctgacagt  ctttccaaat  900
attaaataca  ttggaattgt  tatgtctgtg  tctgaacact  gctcaagcca  tcaagcagtc  960
ttctacagact  ttgcattata  aaactcact  aaattctcca  agaaaaataa  agttgaagaa  1020
tttattttcc  ttgacctgca  tccctctggat  ttctgagttt  cagttcagat  tgtagatgac  1080
aatataagct  gccttcctgaa  attgtcaaca  tctgaagtgt  aagttcattt  tccctctgall  1140
agaagccctg  agttccatga  agtatggatt  accatttgta  tttttcacta  acagtaaatg  1200
tatttttctt  attaatgttt  tgcttagga  atgatgaatt  acattttttg  ttctctcttal  1260
ccataaacat  ctgcattcct  cagctcagcc  ttctctgtat  gttgtttttt  tataaatggt  1320
tgagctgtct  atgcaggtat  tgccaagcta  acagtaaaa  tcattttaa  gaggaagctg  1380
gcgcgtatgg  cagccagagg  gcacactctg  caggacactg  gacaagacag  taaatattca  1440
acttttaatt  ctgattaaag  gagtataggt  aagaatacag  taggtataca  taattggtga  1500
gacaaaatatt  cactttattt  atatttata  tattttttt  tcaatttgtt  aaatactatt  1560
cagttttgta  gttgtccttg  ttgatttggt  tgatattaaa  gtatttagta  taattgccag  1620

```

```

gaaactatca  ttaggggagg  tttagtttgt  tgctgtttgg  actgggaggg  atgatttaaa  680
tttagtgcta  gaaaccaatt  ttagtgtact  cacagtttat  catttgtcag  acgaaaggtal  740
gtttataaag  taccctgtaa  gtccatatca  aaaagtccag  aggaagatta  gtaaactatt  1800
atcaataaaa  ataaacattt  tgtttttcta  atactctaac  atactctccc  ctttagggagg  1860
aagaacgtgc  aaaaactgtg  gagctagagc  gaatacragc  agagaataac  cgaaaaattg  1920
cagaagcaga  agccaaactg  gccgaagaac  tgttgagaat  tgttgaagaa  caaagaagaa  1980
ttctatgaga  aaggtatgaa  ctagaacaag  aagcaaacag  tcaacaaaaa  gaagaacaaa  2040
aaatattcct  gggcaagggg  ctctcagcgc  caaaaactgt  cttctcatta  aaaaccagag  2100
attaaattgt  aaactctgaa  ctttttacaa  agaaaaattg  taatgtagct  taatgtagct  2160
tcagtgtgaa  gttttttttt  gtttttgttt  ttgttttttt  aatttgaata  atctggaaag  2220
ttagcttgtt  ctaataaggg  ctatgtctgc  caattccctt  ttgttttttt  ttgtttcttt  2280
ccactcaagt  caactcctat  ttgtctactg  aagagcagat  cacattgtaa  caacttggaat  2400
gtgtttgtag  tctattatag  gaccccactg  acttcagagt  tatactctgt  ttgtcacatc  2460
gtatctgata  ggtctttact  tttttgtttt  ttatatattt  tataaaaaaa  gaaaaaagtt  2520
ataactgtgt  ttgtgtgac  ccaggggtat  actggaacta  tgtggtgtat  tgttaaaaca  2580
gtgtcttgtt  gatactgttg  ctcttgagtg  tctgtataca  ggttaaggaa  cagttgtgtc  2640
actctgatac  aaagtatata  tatgtctcct  tatgtctcct  gttcattttg  tttttatttc  2700
attgacaaaa  tcaaacccag  attccccatt  gtttaataa  atgattttgc  tgaataaagt  2760
aaagtcttaa  attcaaaaaa  aaaaaaaaaa  gaaaaaaaaa  aaaaaaaa  2809

```

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 910 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

agttcggcac agagaaagta ttttaacctt cctgtagaga tcctcgtcat ggaaggtgc 60
caaaactgttt tgaatggaag gacaagtaag agtgaggcca cagttccccc caccgagggl20
cttttgtatt gttctacttt ttcaagccctt tactttctgg ctgaagcatc cctctggaggt180
gccatgtata agttgggcta tttagagttca tggaacatag aacaaccatg aatgagtggtc240
atgatccgtg cttaatgatac aagtgttact tatctaataa tcctctagaa agaaccctgt300
tagatccttg ttgtgataa aaatataaa acagaagaca tgaggaaaaa caaagggtt360
gaggaaatca ggcataatgac ttataactta acatcagatc ttttctataa tatcctaacta420
ctttgggttt cctagctcca taccacacac ctaaacctgt attatgaatt acatattaca480
aagtcataaa tgtgccatat ggatatacac tacattctag ttggaatcgt ttactctggt540
agaatttagg tgtgagattt ttgtttccc aggtatagca ggcttatgtt tgggtgcatt600
aaattgggtt ctttaaaatg ctttggtggc acctttgtta acagattgct tctagattgt660
tacaacacaa gccataagaca catctgtgaa tacttagatt ttagcttaa tcacattcta720

gaattgtgag ttgaatgaca aagcagttga acaaaaaatta tggcatttaa gaatttaaca780
tgtcttagct gtaaaaaatga gaaagtgttg gttgggttta aaatcttgta actccatgat840
gaaagagaat ttattttata cgtgttatgt ctctaataaa gtatttcattt gataaaaaaa900
aaaaaaaaaa

```

910

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1447 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

gcgcagcgcg cttagaaaagt gcttcctgga gcgcagacga ggtcatgaat catgtgacgg 60
tggtctgagg aggaacctgt ctttaaagct gtccctgaag tgacagcgga gagaaccagg 120
cagcccaqaa accccaggcg tggagattga tccctgcgaga gaaggggggt catcatggcg 180
gatgacctaa agcgattctt gtataaaaaa ttaccaagtg ttgaagggt ccatgccatt 240
gttgctcag atagagatgg agtacctgtt attaaagtgg caaatgacaa tgctccagag 300
catgtcttgc gacctgtgtt cttatccact ttgccccttg caacagacca aggaagcaaa 360
cttgagcttt ccaaaaaataa aagtatcatc tgttactata acacctacca ggtggttcaa 420
tttaactcgt taccttttgt ggtgagtttc atagccagca gcagtqccaa tacaggacta 480
attgtcagcc tagaaaaggga acttgctcca ttggttgaag aactgagaca agttgtggaa 540
gtttcttaat ctgacagtggt ttccagtgtg taccttatct tcattataac aacacaatat 600
caatccagca atcttttagac tacaataata cttttatcca tgtgctcaag aaaggggccc 660
tttttccaac ttatactaaa gagctagcat atagatgtaa tttatagata gatcagttgc 720
tatattttct ggtgtagggt ctttcttatt tagtgagatc tagggatacc acagaaatgg 780
ttcagttcat cacagctccc atggagttag tcgtgtcacc agatatggat gagagattct 840
attcagtgga tcagaatcaa actggtacat tgatccactt gagccgttaa gtgctgcca 900
ttgtacaata tgcccaggct tgcagaataa agccaacttt ttattgtgaa taataataag 960
gacatatatt ttcttcagatt atgtttttatt tctttgcatt gagtggaggaa cataaaatgg 1020
cttggtaaaa gtaataaaat cagtacaact actaaacttc ctttgtacat attattttgt 1080
agtatagatg aatattacta atcagtttga ttattctcag aggggtgtgc tctttaatgall 1140
aaatgaaat tatagctaat gttttttctt caaactctgc tttctgtaac caatcagtg 1200
tttaatgttt gttgtttctt cataaaattt aaatacaatt cgttattcgc ttccaatgt 1260
tagtatgtat gtaaacatga tagtacagcc atttttttca tatgtgagta aaaaataaat 1320
agtattttta aaaatatata aaaaaaaaaa aaaaaataat tttttgttc agactttttc 1380
caaaaatcta aacataatta atatactctt tcagccacat gaataataaa tgagtgtttc 1440
ttgtaaa

```

(2) INFORMATION ON SEQ ID NO. 9:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 671 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

agcgcggtga agcgggggtg ggatctgaac atggcggcgg tggtagctgc tacggcgctg 60
aaggggccggg gggcgagaaa tgcccgcgtc ctccggggga ttctcgagg agccacagct120
aacaaggctt ctataacag gaccggggcc ctgcaaaagg acagctcccc agaggccaag180
gaggaacctg aacctctatc cccggagctg gaatacattc ccagaaagag gggcaagaa240
cccatgaaaag ctgtgggact ggctcggggc atcggcttcc cttgtggtat cctctcttc300
atcctcacca agcggggaagt ggaacaaggac cgtgtgaagg agatgaaggc tcggcgagaa360
atgcggttgt ccaacacggg cgaagtatgag agccagaggt tcagggtctc ctcccagagt420
gcccgcgtcc ctgattgttg gtctgggggt cagacctgag gagcgctgcg accctcttag480
gctattgact gttaaagctc cagggtttgg ccagattcca gttcgtgctt ctgaggtcca540
ccagaggggc catgaagccc aggcgtgtgc caaacctcac cctgccccac accaaggagc600
ccaccaaaag caaataaagt tattgagtgt tttagtagaa ggaaaaaaaaa aaaaaaa660
aaaagtcgac c

```

671

(2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 803 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

gaagatgagg tggagaaga gtcaacagct ttgcaaaaaa ctgacaaaaa ggaattttg 60
aaaaaatcag agaaagatac aaattctaaa gtaaaaccca aaggcaaatg tcatggact120
gggtctccgga cactgtggcag atggaataat tccagcaatg atgaaagtga aggggtctggc180
agtgaataat catctgcagc ttgagaagag gaggagaaga aggaagtga agaagccatc240
ctagcagatg atgatgaacc atgcaaaaaa tgtggccttc caaaccatcc tgagctaat300
ctctgtgtg ctctcttgca tagtggatcc cactactgct gccttcgccc tctctgatg360
atcatccagc atggagaatg gtcttgccca ccttgccaac ataaactgct ctgtgaaaa420
ttagaggaaac agttgcaggg ttgggatgtt gccttaaaaga agaaagagcg tggcgaacga480
agaaaaaagc gcttgggtga ttgtggtatc agtatgaaa acatcattcc tccacaagag540
ccagatcttt ctgaagatca agaagaaaaa aaaaaagatt caaaaaaatc caaagcaaac600
ttgcttgaaa ggaggtcaac aagaacaaag aaatgtataa gctacagatt tgatgagt760
gatgaagcaa ttgatgaagc tatgaagat gacatcaaaag aagccgatgg agggaggt720
ggccgaggaa aagatattcc caccatcaca ggtcatcgtg ggaagagcat ctctactatt780
ttggtgaaa aaataataac gcc
803

```

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 828 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

agcacttcca ggctgggggtg ttgttttga ctggaagaag gagcgccgg gcgaaggcac 60
gtcgagcggg ggagcgccgc tgccgttgga gatcccgcca ggcgcagcagg attcgttggc120
tgccgtcccc gctgctgtgc attgggttaa aaacgacaa caacatcagc catgaaagt180
ccaagtccga gcagtactag cccaagcatc atcaatgaag atgtgattat taacggtcat240
tctcatgaag atgacaatcc atttcagag tacatgtgga tggaaaatga aagaagaattc300
aacagacaaa tagaagagga gttatgggaa gaagaattta ttgaacgctg ttccaagaa360
atgctggaaag aggaagaaga gcatgaatgg ttattccag ctcgagatct cccacaaact420
atggacaaaa tccaagacca gtttaatgac cttgttatca gtgatggctc ttctctgaa480
gatcttggg tcaagagcaa tctgaatcca aatgcaaaag agttgttctc tggggtaga540

tacggaataa tttagatga cggggccctc tttagtgga ttagcacaaa ttccacact600
gtgaagccag tattagaaga cttaattgta aaagctctct tgctactgtg ttacacttat660
gcatcgcaaa agttttttgt agtcttgcat gcttaataaa agtgctcgga cactgtttac720
ctaagtaaaa agcctggtcc aaacccatctt actgggaaaa taggatggg gccccatggc780
cttgatggtt ggaagaccgc caaggggaag gaaccaccag gcccaagt 828

```

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 552 base pairs
- (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

ttggtttccg ggcgcaacca atgtgggagc tgaatagta agagcttctt aaccaaagct 60
tggatattacc gtgtgggggt tcgttttttt cgtgggggtt tatitgattt tgattttttt120
ttcttttatg tgattctttg gaaaacacat tcagaattat atctcgttct tctttaaagt180
tagtgcttag ggttaatttt ttgtactgaa gctcttattg gtgggtgcat gctactggga240
acaagttttt gtacaaaagc ttcaatcaga atcacgtgct gtttgggtgc attactgaga ctctgtttat300
cattagcctt cgtccctccc cgcagaagac tgttggatgt aacaaaataa tatgtatttt360
gatttactta aagtgcctgt aaatttctta gggacctgcc accttttgact gtggatcagt420
tgatgtacac ttgtattatt aaagcactca ataatcact gtggctgata actgcaaaaa480
tgggaacccg acatttgctt tgtgtcctgg tgaccgctgt agccctacgt gcagtggagg540
cttgctaat tc

```

552

(2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 993 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

ggcgatataa tatttaattt atttttttta cttataggtc atgttgatgt ctatgataaa 60
cagatgtttt gccctcgaca gcagaaattc ctttcatttt tctcattcgt ttctcttggt:120
gggttcattt ttttgaatca accacacttc attatttcta ttaagcaatt tgacaggact:180
gttgtagcct gcagtgtagt aaaccttttc atcgaaaact ttccactctt cctttaaaat:240
gcttgctaat gtcaaaaagt gtctcttgat cttttgggca ctgaaaaatc catcgaaaag:300
ccgtacaaac acagtcatct cggctctatc ttcaatgaag acatctgact ctaaaagcct:360
gggtggatca aattgctggt cagagggaat atcacgggaa atggtaatgg tagactcact:420
aaaaggacct gaaccaggct ccacgtagct tgtcactgga gctgtcatct tctatttcat:480
ctctttctcg tttttgcttt gaatgtagct gttcagtttc gtaaaagccg tctggatggc:540
tgaattccag tccatagact ccacggagct gctgacccac ttggctgggt catagtgtc:600
gatctcataa cttccgggct gggggccggc gtccctccgg gccctccagg ccggcgctc:660
cacagccttg gccgcgcgct cctcgccgcg ccgggggtct ggctggagcg gctcgggcat:720
ggcgggcggt acgctctggg agcctgggta gccgcgcaga ggccccgcac cccggggccg:780
cccgccctgc tgtgcgcgcg ccgcgcaggg ccgcgagtcg cctccgcaga cccgg:840
cctccccggc gggctggaga cccgagccca ccgatgcgt ctgctctgg accgcaggg:900
ggcgcccgcca ccaaggcggg gccggctcac gaccccgga agctccggcc ggagtccgc:960
gtcctgcccc cgcccccccg cggcgacagg gag

```

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ctggacctta gaaaaaataa gaaaaataca aaaaacaaaa aaacaaaaac aaaaaaagaa 60
ggaaaaactt ggagggtggg cgtgggaact caggaccoca gagtggcgag tgggtggggg 120
agggagagcc tctctcccccc ttctctgtgt gagaggaaact cttagtgtct ggtgcagctca 180
ttaaattgtgc aatgtgtcaa gtatgttgtt ttacacgcta caacatagctt catttgaac 240
ccattgtata agctgtgtat ttacaaatat aacacacaaa tttaactttt ctttagaata 300
caaaaagtca tgcattgtct ggggaaactat atgcttttcc atttttaagt caggtagctga 360
atactgattc cagttaatga gcagctaaaga tccaactctgt ctaataacagt gacccccctag 420
ccactcgggc ctggcaatat acaatttttt ttccccctcca agtttgttaac acctccccctc 480
cagaaaggca ttgtgcaaca caggattatt tttaaatgat cctgaatttg aattaacctt 540
tgggagaatt ctgtgatgcc cttagaagaa attggacacg tatttgatgt cacaaagctg 600
gggctgggaa ttgctgtgtc aatgtttcat tagacttaag aacctaaaaa ttttctcagt 660
tgggtggata aaacccactaa cgttagaaaa ctgttttctc atgcagctat gtttctctta 720
tttatgcctt gaggactaat ttctggtttt ctatgtgtta atgcactgtt gactctcata 780
atggtgcctt acgcaagcga tcccttctgt ggggtgtcca tacaggggtg tgggcgagtc 840
atgctttatt aaggctcttg ttccaactgg cagtgtactg tatcaacgta taatcacaga 900
aaaaaatctc tttaaggctc tctctcacaa agacatagag tgaactctcc ttacatgtc 960
agattttgtt caaaccttta ggcaacttga ctgtcagtgt taaaatggaa aacaggaaaaa 1020
tggaaaaaat tgaccaaattc tgccaccttg agactttcat atagactctg cacacaattt 1080
gtatagatca cacaccggct gtatttaata ttgaacattt tcacacatat taaagatcac 1140
gaagtattaa aaacccccca atgtttaatgt atttgcttaa aaggcaacaa ttccacata 1200
ctgtctagct atctgttgtt aatacacgaa tataactact tttttaaaaa agtgggcaga 1260
attcttgtgt atgtataatt gtgtgtacag tatgtgtatg tgtgtatata tatatattat 1320
atatatagat aatatataaa tatttttttt aaggagaaaa tagaatgttt agctagaaaa 1380
ttccacagcc tgtgaagaaa tatttcaaaa tgggccataaa ggaggtaaaa atgaaaaacc 1440
taacctaaat tttatagagg ctttatcttt taatttaacga tgtgcggagg actttctgt 1500
ctgaactctg tccgggctgt ctgctctgtc catcaaatgg gcaggctcgg aatggggcac 1560
cttcggccgt tcagaagtgg cctgaacaga atgtcggaac ccaggctgga atcggcacac 1620
ctaaaggatt gattttgaat ttcagcctta ttagaagatc taacctaaag gtaagctaac 1680
cacaggattt cttttttaga acacttttta tgcagatgaa gctatttttt ccagcaagta 1740
gtattctcca gtttttccaa ggagtaattt ccccgaaatt gcataccacg cgttggaagc 1800
cagatatctc accoagctgc tggcttgtgt gtgtgtgtct ttgctttata tatatatata 1860
cacatgtgag tctgggtctg ctgttatatt gtttgatctt cctggaaatg agcagtgaat 1920
aacgtctaca taactggttt tttttttata tgggctgatg aatacattta cctaagaaac 1980
cttatttgtt ttaactaaga ggggaagtgc agttttcttt tggcagttca gaatccaagc 2040
acttgattct ctgggttttg aaaaactcct ttttgacctt ctatgtgctt agccataaca 2100
attccattaa gcaagaaagt aagcaaaaaga caaaaaaaa aaagggaaaa aaaaaaaact 2160
tgcaccgggt tcttccactt acgaaaacatg tgcctgggtt ggggtgggtt 2220
accgtacctg tcaatgcctg ggattttcca taaatttagc acgggacata aag 2273

```

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 986 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

gcgcgatata aacagttgga agagaaaaatg gtacagcagt tacaagagga tctggacatg 60
gaagatgctc cttaaaaaatc tctgtaacca tttcttttat gtacatttga aaatgccott120
tggataacttg gaactgctaa attattttat tttttacata aggtcacctta aatgaaaagc180
gattaaaaaga catcttttcc tgcattgccat ctacataata tcagatatta cggatgttag240
attgcacttc agtgttaaat ctttactgat agatgtacct aagtaaatca tgaataatct300
acttgttaact atagaagtga attgtggacg taaaaatgggt gtgctatttg gataatggca360
ctaggcagca tttgtatagt aactaatggc aaaaatccat ggctagtgat gataaaaaa420
aaatattctt tgcaagtaaaa tattcccttt gttaattgta tagaaggggg gatcaaaaa480
ggaactaaca atttgtatgg cagtgtcaga tattttttat ttagtatttc ctgttttgg540
ttatttgcac cttagaagag cataatgaca ttgtttgat aagcctaatt atgctggact600
gttttgacct ggtttaacc tcttgatagg tagtttgga tgctggggat gagaactgaa660
taactctttg ctggagtgac actcacctct agaatttcca ctttgagaa tactcagt720
caacttga ttcctgatag aacagacttt acttttctag ccagcacttg atctagaagc780
agaggaatcc cagcgccttt taaaagtgtg tatgtgggtt tcttttaaaa agctcctcgt840
tttggaaagt agaatttatg ggtacaacgt atgttcatta tttgtacata aaataaaacc900
attttaaag ttaaaaaaga aaaaaaaaag gggggaaaaa aaaagagaaa aaggaaagg960
aaaaagaaaa agggggggag aagaga                                     986

```

(2) INFORMATION ON SEQ ID NO. 19:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 526 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

gcgtctatat tacatttatt gacactggat atttattatc tgttatatac caggcaaaaat 60
ggacacacca tcaggagata agacctgtat cttacgtgta agatgaaact tatgcaaaag120
gcacagaaca aattattttgt tcacagttac ttttaactct ttcagcaatg cctgagtcct180
ctttatagaa acctcatcttt gctaagttag caaccattca tttttttggt tactcttcat240
gtatagtttt ctcaagtgtc tcttcaaata ctgcataatg gtatagacca tttaatatcc300
caaacataat ctgaaagact agaggaatcg ccattaattt catttggttt tgacaaagcg360
tcatccaatg gattaaaacc ctctcttttg gtggcagtgg aacggtatga tacctaaaaa420

gaaaaaagag ttaatcacct ctcttgata tgaatgctat tagaagtttg ttgactcttc480
ctaaaattgat aattgccttt ctgacttat aatgtagaga gcaaaa 526

```

## (2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1765 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

tttttttttt tttttttttt gctgtttttt atttattttg gatgtttgtc aaataataat 60
tttttttttt aaaaattctcaa aacatgtttc aacacattca gtgcaaaaga tccaccattg 120
gtcacacacat taagaaagca caccacacatg gcttctagtt gggcttaatta aaatctctat 180
gggtcgaaag gtggttgggt gtacttaatt aagctttttt gaagtgcata gctatgcata 240
acagatgaag ttgaaagctg cagagtttaa gatagactta atttttcatt attttcccaa 300
agccagtcatt gatatttatt taatttgggt tcttcagggt gcaccaatcc catgaagctc 360
aattggatag ttccactgct ttgtcaggta ttctctgag aacttgacaa tgggtttttg 420
ccgaagatcg tagagaccaa gaggttttaa aagttctgac acatctctcc agtctgcggt 480
tttctctacc tcagctgaag gatactttct cagaaccttc caaagccagc gtattgccat 540
ttgtccctgag gtccactga gaaataatag agcgtatgaga agcttccatg gatcatgaaa 600
aagtgttttc tgaacgagat taaaagggtc ccgaggaggt gtccatttct taaaggcttt 660
acgtcgtggg gggctaaagag cttctttgtt atatttctg gaaaaataca ggtgtgtttt 720
ccttctttct atctgtgttc gtgggaggtt atcttcagtg aagtcctttc tgggttggtga 780
gcagtgtgtt tccatttcag agccacgttt taaaatgtca gtatgcacaa gtctcttctt 840
ttccacaact tctacttttg ttccgatttc ttcatagttt aaaaaggtat cctcatactt 900
ctcgttgtgt tctgagttct tggctgaaca aaatttgttt atgatgccag aagttttttg 960
ttcagaacaa aaatttgatc ctgaactcaa tgacttttct ttttttttta caaggctgtt1020
ttcttcaact gtccactga ggggtctcacc acatgtctca gcacagaaa tgcagacagt1080
ttcttcaagc tgactttttt gtgcaacagg ttcaacttca gcactctgctt tattcacacac1140
agattctctt ttgctatcac ttgcaacaaa acctgaacag ctcttctcat attcctttttt1200
agttttctta attgggattc ctttcaaaat agtcaccttt cttttgggct ttctaacctt1260
ttcgaagtta acatcatcaa caccctcatc ttctttcaaa agcaaatgag tggaaagtaaa1320
gttagagagt cctctgctct cctgcaactc tgaactacta cttggcgcca taaacacatc1380
ctttttgcac ttgcttcggg tcttgaggtt ccagtttgaa ttgttacttt ggtttttaga1440
atgggatgtc agggctgcga tgctgcagtc ttatatctt gacttgatac cctttttaga1500
aagtacagta aaatcaaaat cttctggctt aagagaagtc ttccatttt ttgtaagata1560
attagcaagt gaacttttgg atctgaactt cagtccttgt gggctagaaa atgataataa1620
aggaaactta ctgctagtaa atagaaggga cttttaaaag aactggacca catttcagat1680
ttctaattaa ttccaaatg ttgccatagg tatctgtcat ttaaaaatga aaaagagtga1740

```

taaatggcac ttttaaatgg ttttc

1765

## (2) INFORMATION ON SEQ ID NO. 21:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gttttttttt gttttcttta aatttggatg tctctacacc actcctgatt tgtaggacta 60
aatagatcta ttatttccaa tgc aaattgt gtaacattta tttcttccctt gatttttaaa120
aatacttttag tattcttaac tatgtatgtg ccttctctta cactgagttc ttttttgc180
ctttcagctg ctccacacaat cctgtctgtt ggagtcatag ctgctaatto catattattt240
ccttcacacac ctggaacatt tagtgtatta ctggtagccct tctgtgttcc aggaaca300
tgaattgcaa actggacttg taacaggatc atacatagag caacaaatta gctactggcc360
ttgtaagata gtaagttagg aatttcacag tcattgtctcc aaatttctat gcagattt420
aaaaacaata taagactgtg gtaaggtaaa aacgcaaatg caatttgcgt tgactaattt480
cctaggactt atttccctat gtaaaacccc tgttcttctt ttcttgccac aagacagggt540
acaaagcttt ctaaaacatg ccttcagggt tccacacctg agacattgct ttgtggatac600
cttcaaaagt gtccaacaa gcaaaaaatc agaccataat ctaagagcaa gtaacttata660
cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaaa gtaagctttt720
tgttaaaata ctaaaaaat agccgc

```

746

## (2) INFORMATION ON SEQ ID NO. 22:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agcagactca caccagaact acattccctg gccccctgcc tgtgtgtctc tggccaggcc 60
tgggttgcca agcttgaccc gagaaaaagga tctgcagaaa atcagactat: gggatcactt120
tgtttgtgca ttgggaatga cattctttcc caccocaggga aaacctttgg gactttcaga180
gacattgtgg ctaggccaacc acatgggtcag cctcaaaagt gaggaggctca gtaacccctcc240
tatccctaga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc300
tgtctctctc tgggaagtatg ctatgtgtgtg tatattctgc atccaaagcc agagggaacc360
acaaagacta gtaaaaacggc ggtctccaatg cccacttagc ctctgcctct gaatttgacc420
atagtggtgt cagctcgata gagcgggaag aagaataatg cattttttat gaaaaataa480
atatccaaag gaagatgaaa ctaaaaggag aaattgaaat caattctactg gaagaaaaa540
tccaatctct gaaastgag attgctgaga agcaaaagca aatttgtgtg acccagaaat600
tactgcagc caagaggctcc ctggatgccg acctagctgt gtcaccaatt cagttttca 659

```

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 357 base pairs
- (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

cgcagtgcgc agccgtgggg ctctctcctt gtcagtcggc gccgcgtgcy ggctggtggc 60
tctgtggcag cggcgggcggc aggaactcgg cactatgagc ggcttcagca ccgaggagcgl20
cgccgcgccc tctccctcgg agtaccgagt ctctctcaaa aatgagaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcattcctt gtttttggac240
acagtcctctt taccagagtc agctagtctc acatatgaat tttcttatat gtctctcaac300
aagtgcttaa aatgcctcgt tgtgctgtga gtaaaggctc gttgattagg ctggggcg 357

```

(2) INFORMATION ON SEQ ID NO. 24:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 890 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

cgtaggcagc ggaagaagcga gccaggccgc tgcgcgcgtg gaagagtagg ttcagagtag 60
attccgggac ccggggcgcg gcgcactgcg caggccggccg gactccgctc agtttccggt120
gcggcggaaca ccaaaagtcgg ggaacttaag catcttcggg ttctaggggtt gttacgaagc180
tgacggagcg agatggaggt ggaagcaccg ggtgttgatg gtcgagatgg tctccgggag240
cggcgagggtc ttagcgaggg agggaggcag aacttcgatg tgaggctcca gcttgggca300
aatggggttc ccaaacacac ctaactgggt gacctctggc ttttcatctt ttccgatgtg360
gtggtgtttc tctttgtgta tttttggcca tgactgtgtc gctgatatct aaataagaa420
gtggtgtttc gagtgaattc tgaaaatggc taacaaacttc tgataaaaag aagacagga480
tctcaataga aqaatttcac atctccaaag gacctctctc ttcattttac actttgttac540
taatttgcag aactctatta attgggtagg atttcaacca tctctagcta agtttctaaa600
attaaacccct ttggttcgtg tttaaaaact ttcacacatc tgatgggttt acagggggtt660
aatataaaaag catctgtact taagggtctt ggtatttcac taagaaatat agtaatgtct720
tttaattgttt taagaggtga tcagggttta ctatggatgt caagtaatat ggaatgata780
taagggggaag gtttttatgg aattcaaaa gtaaatttat tcaaaaagcg ggggaaagg840
ttttgagagg agggggggccc aaggtgttcc tgggggttgc cgaggaggcg 900

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 651 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

gccgtatatt gcatactaca tcagcaaaaag gtgttcgcgc tttataagcg ggcgctacgc 60
cactctcagat cgtgggtcgt ccagagagac aaataccgat actttgcttg ttgatgaga120
gcccggctttg aagaacataaa gaatgaaaag gatattggcg agggccaccca gctgctgaag180
gaggccgaggg aagaattctg gtaccgtcag catccacagc catacatctt ccttgactct240
cctgggggca cctcctatga gagatacgtat tgctacaagg tcccagaatg gtgcttaga300
gactggcctc tttctgagaa ggcaatgtat cctgattact ttgccaaag agcaacagt360
agaacacgcg ggagggaagg ctgggaacga gagggttaagc agctgcacga ggaacgcga420
ctggggggctc ctttaactga agctttgccc cctgcccga aaggaaggtga ttggcccaca480
cttgggtgtt atattgtgac cagaccgccg gaggcgccca tgtagaaaga gagagacctc540
atctttcagc ctggcaagtg aaatatgtta cagaacatgc acttgcccta ataaaaaatc600
agtgaatagg taataaaaaa agtgccattg tagtatgc aaataagcgg c 651

```

## (2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1256 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctcgagccga attcggtctg agcttttcac tgaccatcca tatccaatgt tctcatttaa 60
acattaccga gcatcattgt ttataatcag aaactctggt ccttctgtct ggtggcactt 120
agagcttttt gtgccataat gcagcagtat ggaggggagga ttttatggag aaatggggat 180
agttttcatg accacaaata aataaaggaa aactaaagctg catttggtgt ttgaaaaagg 240
ttattatact tcttaacaat tcttttttca gggacttttc tagctgtatg actgttaact 300

aaactatcta aaatagagca ttttgggtac ttctcatcga ccatccatat ccaatgttct 360
cattttaaca ttaccagaca tcatgtttta taatcagaaa ctctggtcct tctgtctggt 420
gtgacattaga gctctttttg ccataaagca gcagtatgga gggaggattt tatggagaaa 480
gggggatagt ccttcagacc acaataaata aaaggaaaaac taagctgcct tgtgggtttt 540
gaaaaggctta ttatactttt taacaattct ttttttcagg gacttttcta gctgtatgac 600
tgttacttga ccttctttga aaagcatttc caaaatgctc tatttttagat agattaaact 660
taacccaact aatttttttt agatcgagtc agcataaatt tctaagtcag cctctagctg 720
tggttcatct ctttcacctg cattttattt ggtgtttgtc tgaagaaaag aaagaggaaa 780
gcataataga attgtactat ttgtaccaas tctttgggat tcatgggcaa ataatttcag 840
tgtgtgtgat tattaaatag aaaaaaaaaa ttttgtttcc taggtttgaag gtctaattga 900
tacgtttgac ttatgatgac cattttatga ctttcaaatg aatttgcctt caaaaataat 960
gaagagagag tgcctctctt tctcttttta agtgttcagc tgtggcargc tcagagggtt 1020
ctgctgggat caagctggag cgtgtgtata cctctttttt tcagctgttc gtcctctctt 1080
ttctttgatt caccaaagtg gagacaaata catgatctca aagatcacac gtacctactt 1140
aatttcagct gatggagac caaagaattt gcaagtgat ggtttggtat cactgtaaat 1200
aaaaagaggg cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 1256

```

## (2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 694 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtttcraaag gatgtgtaag aaaccagagg taaagggtctc gcgatatctt aagacatccg 60
gcgtagtaac cttcagtgag ccacagcgct agagaagtag gagaagctcg cgaatctgr120
gcccttgccg aggaagactag gagggggagg agagggggtc tcgcgaaag aaagaggtcg180
ggagcgctcg cgaatctctg gaccacccaa cctgaaaggt gcttaggaag ttgaaaggcc240
cagaggaagc ctcggggcaa atggccggag ctggaccgac catgctgcta cgagaagaga300
atggctgttg cagtggcgt cagagcagct caagtctgg ggattctggac ggagagcgcg360
aggaactcggc ggctgagcgc gccgcacagc agctagaggc gctgctcaac aagactatgc420
gcattcgcat gacagatgga cggcacatgg tcggtctgt cctctgcaat gaccgtgact480
gcaatgtcat cctgggctcg gcgcaggagt tctccaagcc gtgggattcc ttctctggcg540
gggagccccc tgtgtggggc ctggccatgg tacccggaca ccacatcgtt tcaattgagg600
tgacagagga gagctgacc gggcctccgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaaa aaaa 694

```

(2) INFORMATION ON SEQ ID NO. 28:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1927 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ggagagtattt attttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
agcctgtttta acttttgata caaagtaaca ttttagtaca gaaaatccca gtcgtgcagc 120
tcagtagcttg tctgtgcaca ctgtaccatc tcagtcaccac tctgctgtga acttagaaaa 180
cagccctac cccagagggt tctgcgagtt aatccttga gaatagtcta cagtttttca 240
tagttgtct gagctagaaa acttgtaact gtaaaacaaa ggacagcatt gaggactgaa 300
acttgtctct tttttgaaca actgtgcaag aaaaatatac cttttttaaa aaacatcagt 360
tatggctaaa ctacaatcta gtgtctagaa ttacaaagaa taaatgaaa tcaaagattt 420
ctcgttagta aaatgaaagt ttaggaacag tattaataa taggtctcac cccaacgaca 480
cttacacaga gccacgtaca gtacctatta ttaacaggac gcatagctta aggaggaacc 540
acatcaaatc ttacgcccaga catatctagc ctacagagtg caaaaaaaa aaaagccccc 600
aaacgaagac acccacactg agtaggggtg atgcctgtag tgctgtaac aagattaaaa 660
agacctcagt tttcttttt agactgttga tagtgacaat aaccattatg ctccccctaa 720
aagctctcaa ttcaatgtct gaaacatgaa tgttttcata tcaaaaagaa ctgatgtacc 780
tgccaccctc taaaaagttt aagaattacc ctgcaaacat tgcaactgatg aaggctgtca 840
cgacttacag agcctaagga ggacccaatg gcaggcatca gcacagctga acaccacctg 900
gacccacactg cagccctgac cagcgagctc tcacggagca gacacagctc tcaagtaata 960
agcacagatg gaggagaaac gagaggctgt ggaaggcagg agagaaaggc cgagagacga 1020
gtttgtgaaga atgcaaaagt cactctcccc attgtgggag gaaaatgcca aaggcactgg 1080
ttctgtctgcc acaggcagtc tgagcacctg gagtgtgtac gtccttccag gagagggtgc 1140
accaagggagc aggaggtttt tcaaaagctct ggtccaccaca acaagaacct cccaagcaal 1200
agcagccccc attgaggttc caaggtcgtt ttgctgaaga cgggaacgaa accaacacca 1260
aagcgacagc ggggtgacag aggggacagg ggctgggacac cggcaacatg gagccgttca 1320
agtaaacata aaccacaaaa tacttagaaa aggctgttaa acgagtgatc cgaaaagttc 1380
tctttgcagc atctctgac agctggctaa agaaaagggt gtgctgaacc cgtctttagt 1440
gttatctgtt ttgtgttaaa gcacacgtgt gacacgggca gagtgtgtg gccctgggct 1500
ggatcgacgc cagccgtggc cctctgtcta caaaggaggt gcttctgggt cctgggtccg 1560
gatcctctcc ccgcattgtc atagacggac agaactctac tttcagtgc tagaaaagag 1620
ctgagttctg ttgcccccca ggccggccagc tgcagtcac caccagcacg cattctctca 1680
gagcgggcag gctggaatcc acaggacttt attttgttct tgattgacca tgccaagat 1740
ctgagtgcaa atgcttgaca gggctctccc ctggatgacc cctgcataaa agccccccag 1800
acacgtcatt cagctcagag taagacccca ggttgaggc aaggcagtac agcttgact 1860
ctttctactg tgtggctgtc tgctttgtgc tccttgccac tctgtccat cccaccctga 1920
ctctect

```

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 672 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```

gcctttttat tttttttttt tggctggtat gctgcattta ttatgagaat caacagtcac 60
cagttaatga ttgactaact cttgttggtc actctggaca ttaacgaaaa agactggaaat 120
agggctacag cgctgctttt atgctacacg ggttatgctt ggactctgac tccacgacgc 180
aggtagattc aggaattcat ggcagtga ca ttcaccatca tgggaaacac cttccctttt 240
cttcaggatt ctctgtagt gaaagagaca cccagtggtg ggctgaaaa acctgaaagt 300
agggagaaga acctaaaaa atcagtatct cagagggttc taaggtgcc aagaagtctca 360
ctggacattt aagtgccaac aaaggcatac ttctggaaac gccaaagtaa aactttctaa 420
cttctgtctc tctcagagac aagtgaagct caagagtcta ctgctttagt ggcaactaca 480
gaaaactggt gttaccocaga aaaacaggag caattagaaa tggttccaat atttcaaac 540
tccgcaaaac ggaatgtgct tcccttgccc atttagggtt tcttctcttt cctttctctt 600
tggttagtct tctgtctctt ttccagtttc catcagatct cccctctgtg ccactggaat 660
ctcagaggtt gc

```

672

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

ccgcattccta gccgcggact cacacaaggc aggtgggtga ggaatccag agttgccatg 60
gagaaaattc cagtgtcagc attcttgccc ctgtgggcgc tctctacaa tctggccagg.120
gatagccacag tcaaaccttg agccaaaaag gacagggaag agtctcagc caaactgcgc.180
cagaccctct ccagaagttg gggtagaaca ctcatctgga ctcagacga tgaagaagct.240
ctataaaat cgagactagc aactaaccc
                                         269

```

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 604 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

tgcgaggggc ggatagctgt ccaaggtctc cccagcagc gaggagctcg cctgctgcc 60
tcttgccgcg gggaagcagc accaagttca cggccaacgc cttggcacta ggggccagaa.120
tggctacaaac agtccctgat ggttgccgca atggcctgaa atcccaagtac tacagacttt.180
gtgataaggc tgaagcttgg ggcattctcc tagaaaaggt ggccacagcc ggggttgtga.240
cctcgttggc ctccatgctc actctccgga tctctgtctg caagggtgcg gactccaaca.300
ggcgaaaaat gctgcctact cagtttctct tctctctggg tgtgtgggc atctttggcc.360
tcacctctgc ctctcctcgc ggaactggag ggaacacagg gccacacgc ttcttctct.420
ttgggattct cttttccatc tgcttctctc gcctgctggc tcatgctgtc agctcgacca.480
agctcgtccg ggggaggaag cccctttccc ggttgggtgat tctgggtctg gccgtgggt.540
tcagcctagt ccaggatgtt atcgctattg aatatattgt cctgacgatg aataggacca.600
aggt
                                         604

```

## (2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 781 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ctttaatgtg cctagagcaa tggaaatgggg cactttgggg ggggtggaat tcaagacgct 60
ctggctgaag attcagaagt atcgggtaac tctcttttcc ttctgggcat cctctctctt120
gttctaattcc tcccttacac tcattctctgg tccattgtat tctgaccaca tcccttaatca180
tgggtcaaac tattgagtc tgggcacatt ggtcatgaa gacacagaag gcaatgagag240
actctcatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaa gggccagcac300
tggccaagct cttatgcttg ctctgaaacc ttcttgggag gagtcaaat ggtctctctt360
tgaaaagtgc cctggccttt tgagaaaagca gtgtggttga gggagatggt tctggcaggga420
gacctgaatg gttgttttct acttgggatt tcttctctgc tttaggagat ctattggaaa480
actctattata accactcggg caccatcgat gccacagaga tgaggacagc cctcaggga540
gcaggtttca cctcacaacg ccaggctcag cagaccattg cctcgcggtg tgcggtcagc600
aagcttggca tcaactttga cagcttcctg gcttgatga tccgcctgga gacctctt660
aaactattca gccttcttga cgaagacaa gatggcatgg ttcagctctc tctggccgag720
tggctgtgct gcgtgttgg ctgaccgcc aaacttgacc tagaagatgg ggggggcctc780
c

```

781

## (2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 304 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
ggccactcgc gcgagacggc aggaactgtc gctcgtactc gtgcgctcgc ctttgccttt 60
cctccgcacac catgtctgac aaaccccgata tggctgagat cgagaaattc gataagtcca120
aactcgaagaa gacagagagc caagagaaaa atccactgcc ttccaaagaa acgattgaac180
aggagaagca agcaggcgaa tcgtaaggag gcgtgcgcgc ccaagtatgc actgagatgc240
gagaagtgtt gcctcgaaat tacctgcttg agggggtaaa gttgggaagg tggaaaaagg300
gtgg
```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1528 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
aattcggatc catgggccac agtggatggc ttgaaatgtg gctgagcgct tcggacactt 60
cggtaccatg gtggccaccc caagacgcgc cccagcccgc catggcccgc atcctccggg 120
atcctgcctt ctgtccctgc tcttgccggg gtttgttccg ccggccggg gacaagagaa 180
gtctaaagaca gactgccaat gcggtatgag tggtagcatc tacgagtatg gagccctcac 240
catcgatggg gaggaataca ttctttttaa gcagtatgca ggcaaatata tctctttgt 300
caacgtagcc agctactgag gtctgacaga ccaatacctt gaactgaatg cactacaaga 360
agaacttggg ccatttggct tggtagctct gggcttccct tccaaccaat ttggcaaa 420
ggagccaggc gagaactcgg agatactccc cagtctcaag tatgttgac cagggtgggg 480
ctttgtgcct aatttccagc tctttgagaa aggagatgtg aacggggaga aagacagaa 540
attctacatt ttctgaaga actcctgccc tcccactgca gaactcctg gtctcactgg 600
ccgctctctt tgggaaccaca tgaagatcca tgacatccgc tggaaacttg agaagttcct 660
gtgtggggca gatggcatac cgggttatgc ctggtaccac cggaccacag tcagcaacgt 720
caagatggac atcctgtctt acatgaggcg gcaggcagcc ctgagcgcca ggggggaagta 780
actgagtcgc ccaacctacc cctaccacct gcccatcatg caaggccgga gggggggctc 840
ttcaggaaag aagccacatt cccagtcatt ctacccccac cccagattct ctttcttatt 900
acataaaaga caagcctggc acaactgtgt gtctgaacca ctgtggacac gtgacaattg 960
```

```

ccccagtgctg  tgcattggccta  cacagcccaag  tatctgccttg  ctgaaacccc  agggatggtc:1020
catctgctgtt  tacggccttgg  cacaacacccc  tcatactttt  ttcagctttc  tgttccaaat:1080
gagcccaaaag  gaaacacaaag  ttctaggctcc  aatgggtcttg  ctcaaaccttg  aacatctatt:1140
ttggggccaa  catctccccc  atgcccacac  tacacacccc  cagcctcctt  ctctctcctt:1200
gaagtagccct  cctgagccccc  caagcccaatc  ccacagtgtct  cctgagacca  gccaaagacaa:1260
ctgttagcgc  catggcccttg  taacccaggtt  cagggttggt  gtctctatga  aggaaggggct:1320
cgaagccctt  gtgggcgggc  ctcccttgag  cccgtctgtg  gtgcagccc  ttatgctatt:1380
caggtctagg  ctcccaggcca  ggaacactac  cccgcgcctt  ctggagacca  tgcctcctct:1440
tcactctgtc  cactcgtatc  tcaacacccc  catctgcctc  gtaaaaggtct  ttctgcagca:1500
aaaaaaaaaa  agaaaaaaaa  aaaaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

ggcaggcttc  agcgtctctc  cccctgctcc  gctcctctgc  agggcccagg  cgcctctggc 60
cttaggacc  aacttctctt  accgccatgg  agttcgacct  gggagcagcc  ctggagccca:120
ctcccaagaa  gcccggtgtg  gggcggggcc  acgggggaga  tcccaagctc  agtccccaca:180
aatctcagg  ccggtcggag  gtagggcgag  gtccgggtcc  aaagcaagga  caccacagct:240
cttccgact  cagcagcagc  tcacgcgatt  cggacacgga  ttrgaagtcc  cagctcgtc:300
gctccaaaga  gcacgagagc  atcccgggca  aggccaaaga  gcccaagtg  aagaagaagg:360
agaaggcaca  gaaggagaag  ggcaagaaga  aggaggtctc  ccactgaag  gccctggaca:420
gggtcatta  aacctctctc  tctgcctacg  agtaccaccc  acctggagct  aagatgctta:480
ggtgggggg  ggccgccga

```

## (2) INFORMATION ON SEQ ID NO. 36:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gggcaccctg tagttgggaa cagcggaacg ctggtcccg ggaactgagta aggtgtctgg 60
atcgaggga ggttcgggtg ggcctcgggc ggctggaaga gctcgactcg tcccgctggg 120
aaagcgcgag tctgagtgga accctggagc acttgacagag cggctggcgc agtcatggcg 180
gactactgga agtccacagcc aaagaaattc tgtgattact gcaagtgcgt gatagcagac 240
aataggccta gtgttggaatt tcatgaaaga ggaagaatc ataaggaaaaa tgtggcaaaa 300
aggatcagtg agattaacaa gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtgtg ctgcaatgga ggcagctgcc ctgaaagcat accaagagga tttgaaaaa 420
cttggtcttag agtcagaaat tttggagcca agcataaacac cagtaaccag cactatccca 480
cctacctoga catcaaatca acagaaagaa aagaagagaga agaagaaaaa aagatccttc 540
aaagggcaga tgggtagaag gcataacctc tgagggttac cattactatt atgatcttat 600
ctcaggagca tctcagtggtg agaaacctga aggatctcaa ggagacttaa aaaagacagc 660
agtgaagacc gtttggttag aaggtttaag tgaagatggt ttacactatt actataatac 720
agaaacagga gaatccagat gggagaaacc tgatgatctt attccacaca ctagtgatct 780
gcctcttagt aaggtcaatg aaaattcact tggcacccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg gggaaacagg aacagaagaa ggaggggtct ctacagagac 900
agaaaagcca aaaaataagt ttaaggaaaa aataaaaaat agtgatggag gaagtgaacc 960
agaaacacag aaagaaaaaa gtattcagaa acagaattca ttgattctaa atgaagaaaa 1020
atcgaaaact cttaaagaaat caaacccata tggagaatgg caagaaatta aacaagaggt 1080
tgagtctcat gaggaggtag atttggaaat tccaaagcact gaaaatgagt atgtatcaac 1140
tccagaagct gatggtggcg gagaacccaa agtggatatt aaagaaaaaa cagtcacttc 1200
tcttggaagt atggcagatg gagtggcccc agtctctcaa aagagaagaa cttgaaaatg 1260
ggaaaatctt aggaaaaattt aagggcaacg aggtgatgat ccaatagttt cgagggagag 1320
ctttttgtt acatgctttt tagggaccag aatggggaga ctttttgcca ccccccaagt 1380
ttgtcccggt ttttgt

```

1396

## (2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 808 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cctctgtcca ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacctc 60
ttggagtcct tctagctcct gccctagcta actataatat caacgtcaat gatgacaacal20
acaatgtctgg aagtgggcag cagctagcta gtgtcaacaa tgaacacaaat gtggccaatg180
ttgacaataa caacggatgg gactcctgga attccatctg ggattatgga aatggctttg240
ctgcaacccag actcttttcaa aagaagacat gcattgtgca caaatggaac aagggaagtca300
tgccctccat tcaatccctt gargcactgg tcaaggaaaa gaagcttcag ggtaagggaac360
caggaggagac acctcccaag ggcctgtgtg actcagtcac cccaacaaa gtgcagtacc420
tgagcaagtt cggaaaaaac attgcaaaaa tgtgtcgtgg gattccaaca tacatggctg480
aggagatgca agaggcaagc ctgttttttt actcagggaac gtgtcacacg accagtgtaac540
tatggattgt ggaacatttcc ttctgtggag acacgggtgga gaactaaaca atttttcaa600
gccactatgg atttagtcac ctggaatagc tgtgcagaaa aaatatgggc tccagtggtt660
tttaccatgt cattctgaaa tttttctcta ctagtattgt ttgatttctt taagtttcaa720
taaaatcatt tagcattgaa acggagaact ctgcgggcta gtaaccacaa ggtacggagc780
aaagatcacc cagggtgggaa gaggtgga

```

## (2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1139 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO



(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gcccacgcgt ccggtcgccg ccggcagcga acagcagcag cagtcagcct tcattcagga 60
aagcacagcca gttgctctca tgcgtttatt gtctttcaat gtgcctcata ttaaaaaacg 120
cacaggagaa ccaatatgga aggtactcat ttatgacaga ttgggccaag atataatctc 180
tcctctgcga tctgtgaagg agctaaagaga catgggaatc actctgcata cgcttttaca 240
ctctgatcga gatcctattc cagatgttcc tgcatatac ttgttaatgc caactgaaga 300
aaatattgac agaattgtcc aggatcttgc aaatcaacta tatgaatcat attattttaa 360
ttttatttct gctatttcaa gaagtaaaact ggaagatatt gcaaatgcag cgttagcagc 420
tagtcagata acacaagtag ccaaggtttt tgaccaatat ctcaatttta ttactttgga 480
agatgatatag ttgtattat gtaatcaaaa taaggagcct gtctcatatc gtgccattaa 540
caggccagat atcacagaca cggaaatgga aactgttatg gacactatag ttgacagcct 600
cttctgcttt ttgtttactc tgggtgctgt tctcataatc agatgttcaa gaggaacagc 660
agcagaaaatg gtacagtgga aactagacaa gaaacttcga gaaaattcaa gagatgcagc 720
aaacagttctt ttacagggtg atacacttgg agctggccaa ttcagcttcc agaggccctt 780
attagtcctt gttagacaga acatagattt ggcaactcct ttacatcata ctgggacata 840
tcaagcattg gtgcacgatg tactgtgatt ccattttaa acagggttaatt tggaaagatc 900
ttcaggagtg gaaaactctc cagctggtgc tagaccaaa agaaaaaaca agaaagctta 960
tgattttaat ccggttgata aattttggca aaacataaaa ggaagtccat tccagaagt1020
tgacagaatca gttcagcaag aactagaatc ttacagagca cagggaagatg aggtcaaacg1080

```

```

actttaaagc attatgggac tagaagggga agatgaagga gccataagta tgccttctgall140
caataccgct aagctaacct cagctgttag ttctttgccca gaactccttg agaaaaaaag1200
acttatgac tcccatacaa atgttggccac tgcgtttta gaacatataa aggcagaal1260
attggagcta tattttgaat atgaagaaaa aataatgagc aaaaactactc tggataaatc1320
tctctatgat ataactatcg accctgatgc aggaactcca gaagataaaa tgaggttgc1380
tctatctat tatataagca cacagcaagc accctctgag gctgatttgg agcaataa1440
aaaagcttta actgatgcag gatgcacact taactccttta caatatatca aacagtggaa1500
ggcttttaac aagatggcct cagctccggc cagctatggc agcactacca ctaaaacaa1560
gggtctttta tcaagagttca tgaatacagg atcacagttt gtgatggaa gagtgaagaa1620
cctgggtttg aaacagcaaaa atccacctgt tactcgtatt ttggacaatc ttatggaga1680
gaagcacaac ccggaactg atgaactatg atattttgat cccaaaatgc tgcggggc1740
tgscagctca gttccagaaa atcaaaaatcc attccaagag gccattgttt ttgtgtgggg1800
aggagcaca tatcttgaa atcagaatct tgttgactac ataaaaggga aacaaggcaa1860
acacatttta tatggctgca gtgagcttt taatgtcata cagttcataa aacagttgtc1920
acacacttga caaaagttaac acagaagaac cttaacctga taactactt ggaatgtgaa1980
taaaagttaa aggaagaaaa gttagaagag caatatgttt ccttctctgt aacaggttcc2040
taaacagtaa aatcagagtt atttgcata ttttaaggaa attatatac taatagtat2100
tgattttaaag aaacatttca gaaataaaat ttcaacttgc taaaaaaaaa gtcggctacc2160
taacagcata atatcgc

```

2177

## (2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 402 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ggcgccagcc ccagccagct caggctacac tatcccagga tcagcatggc cgtccgccag 60
tgggtaatcg ccttgccctt ggctgccctc ctgtgtggg acaggggaagt gccagtggccl20
gcaggaaggc tccctttctc aagaatgcc cttgtggaac acatggtaga gtctccaacc180
tggtcccaga tgtccaacct ggtctgcggc actgatgggc tcacatatac gaatgaatgc240
cagctctgct tggcccggtt aaaaaccaa caggacatcc agatcatgaa agatggcaaa300
tgctgatccc acaggagcac ctcaagccat gaagtgtcag ctggagaaca gtggtgggca360
tggagaggat atgacatgaa ataaaagatc cagcccaact ga 402

```

## (2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1349 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

cttcttttgc catcccattt ccttggcact gcaccatttc cccaattatt ggccaatccc 60
taggctttct gggttttaca atgggttgca ccacaatcac gctcatagat ggctccaatt 120
taaaaaaaaaa ggtaatgggt atggataaaa taagcagatc aaggggaagtg tgctatcata 180
aaataaactgt agcttcaaca tcttgagtac cagtttccgt gcagatagta aacatccaat 240
cacaagggat ttttctcgaa ggggtgtaaag ctggtttgaa aattcttcag tcacagagca 300
gcctacacat gccaaattaga aactgacaga cactagatgt gcttggaaga ttaaacacta 360
cgtaacagaaa cagcagttac taagctccct agtagtttct tgtctttttt aagtttcgct 420
gaatcgacag tttgcacaac gtgctatatt ctgtgggtca aaaccaagta aatactgtgt 480
aaagtgggca gatttttcca gctaagatca agaaaaaaca aattttctga taaaacaggt 540
ttagagtcag aaacactctc taaagtgcac aactgatggt ccacgatctc aaatagctaa 600
aactcctgca gaatgggaag gagagacgtg aaacagggaa ataaattaca gtcagtgcata 660
gttaatttag gaaaaggaaa aataaaacca aactcaagtc ggtaaaagtt atcaaaatat 720
tcaatgatgt agctttcccc actctctgtc acacacgctt gtaacaagat atattaaatt 780
aaggccaatt ttaactcgaa tgcgtttttt tttttctttt tattaagatc tgagatagga 840
acggtcatac ttagtactga aaggcagaca ataaaaatggg ccatgaaaag ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac ctatatcaaa gcatgtgtgt 960
agctcgaaat aaaaaataaa gactatttct atgtcatgac tgcgtgtgtg ctctctctc 1020
atattgcttc cctgtgccat tctgtacata ggtgaaacca gaaccaaggc catcaaaatg 1080
accacaatat ttggcatcat caatatgac ttcaagaaac atttctctca ttttgaaaaa 1140
ggccatttct gtgagcaagt aatcagatcc tgcctgatgt tgtgggtcta tccgttccag 1200
ctctaactgt tctgccacct cctgtaatcc acctttgaga tttttctctg catttatgat 1260
gtgaagtacc tcatgaagag ctgcacaaat ctctaactgt tctgccacct cctgtaaatg 1320
cgaagtcagt attgacgaaa taatagtgc

```

1349

## (2) INFORMATION ON SEQ ID NO. 43:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3552 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

attlaattctt cattctctcta ctatccccc aaatcatcaac ctaattaaac 60
acatcaaatc cccactgtac accaccacat caatcaaatc ctccttcatt attagccctc 120
taccoccttat aatatctttc cacaaataa tagaatatat atttcaacc tggcactgag 180
tcacccaata ttcaatagaa cttaaaataa gcttcaaaac tgactctctc tctatccctg 240
ttacatctgt agccctcttt gtccacatgat caattataga attctcttca tgatatatac 300
actcagagccc aaacatcaat cgattcattt aatatcttac actattccctg attaccatgc 360
ttactctcac ctccagccaac aacatatttc aacttttcat tggctgagaa ggggtgggaa 420
ttatctcttt cctactaatt ggaatgatgt acggagcgaac agacgcaaat actgcagccc 480
tacaagcaat cctctataac cgcacggag acatcggatt cattttagct atagtttgat 540
tttccctaaa cataaacctca tgagaaacttc aacagattat attctccaac aacaacgaca 600
atctaaatcc acttataggc ctatttaactg cagctacagg aaaaacagca caatttggcc 660
tcaccccatg actaccatca gcaatagaag gccctacacc agtttcagca ctactacact 720
caaagtacaat agtagttgca ggaattttcc tactggtccg attccacccc ctacagacta 780
ataataactt tattttaaca actataacttt gccctggagc cccaaccaca ttatttacag 840
taatttctgc tctcacccaa aacgacatca aaaaaatcat tgcttctct acatcaagcc 900
aactaggcct gataatagtg acgctaggaa taaaccaacc acacttagca ttctcacaca 960
tctgtaccca cgcattcttc aaagctatac tctttatatg cctgggtcca atcattcata 1020
gctgggcaga cgaaacagac atccgaaaaa taggaacacat cacaaaaatc ataccattca 1080
catcatctg cctagtaatc ggaagcctcg cctcaccagg aataccattc ctaacgggtt 1140
tctactcaaa agacctaatt attgaagcaa ttaatacctg caacaccaac gcttgagccc 1200
tactaatctac acttaactgc acttctataa cagctatgta cagcatcaga atcatttact 1260
tcgtaaccaat aacaaaaccg cgttttcccc ccttaacttc cattaacgaa aatgacccag 1320
acctcataaa cccaatcaaa cgcctagcat tcggaagcat ctttgaggaa ttgtctatc 1380
cataataact tcaccaaac ccgattccag tcttcacaa accatgattt ttaaaaacca 1440
cagccctaact ttttcagta ttaggattcc taatcgact agaaactaac aaaaacca 1500
taaaactatc aataaataaa gcaaatccat attcatcctt ctcaacttta ctggggtttt 1560
tcocctctat tattcaaccg attacacca taaaactctt caaccttaag ctaaaaacat 1620
ccctaactct cctgacttg atctggttag aaaaaaccat cccaaaatcc acctcaactc 1680
ttcacacaaa cataaccact ttaacaacca acaaaaaggt cttaattaaa ttgattttta 1740
tatcattctt aattaacatc atcttaatta ttatctata ctcaattaat ctgagtaatt 1800
ctcgataata ataaaaatc ccgcaaacaa agatcaccca gctactacca tcaattcaag 1860
agcacaacta tatattgcg ctaccccaat cctcctctcc aacataaact caacatcatc 1920
aacctcatac atcaaccaat ctcccaaac atcaagatta attactcaa cttcatcata 1980
ataatgaag acacaaatta aaaaaacct tataatcacc cccaatacta aaaaaccaa 2040
aattaatcag ttgatctccc aagtctctgg atttctcca ctatctaaac ctaaaaacga 2100
tcacaacaca accaacatcc cccctaataa aattaaaaaa actattaac ctaaaaacga 2160
tcacacaaac cctaaaaacca ttaaacaccc aacaacccca ctaacaatta accttaacc 2220
tcacataaaa ggtgaaggct ttaattgtaa cccaagacaa ccaacaaaaa ataatgaac 2280
taaaacaaaa atataattat tcatattttc tacaacagat tcaactgcga ccaatgacat 2340
gaaaaaatcat cgttgtaatt caactacaga aacaccattc ggatccatga aaaaacacac 2400
cattattttta aattattaac cactcattca ttgacctacc tgccccatcc caacttttat 2460
catgatgaaa ctttgggtcc ctctcaggag ttgcctaat agtccaaact attcagggt 2520
tttctcagc catcacatc acatcagata caataacagc cttttcatc gtaaacaca 2580
tttgcgaga cgtaaatcag ggtgactaa tccgatatat acacgcaaac ggagcctcaa 2640

```

```

tatatttttat ttgcttatto cttcagtgcg gacgaggcct atattatgga tcatatatac2700
ttatagaaaac cggaaacatt ggagtacttc tactgttctgc agtcatagcc acagcattta2760
taggtctacgt ccttcccatga ggacaaatatt cattctgagg tgccacagtt attacaaacc2820
tctctaccagc catcccatat attggaacaa cctcagtcga atgaatttga gggggctctt2880
cagtagacaaa agccaccttg acccgattct tgcctttcca ctccatttta ccatttatta2940
tcggggccctt agcaatcggt caccctcctct tcttccacga aacaggatca aacaaaccca3000
caggattaaa cccagatgca gataaaattc catttccccc ctactatata atcaagata3060
tcttaggatt cctaatcata ttcttaattc tctaatacct agtattattt ttcccagaca3120
tactaggaga cccagacaac tacataccag ctaatccact aaacacccca ccccatatta3180
aacccgaatg atatttccata ttgcatagc ccaattctacg ctcaatcccc aataaactag3240
gagggtctct agccttaattc ttatctatcc taatttttagc cctaatacct ttccctcata3300
cctcaaaagca acgaagcctta atattccgcc caatcacaca aattttgtac tgaatccctag3360
tagccaaacct accttatctta acctgaattg gggggccaacc agtagaacac ccatttatta3420
tcatttgccc actagcctcc atctcatact tctcaatcat ctttaattct ataccaattc3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaaaa acgatcgggt3540
gacatatagg gc
3552

```

## (2) INFORMATION ON SEQ ID NO. 44:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 601 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

tttttttttt tttttttttt tgcaattcaa atgaacgttt atttcttaaa cccacacaga 60
gtaagggcag agcttagaga tgccctggcag agcattttctc atccaggatc acttctcctgt120
tctttctctt ttgctggggag catcttagat ttatatcatt ttctacaaag acaatatcct180
gaatggcagt cgcagggtta ttccaaggtt ggagtctctt caggaaagtag gggagactgt240
attcccagct aatggaaatt tcactgtgat gtctgtgttc tcagtgaatt ctccagaaaa300
cgccgaggag actgtctcaa catcagttaga gaactcagaa ttctgtttgt ttgcggctgt360
cgtgaagctc atgatctgct cagagtcagt gcttaaatca tcatctgtat aatcctctag420
aggagctttt gtccctctgt atgatccag ttggtcaaa actgagttta gtaggccaat480
gattgaattc ttgagttctt tattgattga aactaattct gacaggggga aagccacagt540
cagaccacag aagacagtga tcaccaggac ctgaaaagc atcatgcttt agtagggta600
a
601

```

## (2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2147 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

agaaggggaa caaaaaaaa aatatactgaa tttagaaaaa ccacaaagct acaacactga 60
ccctcctctt ttcttgagac ggagttttgc tcttgtaacc caggctggag tgcagtgagg 120
tgatcttgga tcactgcaac ttccgtctcc ogggttcaag tgattctccg gccctcagct 180
cccaagttag tgggtttata ggtgccggcc accagaccgg gctaattttt tagttttagt 240
agagaagggg ttccaccacg ttggccaggc ttggtctaaa tgaccctctt atttttaact 300
tggataccgt ctattctgcc aaaaagacaat ttctagagta gttttgaatg ggttgatttc 360
cccacactcc acaactctgt aagccagttg ctgacttact aaaaaaagag ttgtatataa 420
tcttttaagt gctgagtatt tcataggaaa gctgaaatgct gctgtaaagt gctctttaag 480
tctttttttt tttaataccc ctctcaatga atgaaactag gggaatttca gggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt cttctgtttt tgagaagcag 600
tggttggggc atttttaaga tggctggcta ctctgttttt ccttcattgt aataaatttg 660
tctataacta gtaacatgaa cttgcccta gaggtagttg ttaataattt tgaatatta 720
aggctctgcc aagcttctga tgattcacac ctgtactact gattattaag caggcacagac 780
acttgacctt atattgttga tctgtgacct cctctcatat taatatttga taaagatttt 900
aatttatgta aaactttctaa agcagaatca aagctcctct tggggaaatg gcaagctctt 960
aggataggca agacccttga tgaatagttc caaagcatta ccgcatggta gagaacacac 1020
tcgatataaa atgttaagct atctgaaaaa taaaatgtgc aagtcttcag gatggccacaal 1080
aacaaaggtt aatgcttctt ggggcacatt ctctgaggtt ctctgaggtt atgataat1140
atctgacttt tgtttgtgtt acatgacttc tgtgacttca ttgaaaatct gcacaattca1200
gtttcagctc tggatattct cagtgacctt ttgtgaaggt ttttatctgt ctactctgtat taaaagttaal 1320
gtttgacttt gttttagcct atttaatttt tattttcttt ttttggtttg gctctttta1380
actataaaa agaaaaagag ttgtggtttt cattaataag aacttagagc tcttcaatcc taagattttc1440
gtcaggcttt ctgaacattg agatatcctg aagctactct ctgcctcttt atagtataat1500
tcagaaaaag cttcacttga acccaaaacc aagctactct caaaatgagg gagaacaact tgctgtcct1560
tcaggaaaag gactcagttg ttatttttta aactgcattt taataatttg atagtataat1620
gtaatacaaa gactcagttg ttatttttta caccctgtag ttttatagtt ctttaactaal 1680
aacataaagg agtaaggcac cttttatagg ctacatgctt acaagccacc atagtcacag1740
acctatacag ttctcttctt ttgaaaaaaa cctacatgct cagttcttga ggtgaattac aaaagtcacag1800
ccattatcat cctctcaggt tatttgaagt gtattttttt gtacattttg gctgcagtt1860
tgggtgtaga atatactata atatggatca tctctacttc tgtattttat tatttttaac1920
tgagactcaa ccacagttct cttttccccc tccaccctct ttgtgctgt aggatgtact1980
gtatgtagtc atgacatttg tatttaataa tttagaatct acagatctgt tttgtacttt2040

```

```

ttatactgtt ggatacttat aatcaaaact tttaactagg tatgaataa atctagctct2100
actagaataa aaaaaaaa aaaaaaaa ctcaagacta gttctctt
2147

```

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 623 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

ccccagcgctc cccggaacg gcgcgcgcg cgacaggacc gaggggcctt agttggtggg 60
caagtcgggg atcccagaaa gagaagcggtg acccggaagc ggaacacgggt gtccgtcccal20
gtctcgggcct gccagtgagc ttctaccatc atggacctat tgttcggggc cgggaagacg180
ccagagagagc tactcgggca gaaccagagg gccctgaacc gtgccatgcg ggaagctggac240
cgcgagcgac agaaactaga gacccaggag aagaaaatca ttgcagacat taagaagatg300
gccagccaag gccagatgga tgctgttcgc atcatggcaa aagacttggg gcgcaccccg360
cgctatgtgc gcaagtttgt attgatcgcg gccaacatcc aggcgtgtgc cctcaagatc420
cagaccactca agtccaaaca ctcgatggca caagccatga aggggtgtcc caaggccatg480
ggcaccatga acagacagct gaagttgccc cagatccaga agatcatgat ggaagtttag540
cggcaggcag agatcatgga tatgaaggag gagaggattg aattgttga tttgatgatc600
cgtggggtt tggggaagtt tta

```

623

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 781 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN



## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gcgggtatat  tccaagcttg  aaaaactaaa  agatctctga  aagatgctgc  caagaaggcc 60
cagaaggatg  tctgcatagt  tctggccaag  gagatgatca  ggtcaaggaa  ggctgtgagc 120
aagctgtatg  catccaaagc  acacatgaac  tcagtgtcca  tggggatgaa  gaaccagctc 180
gcggctcttc  ggtggtctgg  ttccctgcag  aagagcacag  aagtgatgaa  ggccatgcaa 240
agtcttctga  agattccaga  gattcagccc  accatgaggg  agttgtccaa  agaaatgatg 300
aaggctggga  tcatagagga  gatgttagag  gacacttttg  aaagcatgga  cgatcaggaa 360
gaaatggagg  aagaagcaga  aatggaatt  gacagaattc  tctttgaaat  tacagcaggg 420
gccttgggca  aagcaccaga  taagtgact  gatgcccttc  cagagccaga  acctccagga 480
tcgatggctg  cctcagagga  tagggggcag  gaggaagagg  ctctggaggc  catgcagtc 540
cggtcgccca  cactccgcag  ctggggcctg  cctaccctcg  tgggtgtgca  cacactcttc 600
tcaagagctc  ccattttatg  tctctcttgc  actacacctc  tggtgtgagg  actaccattt 660
tggagaaggt  tctgtttgtc  tcttttcatt  ctctgccacg  gttttgggat  cgcaaggga 720
ctgttcttat  aaaagtggca  taaataaatg  catcattttt  aggaaaaaaa  aaaaaaaaaa 780
a

```

781

## (2) INFORMATION ON SEQ ID NO. 48:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1714 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gttgccacat gcagtcgcgc ggaggaactg tgctctttga gccgcacgct agggggcccg 60
aagggaact gcgagggcgaa ggtgaccggg gaccgagcat ttcagatctg ctccgtagac 120
ctggtcgacc accaccatgt tggctgcaag gctggtgtgt ctccggacac taccttctag 180
ggttttccac ccagctttca ccaaggctcc cctgttgtg aagaattcca tcacgaaga 240

tcaatggctg ttaacacctt gcagggaata tgccacaaaa acaagaattg ggtccggcg 300
tgggagaact ggccaagAAC tcaaaagggc agcatrgaa ccatcgatgg aaaaaattt 360
taaaattgat cagatgggaa gatggttgt tgctggaggg gctgctgttg gtcttgagac 420
attggtctac tatggtctgg gactgtctaa tgagatttga gctattgaaa aggtctgaat 480
ttggctcag tatgcaagg atagaattca ttccacctat atgtacttag caggggagta 540
tggtttaaca gttttgtctg ccatagcaat cagcagaacg cctgttctca tgaacttcat 600
gatgagaggc tcttgggtga caattggtgt gaccttttga gccatggttg gagcttgaat 660
gctggtacga tcaataccat atgaccagag cccaggccca aagcatcttg ctggttgtct 720
acattctggt gtgatgggtg cagtgtgtgg tctcttgaca atattagggg gtcccttctt 780
catcagagct gcattgtaca cagctggcat tgtgggaggc ctctccactg tggccatgtg 840
tggccccagt gaaaagtttc tgaacatggg tgacccctgg gagtggggcg tgggtctctg 900
ctttgtgtcc tcaattggat ctatgtttct tccacctacc acgtggctg gtgccacctt 960
ttactcagtg gcaatgtag gtggattagt tcttttcagc atgttctctt tttatgatac 1020
ccagaaagta atcaagcgtg cagaagtatc accaatgtat ggagtccaaa aatgatgacc 1080
cattaactcg atgctgagta tctacatgga tacattaaat atattttatg cagttgcaac 1140
tatgtcggca actggaggca acagaaagaa atgaagtga cagcttctg gctctctgcl 1200
tacctcaaat atctgttta atggggcaga tatgatttaa atagttttga caagcagctt 1260
tcgttgaagt ttagaagata agaaacatgt catcatattt aaatgttccg gtaattgtat 1320
gcctcaggct tgcccttttt tctggagaat aaatgcagta atccctcccc aaataagcac 1380
acacattttc aattctcatg tttagtgtat tttaaaaatg ttgttgaaat gtgaaaacta 1440
aagttttgtt catgagaatg taagtctttt ttctacttta aaatttagta ggttcaacta 1500
gtaaactaaa tttagcaaac ctgtgtttgc atattttttt ggagtgcaga atattgtaat 1560
taattgcata agtgatttgg agcttttgta aagggaccag agagaaggag tcccttcag 1620
tcttttgttt ttttaaatat ttaggaaact agcacctggg gttatttgga ttaggtgagg 1680
gagcccggtt ggaacagcgg ggtattgggg aaca 1714

```

## (2) INFORMATION ON SEQ ID NO. 49:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 831 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

caccoccagc cccgtctctg aggcaccgag aaacgaggag gcccgtagcg agtctccacg 60
tgggtaccgg cgtctctcgg gcccgtagcc acccgcccgc cggaagccga catctcgagt120
tctggcagaa gcaatttgcg cggcgaggag cggacgggca ggaacccaat aagctgcttc180
gctctggagc tgaagcccgct actcaagatg gcggtctcgg gcggcggtgg ccagtgacta240
gaaggcgagg cggcgcgga ccatggcggc ggcgcgggac gaggcgagtc cagaggacgg300
agaagacgag gaagaggagg agcagttggt tctggtggaa ttatcaggaa ttattgattc360

agacttcttc tcaaaatgtg aaaaataaat caaggttttg gccattgaca ctgagagccc420
gattctggaa gtggacagct gtgtcttttg tggggagtat gaagacactc tagggacctg480
gtttatcttc gaagaaaatg ttgaacatgc tgatcacaga ggaataataa aaacagtgtc540
aaaataataa tgcataccta tgaagaaagt cagcatgaca agaactctcc tgacagagaa600
gaaggaaagg gaagaaaaca taggtgggggt ggaatggctg caaataaagg ataagtattc660
ctcttatcga cccaacatga ttgttaactt tctacatgaa aatgaagacg aagaagtgtc720
agcttcagcc ccagataaat ctttgggaatt ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaaaccg ggggttgttg aaacggggga acccattgcg ccttgggaat t      831

```

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

tgaagcttcta agagctttcc aagtttggga aggtgtccgg gttttctcgg attacttctc 60
tgagcatgaa cgggaagtcac cctttgtgcc ttatgcggtg attttaatga taggtgtcat120
atataggacg gagtaatctg ttacattctt gttcttctcg atgcactcac aagcgggtaa180
ctaggtgaca agaaaacaaa gatcttattc aaaagaggtc ttacagcaac ccaacgtctc240
atcttcccat agtaaaagatg acggcgccctt gaggtaaagt acaggcaaca ccacttccgc300
gtttctcttg cgccttggtc caagatggcg gatgaagcca cgcgacgtgt tgtgtctgag360
atcccggtgc tgaagactaa cgcgggaccc cgagatcggt agttgtgggt gcagcgactg420
aaggaggaaat atcagtcacct tatccggtat gtggagaaca acaagaatgc tgacaacgat480
tggttccgac tggagtcctaa caaggaaagga actcgggtgt ttggaaaaat ctgggtatct540
catgacctcc tgaatatatga gtttgacatc gagtttgaca ttcttatcac atatcctact600
actgcccacg aaattgcagt tcttgagctg gatggaaaga cagcaaatgt gtacaggtg
gactgaatag gagatggcaa agagtcaaaag aaagccttaa ggaagaacct cgtggcgg
gggagagcat caggaagagt agct

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2017 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

TGGGACCCGA GGCGCCGAGC AAGATGGCGG CGCGAGTGCT GCGGCCCCCG GGAGGGCGTG 60
GGCGGGCGGG CCGCTGCAGC GGGCGGCCCC CTGCAGCTCTC CTGCCGAGCG TCCGGGCAATG 120
GACATCTCTCC AGCAACAGAT CTGAGGAAGA CAGCTGGCTA AATCCTTAT TTGTCGGGAA 180
AGTTGATCCA AGAAAAGATG CCGACCTCAA TCTCTAGGCC AAAAAAGGAA CAAGCAATCT 240
ATACAAATTA CAGTTTCACA ATGTTAAACC GGAATGCCTA GAAGCATACA ACAAAAATTG 300
TCAAGAAGGTG TTGCCAAAGA TTCACGAAGA TAAACACTAC CTTGTACTT TGGTGGGGAC 360
TTGGAACACG CTGTTATGGC AGCAGGACCA AGCTGTCCAC CTTGGAGGT ATGGAAGGAG 420
CTATCCAGCC CTCACAGAAG TCATGAATAA ACTCAGAGAA AATAAGGAAT TTTTGAATT 480
TCGTAAGGCA AGAAGTGACA TGCTTCTCTC CAGGAAGAAT CAGCTCCTGT TGGAGTTTCA 540
TTTCTGGAAT GAGCCTGTGC CAAGATCCGG ACCTAATATA TATGAACACA GGTCTTACCA 600
ACTCCGACCA GGAACCATGA TTGAATGGGG CAATTAATGG GCTGTGCAA TCCGCTTCAG 660
ACAGGATGGT AACGAAGCCG TCGGAGGATT CTTCTCTCAG ATTGGGCGCG TGTACATGGT 720
GCACCATCTT TGGGCTTACA GGGATCTTCA GAACAGGGAA GACATACGGA ATGCAGCATG 780
GCACAAACAT GCGTGGGAGG AATGGTATA TTACACAGTT CCACCTTATC AGGAAATGGA 840
ATCCGAATC ATGATCCACC TGAAGACCTC GCGCCCTCCG TAAAGCTGTA GAGTCTCTAT 900
GTGCTACAT ACATTTCTGT GACAAATATT TGTCTAAAT TAATTTTAA TGTGTATCAA 960
GTGAAAAGA AACACTGAGG TTTAAGCTG CTGTATATAG CTTGTGAGAA ACCCTCTTTC 1020
TTTAAAAATT ACATAATCAC AAGAAAGGAA AGAATTACAG TTGGACTGAT TGTGACAGTG 1080
CCTTGTCTGT CCTCTTGAAC CACCCCGTGT TGTCCAGTAT ACCCTATAAC ACTTAGCCAC 1140
TCTCTCCACC CCTCCAGAAG GGTCTCCAGT TGAATCTGA ATCATCTGA AATAAGATT 1200
CCAAACCAAA AAAAAATTA GCCATTTCTT TACTAAAAAA AACCAAAAAA CAAATCTGTT 1260
TTAATATCAC AGATTTTITAG ACAAAATTTCT TGTATCAGGA AGAAATACAA ATTTTGTAT 1320
GTTTCTCAAG CAGTTTITCT GAGTAGTTTC TGAGGAGGAA CAAATACAA GTGATCCCAA 1380
TAACGTGAAA TGTTTTAACT CACTCTCAAT TGTAAAGCAG CCACATAGTA GACCAATGGT 1440
TTTCCAGCT GGGCAAGGTA CATTTAATCA GTAATCAGT TTCACATCAT GTATTGTAT 1500
GTTTCAATGT GAGACACAAA AACAAATGGT TGAACCTTGT GTATCATATG TGATTTGAA 1560
ATGAACCCCT TGAATAGCAC TAATTTTAT TTGTGGTATT TTTCTATAAC AAAACAAGTA 1620
GCTCTAGGAA AAGAGGTTT ATTTGTAAA CGATCATTTG TGACCTCAGA CACTCTCTGG 1680
CTAATATTT AATAAGCTCA CAGCAGATAA TCTCGAGATC ATGGGTGAGG GGTGGTGAT 1740
GTTGAGATTT AAATGTCAT AAAGCTGCAT ACTTTTGTCT TAGCTGTTG ATTTCAATTT 1800
TTAATATAT ATGCCAATT TGTGACTGTT ACCATGTGAA AGTCCGTGTG AAATGAACAA 1860
TTGTCTGCC CACAATCAAG AATGATGTG TAAAGTGTGA ATAAATCTCA TATCAAAATG 1920
CAAACTTTA CATGTGAATG ATTTCTCTCA AGAACATAGA AAAGTCAATA AATCCTCTT 1980
AATTTCACA AAAAAAAAAA AAAAAAAAAA AAAAAAAA

```

2017

01  
 02  
 03  
 04  
 05  
 06  
 07  
 08  
 09  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525  
 526  
 527  
 528  
 529  
 530  
 531  
 532  
 533  
 534  
 535  
 536  
 537  
 538  
 539  
 540  
 541  
 542  
 543  
 544  
 545  
 546  
 547  
 548  
 549  
 550  
 551  
 552  
 553  
 554  
 555  
 556  
 557  
 558  
 559  
 560  
 561  
 562  
 563  
 564  
 565  
 566  
 567  
 568  
 569  
 570  
 571  
 572  
 573  
 574  
 575  
 576  
 577  
 578  
 579  
 580  
 581  
 582  
 583  
 584  
 585  
 586  
 587  
 588  
 589  
 590  
 591  
 592  
 593  
 594  
 595  
 596  
 597  
 598  
 599  
 600  
 601  
 602  
 603  
 604  
 605  
 606  
 607  
 608  
 609  
 610  
 611  
 612  
 613  
 614  
 615  
 616  
 617  
 618  
 619  
 620  
 621  
 622  
 623  
 624  
 625  
 626  
 627  
 628  
 629  
 630  
 631  
 632  
 633  
 634  
 635  
 636  
 637  
 638  
 639  
 640  
 641  
 642  
 643  
 644  
 645  
 646  
 647  
 648  
 649  
 650  
 651  
 652  
 653  
 654  
 655  
 656  
 657  
 658  
 659  
 660  
 661  
 662  
 663  
 664  
 665  
 666  
 667  
 668  
 669  
 670  
 671  
 672  
 673  
 674  
 675  
 676  
 677  
 678  
 679  
 680  
 681  
 682  
 683  
 684  
 685  
 686  
 687  
 688  
 689  
 690  
 691  
 692  
 693  
 694  
 695  
 696  
 697  
 698  
 699  
 700  
 701  
 702  
 703  
 704  
 705  
 706  
 707  
 708  
 709  
 710  
 711  
 712  
 713  
 714  
 715  
 716  
 717  
 718  
 719  
 720  
 721  
 722  
 723  
 724  
 725  
 726  
 727  
 728  
 729  
 730  
 731  
 732  
 733  
 734  
 735  
 736  
 737  
 738  
 739  
 740  
 741  
 742  
 743  
 744  
 745  
 746  
 747  
 748  
 749  
 750  
 751  
 752  
 753  
 754  
 755  
 756  
 757  
 758  
 759  
 760  
 761  
 762  
 763  
 764  
 765  
 766  
 767  
 768  
 769  
 770  
 771  
 772  
 773  
 774  
 775  
 776  
 777  
 778  
 779  
 780  
 781  
 782  
 783  
 784  
 785  
 786  
 787  
 788  
 789  
 790  
 791  
 792  
 793  
 794  
 795  
 796  
 797  
 798  
 799  
 800  
 801  
 802  
 803  
 804  
 805  
 806  
 807  
 808  
 809  
 810  
 811  
 812  
 813  
 814  
 815  
 816  
 817  
 818  
 819  
 820  
 821  
 822  
 823  
 824  
 825  
 826  
 827  
 828  
 829  
 830  
 831  
 832  
 833  
 834  
 835  
 836  
 837  
 838  
 839  
 840  
 841  
 842  
 843  
 844  
 845  
 846  
 847  
 848  
 849  
 850  
 851  
 852  
 853  
 854  
 855  
 856  
 857  
 858  
 859  
 860  
 861  
 862  
 863  
 864  
 865  
 866  
 867  
 868  
 869  
 870  
 871  
 872  
 873  
 874  
 875  
 876  
 877  
 878  
 879  
 880  
 881  
 882  
 883  
 884  
 885  
 886  
 887  
 888  
 889  
 890  
 891  
 892  
 893  
 894  
 895  
 896  
 897  
 898  
 899  
 900  
 901  
 902  
 903  
 904  
 905  
 906  
 907  
 908  
 909  
 910  
 911  
 912  
 913  
 914  
 915  
 916  
 917  
 918  
 919  
 920  
 921  
 922  
 923  
 924  
 925  
 926  
 927  
 928  
 929  
 930  
 931  
 932  
 933  
 934  
 935  
 936  
 937  
 938  
 939  
 940  
 941  
 942  
 943  
 944  
 945  
 946  
 947  
 948  
 949  
 950  
 951  
 952  
 953  
 954  
 955  
 956  
 957  
 958  
 959  
 960  
 961  
 962  
 963  
 964  
 965  
 966  
 967  
 968  
 969  
 970  
 971  
 972  
 973  
 974  
 975  
 976  
 977  
 978  
 979  
 980  
 981  
 982  
 983  
 984  
 985  
 986  
 987  
 988  
 989  
 990  
 991  
 992  
 993  
 994  
 995  
 996  
 997  
 998  
 999  
 1000  
 1001  
 1002  
 1003  
 1004  
 1005  
 1006  
 1007  
 1008  
 1009  
 1010  
 1011  
 1012  
 1013  
 1014  
 1015  
 1016  
 1017  
 1018  
 1019  
 1020  
 1021  
 1022  
 1023  
 1024  
 1025  
 1026  
 1027  
 1028  
 1029  
 1030  
 1031  
 1032  
 1033  
 1034  
 1035  
 1036  
 1037  
 1038  
 1039  
 1040  
 1041  
 1042  
 1043  
 1044  
 1045  
 1046  
 1047  
 1048  
 1049  
 1050  
 1051  
 1052  
 1053  
 1054  
 1055  
 1056  
 1057  
 1058  
 1059  
 1060  
 1061  
 1062  
 1063  
 1064  
 1065  
 1066  
 1067  
 1068  
 1069  
 1070  
 1071  
 1072  
 1073  
 1074  
 1075  
 1076  
 1077  
 1078  
 1079  
 1080  
 1081  
 1082  
 1083  
 1084  
 1085  
 1086  
 1087  
 1088  
 1089  
 1090  
 1091  
 1092  
 1093  
 1094  
 1095  
 1096  
 1097  
 1098  
 1099  
 1100  
 1101  
 1102  
 1103  
 1104  
 1105  
 1106  
 1107  
 1108  
 1109  
 1110  
 1111  
 1112  
 1113  
 1114  
 1115  
 1116  
 1117  
 1118  
 1119  
 1120  
 1121  
 1122  
 1123  
 1124  
 1125  
 1126  
 1127  
 1128  
 1129  
 1130  
 1131  
 1132  
 1133  
 1134  
 1135  
 1136  
 1137  
 1138  
 1139  
 1140  
 1141  
 1142  
 1143  
 1144  
 1145  
 1146  
 1147  
 1148  
 1149  
 1150  
 1151  
 1152  
 1153  
 1154  
 1155  
 1156  
 1157  
 1158  
 1159  
 1160  
 1161  
 1162  
 1163  
 1164  
 1165  
 1166  
 1167  
 1168  
 1169  
 1170  
 1171  
 1172  
 1173  
 1174  
 1175  
 1176  
 1177  
 1178  
 1179  
 1180  
 1181  
 1182  
 1183  
 1184  
 1185  
 1186  
 1187  
 1188  
 1189  
 1190  
 1191  
 1192  
 1193  
 1194  
 1195  
 1196  
 1197  
 1198  
 1199  
 1200  
 1201  
 1202  
 1203  
 1204  
 1205  
 1206  
 1207  
 1208  
 1209  
 1210  
 1211  
 1212  
 1213  
 1214  
 1215  
 1216  
 1217  
 1218  
 1219  
 1220  
 1221  
 1222  
 1223  
 1224  
 1225  
 1226  
 1227  
 1228  
 1229  
 1230  
 1231  
 1232  
 1233  
 1234  
 1235  
 1236  
 1237  
 1238  
 1239  
 1240  
 1241  
 1242  
 1243  
 1244  
 1245  
 1246  
 1247  
 1248  
 1249  
 1250  
 1251  
 1252  
 1253  
 1254  
 1255  
 1256  
 1257  
 1258  
 1259  
 1260  
 1261  
 1262  
 1263  
 1264  
 1265  
 1266  
 1267  
 1268  
 1269  
 1270  
 1271  
 1272  
 1273  
 1274  
 1275  
 1276  
 1277  
 1278  
 1279  
 1280  
 1281  
 1282  
 1283  
 1284  
 1285  
 1286  
 1287  
 1288  
 1289  
 1290  
 1291  
 1292  
 1293  
 1294  
 1295  
 1296  
 1297  
 1298  
 1299  
 1300  
 1301  
 1302  
 1303  
 1304  
 1305  
 1306  
 1307  
 1308  
 1309  
 1310  
 1311  
 1312  
 1313  
 1314  
 1315  
 1316  
 1317  
 1318  
 1319  
 1320  
 1321  
 1322  
 1323  
 1324  
 1325  
 1326  
 1327  
 1328  
 1329  
 1330  
 1331  
 1332  
 1333  
 1334  
 1335  
 1336  
 1337  
 1338  
 1339  
 1340  
 1341

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 856 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

cgcaagtgcgc aggcgtgggg ctctctcctt gtcagtgcgc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcggcggc aggaactccgg cactatgagc ggcttcagca ccgaggagcgl20
cgccgcgcgcc ttctcccttg agtaaccgagt ctctctcaaa aatgagaaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggat gtgtttcaca tggtagttga240
agtaccacgc tggctcaatg caaaaatgga gattgtctaca aaggaccctt taaaccctat300
taaacaaagt gtgaaaaaaag gaaaacttcg ctatgttgcg aattgttcc cgtataaaagg360
atatactctg aactatggtg ccaatccctca gacttgggaa gacccagggc acaatgataa420
acataactgc tgttctgtgt acaatgaccc aattgatgtg tgtgaaattg gaagcaagg480
atgtgcaaga ggtgaaataa ttggcgtgaa agttctaggc atattggcta tgattgacga540
aggggaaacc gactggaaaag tcattggcat taatgtgat gatcctgatg cagccaatta600
taatgatata aatgatgtca aacggctgaa acctggctac ttagaagcta ctgtggactg660
gtttagaagg tataagggtc ctgatggaaa accagaaaaat gagtttgcgt ttaatgcaga720
attttaaagt aaggactttg ccattgatat tattaataagc actcatgacc attgaaaaag780
attagtgact aagaaaaacga atgggaaaaag gatcatgttg attgttcaac ttttcgttgg840
gccccctcaa gtgtgc                                     856

```

## (2) INFORMATION ON SEQ ID NO. 53:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 540 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

gcatagacaa agggcctcag aatcgcgag ggcgaattgt gccctgggtc gccaaagatgt 60
cgttcccaaa gtataagcgc tggagcctgc gcactctgcc tgagaccctc gacccagccg120
aatacaacat atctccggaa acccgcgagg cgcaagcgag cggctggcca taagagccca180
gctgaaacga gactacotgc ttcaatadca cgtatccaac cgcgaggggc tcatcgaaaa240
tcttgcttgg cttcgttggg cctatgcaa aacaataaat gtcctacctt atttcagacc300
cactcctaaa aactcaactca tgggagctct gtgtggattt gggccctcca tcttcattta360
ttatatattc aaaactgaga ggcataggaa agaaaaaactt atccaggaag gaaaattgga420
tcgaacattt cccctctcat attaaagtcg gcaatgatga ctatatgtat tcccgcttaa480
ataaatcatc tattaatcat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagtcg540

```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1912 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

tgtgtgaggc ccaacagcgg aatcatcgat gcagggggcct gaattaatgt atctgtgatg 60
ttacaagcctt tcgattatga tcccaatgag aaagtgtaac acaggttatg gttcagttcta 120
tgttttgcctcc aactgaacact tcagatatgg aagcagttatg gaaggaggca aaaccggaaag 180
accttatatgga ttcaaaaactt agatgtgtgt ttgaattgcc agcagagaatg gataaaccac 240
atgatgtaga aataaataaaa attatatcca caactgcatac aaagacagaa acaccaatag 300
tgtctaaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaaggtgaa gttcagagtc tacgggaggga gaacaagcag ttcaaggaaag 420
aagatggact cgggatgagg aagacagttc agagcaacag ccccatttca gcattagccc 480
caactcggaa cgaagaaggc cttagcaccg ggcctctggc tctggtggtt ttgcttctta 540
tcgttgggtgt aattattggg aagatggcct tgtagaggta gcattgcacag gatggtaaat 600
tggatttggt gatccaccat atcatgggat tataatttat cataaccatg tgtaaaaaaga 660
aattaatgta tgaatgacatc tcacaggtct tgccctttaa ttaccctccc ctgcacacac 720
atcacacagat acacacacac aatatataat taacgatctt ttagaaggtt aaaaatgtat 780

atgaactgat tgagggggaa aagaatgac tttattaatg acaagggaaa ccatgagtaa 840
tgcacacatg gcatattgta aatgtcattt taacacattg taggccttgg tacatgatgc 900
tggattaccc ctcttaaaat gacacccctc ctgcctgtgt ggtgctggcc ctggggagc 960
tcccgccccc catgctgggg agtgccgtca gctccacaca gtatgcccca cgtggccccc 1020
tcccgccccc ggcctgcttc cgtgtcttca gttctgtcca agccatcagc tctctgggac 1080
tgatgaacag agtcagaagc ccaaaaggaa tgcaactgtg cagcatcaga cgtactcgtc 1140
ataagtgaag ggcgtgtgtt gactgattga ccagcgctt tggaaataaa tggcagctgt 1200
tctgtcactt aaagggacca agctaaattt gtattggctc atgtagttaa gtcaaacctg 1260
tatctcagaa tcttttaact atatttaact tatctaatgt atttcatccc atgtttctt 1320
attgtcacaa gactacagtt aatgctgcgt gctgctgaac tctgttgggt gaactggtat 1380
tgcctctgga ggcctgtggg ctccctctgt tctggagagt ctggctcatg ggaggctggg 1440
ttatttggga tgcctgggaa gagctgccag gaagtgtttt ttctgggtca gtaataaaca 1500
actgtcatag ggaggggaaat tctcagtagt gacagtcaac tctaggttac ctttttaaat 1560
gaagagtagt cagtcttcta gattgttctt ataccaccctc tcaaccatta ctacacctc 1620
cagcgccccc gtccaaagtct gagcctgacc tcccttggg gaacctagct ggaactcagg 1680
caaatggatc ggcctgcaga gggctagaag cgaggggcacc agcagtctgt ggtggggagc 1740
aaggggaagag agaaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga 1800
attcaattta tgccataaaa gaccacaacca gttctgttgc actatgtagc atcttgaaaal 1860
gaaaataattt aaaaataaag aaaaaaataa gct 1912

```

## (2) INFORMATION ON SEQ ID NO. 55:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN



## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

tttttttttt ttttatcgag caagaatctg ttaacagttt tatttttttt tatgttaaat 60
acctggggag aggatgttaa ggatgaaaaa ctcaagtcac aactgcccra caegggtata 120
gaaaaattct gccatgatat tagcaaaagt aaaggaggaa aaatttacac tgaaggaggg 180
atttttcccc caaggaatac ctcttggcat ttcttgaaat agtgggatta gcaattctaaa 240
taaatcatat ttcaagaggt aacagcaaca gataaaattt aaagggatta ttaaaataac 300
atttcaaga ctctgaacaa ttcttgaact cttattaaaa ccacaagaaa agaacaattc 360
tttttttatg aatttcataa aggactcaat gtgcaactga catctgctag tgaatgatcg 420
ggaatataca acctgtccag tagccgaaca gttttgtttt attgtgtttt taaaccgtaa 480
ggatcatta aaaggcaaac ctatatgacg ctgtacacac aaaaaaatgg tcaccgtggg 540
ccatactacc aatgaaatgg taggtaaaca aatctttttc tgggtcaagag aaaaaaaaaa 600
aaaaaagaaa gcactctgca tgcttcactc tacaagatga atttccctag aaagaatcca 660

atgaaaatgg ctgcaattac aacaagaagt gaagggaagc cactgggtgac attatctctg 720
aaggatggag ttgaggttga tccaggttca tccgaatgg ctacctttct gaqccctaaa 780
cccttcaccc tccaggtggcg attttctctt gatagcttca tcaattctcc ctgaagtctt 840
ttacactctt ccattagctt ccttggttcg gtatctttaa gtgaacact gtgtggtttt 900
ggcatagggt catcttgcct agatgcaatt agtgggaacg ttctgctagg tcccatatca 960
ttcatattat catcttgcct gggcatttca aatagcctac tcaatttggg atccattaat 1020
tcactagggt ttgcctctct ccacaacagct tccatattcg aagtgtttgg tggaggcaaa 1080
agcattactg aaacagctac agttgacccct gggccaataa ttccactggt gggccccaal 1140
cagtagcggc gaggtgctgt agtcttcaact ttgaaaaaca cttttctatc cgaatggatt 1200
cgcaatttaa gacttgaggt gactacatct gtgaaggggc ctttgaattt gaggtctgtg 1260
ggcgagctga gacacagagt ctgctcgctc tcgccatggc ccctgaggcg gaccocatcg 1320
gagagacagt gcagagcagg gggcggtctg ctctcggggg ccgggggacg atggcagag 1380
gggggggggg gcgagttcgc atctctcctt ttccgtggtg gactctgttc aaccacattc 1440
ttatgttggc agatctgctt ccagattgat tttagagca ccatcaactt cacattcct 1500
attctgattt tgtttgttt ttctggggtt ttctggaact taaaaagctg ccccgaaaat 1560
actatatttt taggtttgtg ttctgaaaag ctccgtgctg ctggaatttt ggggggaaat 1620
acaggtacct tcaagcaatga ggtgtttaag atttgcacat agcaatgcaa ttctttctaa 1680
atatggggat atttactctt attaagaaat tatatcaaac attgatgtcc ttgatcatt 1740
tatgtttcca tattactttt gattctacta tgattgtgtg gtggtgaaca aagatcatt 1800
caaaacaaaa ctgtaatttt gttatatttg attcaatgga atttacctaa aaaaataaga 1860
ctaaaaatgt gaaaaaaaaa aaaaaaaa aa 1920

```

## (2) INFORMATION ON SEQ ID NO. 56:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

cggctcgcag ggctcgagat tgcaggtcgt ggtggtcttg gaagagcgtc gaggggggccg 60
tggacgtgga atgggcccag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga atgatatagat ctggcctgaa gcacgaggac aaacgtggag gtacgggatc 180
tcacaaactgg ggaactgtca aagacgaatt aacagagtcc cccaaataca ttcagaaca 240
aatatcttat aattacagtg acttggtatc atcaaatgtg actgagggaaa cacctgaagg 300
tgaagaacat cctccagtgg cagacactga aaataaggag aatgaagtgt aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgaagtgaag gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtgggaaga 480

gggattttgt cttcataaat caaagagtga agaggctcat gctgaagatt cggttatgga 540
ccatcatctt cggaaagccag caaatgatat aacgctctcag ctggagatca attttggaga 600
ccttggccgc ccaggacgtg gcggcagggg aggcagaggt ggacgtgggc gtggtgggag 660
ccbaaaacgt ggagcagcga ccgacaagtc aagtgtctct gctccgatg tggatgacc 720
agaggcattc ccagctctgg cttaactgga tgcataaga caaccctggt tcccttgtga 780
accctctctg tcaaaagcttt tgcattgcta aggatcccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcatcac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aaagtaacaaa tatggtatgt agttttgtat ttgaaaatgt 960
attggtagca gggatgtttt cataattttc agagattatg cattcttcac gaactctttt 1020
gtattgtctg ttgcaaatat gcatctccaa acttgaaata taggtgtgaa cagtgtgtac 1080
cagtttaaaag ctttcaacttc atttgtgttt tctaattaag gatttagaag tcccccaat 1140
tacaaactcg ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac 1200
atgggtcaact gggacatgtt aaactttgat ttgtcaaat ttatgctgtg tggaactact 1260
actatctgta ttttaactta gtttttaata tttaactttt ggggaaaaaa cttttttcac 1320
tcctcagat agctgttata tatatatgct aaacttttt atacagaaat atcagtaact 1380
gaacaaatcc aaaaacacat ttggttttat aacccgtggc tgccttgcca tggggcccat 1440
ttgggggtcca aattataa

```

1458

## (2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2188 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

gggccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 120
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 180
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 240
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 300
cCaacccctcc cccacccccc cccctacaag tcacctgggt aagcCaaccc gaattctact 360
caccctggcg tggaagtatg tatgacagaa tggcagcgagg aggtgatgga tatgatggtg 420
gttatggagg ttttgatgac tatgttggtc ataataatta cggtataggg aatgatggct 480
ttgatgcagc aatgagagat ggaagaggta tgggaggaca tggctatggt ggagctggtg 540
atgcaagtcc aggttttcat ggttggtcatt tegtacatat gagagggttg ccttttcgtg 600
caactgaaaa tgacattgct aatttctct caccactaaa tccaatacga gtctcatattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagtttgtg acacatgaag 720
atgcagtagc tgccatgtct aaagataaaa ataacatgca acatcgatat attgaactct 780
tcttgaaatt tactcctgga ggcggtctct gcattggagg ttctggaagt ggaggctacg 840

gaaagcagtg aatggataat cagggaaggct atggatcagt tggaaagaatg ggaatgggga 900
acaattacag tggaggatat ggtaactctg atggtttggg tggttatgac cgtgggggtg 960
gaggcagctg aggttactat gggcaaggcg gcatgagtg aggtggatg cgtgggatgt 1020
atgaaagca aaaaacacaa catacaagtc ttgacaacag catctggtct actagacttt 1080
tttaacagatt caattttttt tgtattttaa gaactttata atgactgaag gaactgtgtt 1140
tcaaaatatt atttggtaaa gcaacagatt tggatgggaa aatgtttct gtacgtttat 1200
ttgtgcata ctttgactta aaaaataaatt ttatattcca aaccactgat gtgatattt 1260
tttatataat agttactctt aaagatgtgc tgctctcata agatttgggt tgagtattt 1320
tactattagt tccacaagaa ttagtgggtg gtaattttag aggataatgg ttacacctgt 1380
cgtcaactctg aagctctaaq cagcactctg gaatagagct tgacaaataa ttagtgaac 1440
ttttttcttt agttctctct ggacaacact gtaaatataa agcctaagaa tgaagtggct 1500
tcaggagtat aattattttt atattattat ttctcaaatg tcatattatc 1560
ggcatagctc tgaacacttg atgacttaag aggtattgat ttctgaatat tcaataatt 1620
gttaactggg tatgagagt tgggaagctg aattctagcc ctatgatttg gagtaaac 1680
ccttcagcac ttgacgcaaa taccaaaatt gtctccaaaa aattgatagt tgcagggtat 1740
cgcaagatgc ctatagatag ggttaaggtt ctcaagtaca caagaattca gttattatca 1800
cataggttat tactatggag tataattctc scaactgta ttctagtttt ctgcccaata 1860
gagttttaaa aactgtataa atgatgactt taaaaaaatg taagcaacaa gtcacatgca 1920
tttagcaata aaacaatcct gcagttgggt ttgttatctg atccctgctt ggagttttat 1980
tcaaaagaa ctatatgtag caagggaaaag tggcttttta atttttaact ctttgatcaa 2040
tatgggtttt ttccaaaatt gctaattgat caaaatgaaa cctgttgatg tgaattcag 2100
tattgaactt gttacttgtt ttggccagaa atgttattaa taaactgcaa tgtgggagat 2160
aaaaaaaaaa aaaaaaaaaa aaaaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcgctagtt cgatcggtag cggggagcga gagcgagccc cagagagccc tggcagagccc 60
caccgcccgc gccggcctag ttaccatcac accccgggag gggccgcagc tgcgcagccc 120
ggcccccagtc accatcacgc caaccatgag cagcgagccc gagaccagc agccgcccgc 180
ggcccccccc gggccccccg ccttcagcgc ccccgacacc aagcccgcca ctacggggcag 240
ggcgcgaggg agcgtggccc cggggggcct cacatcggcg gcgcctgccg gcgggggaaa 300
gaaggtctatc gcaacgaagg ttttgggaac agtaaaatgg ttcaatgtaa ggaacggata 360
tggtttctatc aacaggaatg acaccaagga agatgtatgt gtacaccaga ctgccataaa 420

gaagaataaac cccaggaagt accctcgagc tctaggagatg ggaagagactg tggagtttga 480
agtctgttaa ggaagaaaag gtgcccagggc agcaaatgtt acaggtccctg tgggtgtccc 540
agttaaggc agtaaatatg cagcagaacgc taaccttat agacgctatc cagctgttagt 600
gtttctctca cgtcaatacc agcaaaatga ccagaatagt gagagtgagg aaaaagaaccg 660
gggatacggag agtgctcccg aaggccaggg ccaacaacgc cggccctacc gcaaggcagag 720
gtttcccaact tactacatgc ggagacccta tgggcctcga ccacagtatc ccaacctctc 780
tgtgcagggg gaagtcatgg agggctctga caccaggggt gcagtgagaa acagtgagacc 840
agtggagcag aactgtatgc ggggatatac accacagctc gcaggggggc ctccctgcga 900
aaagcagcgt agagaggaac gcaatgaaga agataaagaa aatcaaggag atgagaccga 960
aggtcagcag ccaactcaac gtccgtacgg ccgcaaatct ccaacagcag gcagagccccc 1020
agaaaaaccc aaaccacaag atggcaagga gacaaaagca gccgatccac cagtgagaa 1080
tgtctgcctg cccgagggctg agcagggcgg ggctgagtga atgcgcgctt accatcttta 1140
ccatcatcgg gtttagtcat caacaagaa gaaatatgaa attccagcaa taagaaatga 1200
acaaaagatt ggagctgaag accctaaatg ctgtgttttt gcccgctgac cagataaaat 1260
gaactactcg cattatctat cagcagcagg gtttttatta tttttactca aagacgtccc 1320
tttttggtaa taacaaacgt gtttttttaa atggcctggg ttttctcaat acgcttttaa 1380
aggtttttaa attgtttcat atcgggtcaa gttgagactt ttaagaaactt caattttta 1440
ttgtaataaa agtttacaac ttgatttttt caaaaaagtc aacaaaactg aagcaacctg 1500
taataaagggt ctttaataat tgtcttttgc taaaaaaaa ggggaatat 1548

```

## (2) INFORMATION ON SEQ ID NO. 59:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1254 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ggaccgcttc ccccgagcca gcagcagcgt ttgacgtcat cgtgcgtgtg gtgccccctgc 60
tgccggggctt ggtgattgga ggaacccccg tgcctgacgg agggctgtag cctgtgagca 120
gcgagatcca gggacagagt ctccagcttcg ccgctgctgc cgccgcccgc gccacagagac 180
tgctgagccc tcccgctccgc cggccaccacc cactccggac acagaaacatc cagtcatgga 240
taaaaatgag ctgggttcaga agggccaaact ggcgagcag gctgagcgat atgatgacat 300
ggcagcctcg atgaagtctg taactgagca aggagctgaa ttatccaatg agggagaggaa 360
ctttccctca gttgottata aaaaattgtt agggagccgt aggtcatctt gggagggtcgt 420
ctcaagtatt gaacaaaaga cggaaagtgc tgagaaaaaa cagcagatgg ctgcagaata 480
cagagagaaaa attgagacgg agctaaagaga tatctgcaat gatgtactgt ctcttttggg 540
aaagtctctg atcccccaatg cttcacaaagc agagagccaa agtcttctat ttgaaaatga 600
aaggagatta ctaccgttac ttggctgagg ttgcccgtgg tgatgacaa gaaagggatg 660
tcgatcagtc acaacaagca taccagaaga cttttgaaat cagcaaaaaa gaaatgcaac 720

aaacacaacc tatcagactg ggcctggccc ttaactttct tgggttctat tatgagattc 780
tgaactcccc cagagaaaagc ctgctctctt gcaaaagacag cttttgatga agccattgct 840
gaactttgaca caattagtag agagtctatc aagacacagca cgtctaataat gcaattactg 900
agagacacact tgacattctg gacatcgcat acccaaggag acgaagctga agcaggagaa 960
tgaggggaaaa attaacgggc cttcccaactt ttgctgcctt cattctaata ttacacagtl 1020
agaccatttg tcatccatgc tgtcccacaa atagtttttt gtttacgatt tatgacaggtl 1080
ttatgttact tctatttgaa ttcttatatt ttccctgtgg gttttatggt tagttttgggl 1140
ggagtaggag ccagttttaac gtttggggag ttgtctgttt ttctgtcttt gagggtgggl 1200
ccagratggg ggggtgttgg gattttttgt taccagtttt tgagggtgtt ttgg 1254

```

## (2) INFORMATION ON SEQ ID NO. 63:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 954 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

cctcttcttt ttctttttct tctttttttt ttctttttt ttttttgta gagcagggtc 60
actttattgg tatagagact gcagagggac caggggcttt agctgttggc agctatggtg120
tccttaatcc agtcacacata gttgtagacc ttggtgtaga ctccaggcct gtctctctgg180
gcacagccat agccccagga gacaattcct tggagctctc cattggagac cacagggccca240
ccagaatcac cctggcagga atccttgctt cctcagagga agccccacac gaacatgttg300
ttggtaatct ttccagggtg ggaggcttca cactcagcct ggctcagcac agggcatcc360
aggcactgca gctcgtctgg gtatgcggca ccagaactca gagtgttgcc ccagccggag420
atgagggaat cggtgccagc agctggaggg gcagtgggca gagagatggc ggacacggg480
gaattgatga cggcagggtg ggagagcttg atcagcagga tgtcattgtc cagagtcgg540
ctgttgtatt tggggtggcg gatgatcttg gccgcattga tgaactgttc attccctcc600
aggacttcga tgttgtgctc tcccagcttc acctggatgc gggacttgta gcagtgcac660
gctgacacca cccactgttc gctgatgagg gagccaccgc agaagtggta gccagaattc720
aaggacacct ggtaggggac agaattctcc tcacagatgt agcccccaac gatcttgta780
tcacatcaa agggggcagc aacagcagct gcaacaaagg taaggatcag aagtagattc840
atggtgttag agtgtgcctg attgctggtg gagaacccgt ctttatacct ccgaggtatg900
gggagaggag gtgtctgtga ggtgagggtc actgctcttc ccagcacaaa caca 954

```

(2) INFORMATION ON SEQ ID NO. 65:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2213 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

jggcgaccgg cgggggggtcg aggcctgcct ctccgagagc tcttgggcgg gcggtccggg 60
ccggggggccc caggtgcgct tcccttagag agggattttc cgggtctcgt ggcagaggaa 120
caacacagaaa ctgggggctc agtctccacc ccaacgtggg cgggattccg cccggataag 180
accocgtctc tggccctcga taggggttga cctccgcagc cgcagaggag ggcgcagacc 240
ggcctcgaaa agcctctcgt tgggtggctg aactctgac tgcacctaga gtcatggcca 300
ggcgcaaccaa aggaggtact gtcaaaagct ctccaggatt caatgccatt gaaga-gccc 360
agacccctgag gaagcccatg aaagggctcg gcaaccgat agagccatt attagcgccc 420
ttgcctaccg caacacccgc cagcgccagg agatcaggac agcctacaag agcaccatcg 480
gcagggaact gatagacgac ctgaagtcag aactgagttg caacttcgag caggtgattg 540
tggggatgat cagcgccacg gtgctgtatg acgtgcaaga gctgcgaagg gccatgaagg 600
gagccggcac tga-tgagggc -tgcttaattg agatcctggc ctccgggacc cctgaggaga 660
tccggcgcat aagctcaaac taccagcagc aatatggacg gagccttgaa gatgacattc 720
gctctgacac atcgttcatt ttccagcgag tgctgggtct tctgtcagct ggtggggagg 780
atgaaggaaa tta-ctggac gatgctctcg tgagacagga tgcccaggac ctgtatgagg 840
ctggagagaa gaaatggggg acagatgagg tgaaaattct aactgtctc tgttcccggg 900
accgaaaca cctgttgcat gtgtttgatg aatacaaaag gatatacag aaggatatgt 960
aacagagtat taaatctgaa acatctggta gctttgaaga tgctctgctg gctatatgaal020
agtcgatcga gaacaaatct gcatattttg ctgaaaagct ctataaatcg atgaagggtc1080
tgggcaccga tgataaacac ctcatcagag tgatgggttc tcgagcagaa attgacatgt1140
tggatatccg ggcacacttc aagagactct atggaaaagt tctgtactcg ttcatcaagg1200
gtgacacatc tgggacttac aggaaagtac ctctgtttct ctgtggagga gatgtataal260
ataaaaatcc cagaaggaca ggaggtattc caacactttg aattttttta acttcaattt1320
ctcacactgc tattatcatt atctcagaat gcttatttcc aattaaaacg cctacagctg1380
cctcctagaa tatagactgt ctgtattatt attcacctat aattagtcatt tatgatgctt1440
taaagctgta ctgcatttcc aaagcttata agatataaat ggagatttta aagtagaaat1500
aaatatgtat tccatgtttt taaaagatta ctttctact tgtgtttcac agacattgaa1560
tatattaaat tattccatat ttctttttca gtgaaaaatt ttttaaatgg aagactgtct1620
taaaatcact tttttcccta atccaatttt tagagtggct agtagtttct tcattttgaa1680
ttgtaagcat ccggtcagta agaatgccca tccagttttc tatatttcat agtcaaagcc1740
ttgaaagcat ctacaaatct ctttttttag gttttgcga tagcatcagt tgatccttacl800
taagtttttc atgggagact tctttcatca catcttatgt tgaatcact tctgtagctc1860
aaagtatacc aaaaccaatt tatctgaact aaattctaaa gtatgggtat acaaaccatal920
tacatctggt taccaaacat aaatgctgaa cattccatat tattatagtt aatgtcttaal980
tccagcttgc aagtgaatgg aaaaaaaat aagcttcaaa ctaggatttc tgggaatgat2040
gtaatgctct gaatttagta tgatataaag aaaacttttt tgtgctaaaa atactttta2100
aaatcaattt tgttgattgt agtaatttct atttgcactg tgcctttcaa ctccagaaaac2160
attctgaaga tgtacttga ttaattaaaa aagttcactt tgtaaaaaaa aaa 2213

```

## (2) INFORMATION ON SEQ ID NO. 67:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

cctcgtgcag gtgcaccgct tgcctctaaa agctctggag gatggccggg cataatgggtc 60
tccatgtgtc aacaaacaga tccaaagggt cctaattgaa tgcgcagatg aataaataa 120
taatgtggag gctgtggagc tgcctaattc caatcatttg gttcaattgc agcagatga 180
tcttcacta ggcagctcaa tggagaatgg cttaaactac atggctgtgg catttctat 240
gcagttagta aaaaactctg tggtagatga aaggagtggt cctcatgtta ctgaggcaga 300
tctgttccac accattgaaa cctccatgag gattaatgct cactccagag ccaatgtccc 360
agaaggatrg ccccaagctg tggaaagtag gcgatccaac catgaagcaa tgattgatcg 420
tgctcatgga ggcaccaact ttatgatgca ttctgggac tctcaagcct cagagatga 480
tgacctcca ggcctgaggg agaaggcaga gtatctctg aggggaatgg tgaatctca 540
ccattcagca gcagctggcc gcgacagta tcaagctttc tctgcatttg ttggacagat 600
gcacccagca ggaataacta agaccgatga tctcaataca aggttctttc gtctgtgtac 660
tgaaatgtgt ttgaaataga gtacccgtgc tcaggctgag cagcagcaca atcctgtctg 720
caatcccaac atgatccgag ccaagtgtca tcaacaacct gatgcctttg ttogactcat 780
tgcaatgctc gtgaaacact caggggaggg ccccaaacat gtcacaaaga ttaattctgt 840
gaacaaagtc cttgtgtatg tagtggagtg tctccttcag gatcatgatg ttctgcagag 900
tgaaattcag caacttccct accatcgaat ttatatcatg cttctcttgg aactcaatgc 960
acctgagcat ggttgggaaa ccaataattt ccagacactt acagctttct gcaatacatt 1020
cacatctgt aggcctcaca aagctcctgg ctttgtatat ccttggtctg aactgattct 1080
ccatgggata ttattgcgaa gaatgctggc acatacgcca cagcagaagg ggtggcctat 1140
gtatgcagag ctactgattg atttattcaa atatttagcg ctttctctta gaaatgtgga 1200
actcaccasa cctatgcgaa tctctacaaa gggcacttta agagtgtctg tgggttcttt 1260
gcatgatttc ccagagttcc ttgtgataa cctattatgg ttctgtgatg tgatccccacc 1320
taattgtatc cagttaagaa atttgatctt catgttgagt gaaattaaca tgaggtcccc 1380
cgacccattc actcctaact taaagggtga catgttgagt aaaaaggatt tggattccta 1500
tcttaaacat cgatcaccag tcactttctc gtctgatctg cgcagaacct acaggtatcc 1560
aatgaacctg ggaatcgcta caacctccag ctctacaatg caactggtgt ctatgtcggt 1620
actcaggcca ttgcgcacat ccacaaacag ggcagcacac ctccaatgag caccatacct 1680
cactccgac acatgggatc ctccagaagt ttgctgtgtg acttgagcac tggaggtctg 1740
ctctctttc tgaatgcact tgcacaaatg ctccgtacc cactcactac 1800

tccagtgsa ccatgctgta cctttttgca gaggccataa cggagccat ccaagaacag 1860
atcacaaag ttctcttggg acggttgatt gtaaataggc cacatccttg gggctctct 1920
atcaccttca tctgagctgat taaaaaccca gcgtttaagt tctggaacca tgaattgaa 1980
caactgtgcc cagaaatcga aaagtatttc cagtcggtcg cacagtgtct cactgggacg 2040
agcagggccc agcagataat ggaagggaca ggtgccagtt agacgaaact gcactctctg 2100
tgtagcttcc agtctagagg tctcactgca ccgagttcat aaactgactg aagaatcct 2160
tcagctcttc ctgaccttcc cagcctcttg ttgttgggtg atctgcccc aactcgttg 2220
ggatcagcct cctgtcttat gtgggcacgt tccaaagttt aaatgcattt ttgtactct 2280
tggccaaaat ttgaaagatg ctgtgaatat cttttgaaat ttgtgtaaat acatgaaaga 2340
ggaaatgact ttgttcgaa cttctgggett tgtgcaagct gtgtccaagg ccaatgata 2400
aaactgtccc ttgtaatgaa gaggcagctg atgcattgca cttgtctgag ggcatactat 2460
catgtctctt gacattcctg gtgtcccaaa gaatagcaaa aagccagttt gaattatg 2520
taactatttt tttaattggt gacaggggac cttgaaaatc actaagttat taaaaatgt 2580
gatgtgctag aattggatat tccaggaaac atgggaaggg ctcaactattg gaatccatg 2640
atgttccatt ttgtctctac ccaaacgtat ccaaaagctg actgcatttg taccattta 2700
ttctcttttg ggaattatca cctcagcctg ctgagatcgg ggtcagctct ttaataaag 2760
ggaaaacaga ccaggcctaa agcccacccc ctacccctca cccccccaca atcctctct 2820
gaaactctaa aaaccagtgg ggaatttagg gaaagggaac ccaaacccgc atcaattg 2878

```



## (2) INFORMATION ON SEQ ID NO. 68:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

atgatatttt ggatgtagtc ttttgattgt ttaaatctta aaaagtaaat ggatcttttg 60
acactggggt atgtttttatt tttatgtgtg caaattttaa ccatattctt ttctagttaal20
agagagaaaa gcaagttgct ccagaaaaaac ctgtaagaa acaaaaagaca ggtgagacttl80
cgagagccct gtcattcttc aaacagagca gcagcagcag agatgataac atgtttcaga240
ttgggaaaaat gaggtacgtt agtggtcgcg attttaaagg caaagtgcta attgatatta300
gagaataatt gatggatcct gaaggtgaaa tgaaccagg aagaaaagggt atttctttaa360
atccagaaca atggagccag ctgaaggaac agatttctga cattgatgat gcagtaagaa420
aactgtaaaa ttcgagccat ataaataaaa cctgtactgt tctagtgttt ttaatctgtc480
ttttacattt ggcttttgtt ttctaatagt tctccaagct attgtatgtt tggattgcag540
aagaatttgt aagatgaata ctttttttta atgtgcatta ttaaaaaat tgaagtgaagc600
taattgtcaa cttttataag gattactttg tctgtccacc acctagtgtg aaataaaatc660
aagtaataca atcttaaaaa aaaaaaaaaa aaaagtcgag c                                701

```

## (2) INFORMATION ON SEQ ID NO. 69:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 817 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

gttttttttt tttttttttt ttttttttaa gcacagaaaag cttttattac cacagaggaa 60
atcaggaaat gctggaggca gcctcgttag ctgtgtgatc agggaggggga cagcaggcgg120
gaacccgtca tcaatcatgt ctgggcagtc tcccaaccac caggtttgtt tggttcaggal80
gaggcgtttg ctgggctgtg tgtgtgtatg atcaggaagg tcagcctcaa caaatgggct240
tcttcctgga cataggacag ccagaatcgg ggacaccagc tgcacagaca ccacctaaa300
atggaaatca aattaggctc attacatcag gaagtacatt tcacctgat cataaaagag360
ggacaaggga gcactgggct ctactggata gcctttcttt tagataagat gcttttaaaa420
gttaaacatt ggcagggcct tccccctagc taacagcaag cagcacacaa ttccaagtca480
gctgttaaa cttttgttat cttgttatc tgttatatt tggatttga acgaaattga540
tggagtacga gcgggtagag gaatcctggt tgatctggaa attttcctg gagagcccaa600
aaggctggag aaccaagttc ccaagatctt ttaatttacc taacatctct tcttttagtc660
tttcattacg ttcttcaatt tgcttaggta atctcataca agcttctctt gcttgatgta720
ttgatgaagg ttcccgcctg ctgtcccttc cctgatcaca cagctaacga ggctctcca780
gcatttcctg atttcctctg tggtaataaa agctttc 817

```

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2686 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

gcaaggcccta ctgtcgccgt ggaggggagg tgtagccggt cttgggggt aggcggtagt 60
ggcggaagag gttcgccggt tgatggcgga tcaggatcgg aagcctgcgt aactttctcc 120
cttgatccgg gagtorttcc acgagattca caatgacatc cttcaagaa gtccatttgc 180
agacttccaa ctttgcccat gtcatctttc aaaaatgtggc caagagtta cctcctaag 240
cacactcgga atgtcattac accttaactc catatattca tccacatcca aaagatcgg 300
ttgtgtattt caaggttggg tggagtactg ctctgtatta ttacacgttt ttatgtccc 360
ctatgcctga acattattgt gaaggatcaa cagtcaattg tgtactagca ttccaaggt 420
attacctccc aaatgatga tgagaatttt atcagttctg ttacgttacc ctaaggtgt 480
aaattcgtgg agcaagtaca cctttccagt ttccagcttc ttctccagt gaagagctgc 540
ttactatgga agatgsagga aattctgaca tgtttagtgt gaccacaaa gcaggcttc 600
ttgagttgaa aattgsagaa accatgaaag aaaaagaaga actgttaaa ttattgccg 660
ttctggaaaa agaaacagca caacttcgag acaagttgg gagaatgaa agagactta 720
accatgagaa aaaaagatgt gcccaactgc aagcagaaca aaaggtctct actgaagtaa 780
cacaaaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgt gctacatcca 840
aagcccatca gcttgaggaa gatatttgtt cagttaacaca taagcaatt gaaaaagaa 900
ccgaattaga cagttttaa gacaaaactca acatgaaaga gaacaactt 960
aatgtcagtt gaagcacag aggatgaaa aggaacttta taaggtacat ttgaagaata 1020
cagaaaataga aaataccaag cttatgtcag aggtccagac ttaaaaaat ttatagtgga 1080
acaaaagaa cgtgattact catttcaaa agagatttgg caggctgcag ttatgttgg 1140
ctgaaaagga aaatctgcaa agaactttcc tgcattaca ctaagttaa taagtattt 1200
gttttttaaa ggagcaactt cgtaaaagc aggaacaggt tcaggcaact cggaagaag 1260
ttgtctttct ggctaaagaa ctcagtgtg ctgtcaactg acgagacaga gatgtggcag 1320
acctgcatac tgcacgcttg gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg 1380
cagaaactaa actcaatgct atgaaaaaag atcaggacaa gactgtata cctggaacag 1440
aactaagaga aagagttgaa gatctgaact tccgtcttca gatggctgca gaccattata 1500
aagaaaaatt taaggaatgc caaaggctcc aaaaaaactt aaaaaaactt tcagatcaat 1560
cagcctaata taataatgtc ttcaaaaaga aacgggggaa tcagcagaaa gtgaatgat 1620
cttcagttaa acacagacca gccactctcg cctctactgt agatgtaaa ccactacatt 1680
ctgcagcaga gccagatttt gacatagtaa caaaggggca agtctgtgaa atgaccaag 1740
aaattgctga caaaaacagaa aagtataata aatgtaaa caactctgca gatgagaaa 1800
caaaatgcaa taatatgct gatgaacttg tagctgaagt acaggacaat tataagaac 1860
tgaaaattgc tgaaaatgta aaacttgaa cgaagaaatgga agatggagca gatggctg 1920
tttaccocaga tgaataacaa aggcacactg tcagagtccc ctttgggga ctggaagaca 2040
atgttgtctg cagccagcct gctcgaact ttatgtcgcc tgaatggctt gaggaactct 2100
aggatagcaa agaagatgag aatgtgccta ctctcctga tctccaagt caacatttat 2160
gtgggcacag gacagccttt tgctttgatt ccagctttga tgttcacaag aagtgtcccc 2220
ctctgtgagt aatgtttctt cctaactatg atcagagcaa atttgaagaa catgttgaaa 2280
gctcactggaa ggtgtgccg atgtgcagcg agcagattccc tcttgactat gaccagcagg 2340
tgtttgaaag gcagtgtgcag acccattttg atcagaattgt ctcaaatatt gactagttac 2400
tttttattat gagttaatat agtttagcag taaaaaaaaa aaaaaaaacc acacctaaaa 2460
tagacacagt aggagacct agagcggatg ctttctgca ccttttactg cactttctga 2520
ccaggagcta ctttgagttt ggtgttacta ggatcaggg cagtctttgg cttatcaata 2580
aattttaact tctgttaatc ttacaaaaat ttaaaaaaaa aaaaaaaact cgtactttat 2640
ttatccctag ttgcagactg ctgaataaag gtcaaggatt atccat 2686

```

## (2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 922 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cdna library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctgctctgaa aagccatctt tgcatgttc ctcatccgcc tcttgctcg cggcagccgc 60
ctccgcgcgc cgcctctctcc gccgcgcgcgc actccggcag ctttatcgcc agagtcctctg120
aactctcgct tctcttttaa tccctcgcat cggatcaccc gcgtgcccca ccatgtcagat180
cgacgcgtga gacacccagc cccgaatcac caccaggac ttaaaggaga agaagggaagt240
tctggaagag gcagaaaatg gaagagacgc cctctctaac ggggaatgcta atgagggaaa300
tggggagcac gagcctgaca atgaggtaga cgaagaagag gaagaaggcg ggtgatggtg360
aggaaaggga tggagatgaa gatgaggaag ctgagtcacg tacgggcaag cgggcagctg420
aagatgatga ggatgacgat gtcgatacca agaagcagaa gaccgacgag gatgactaga480
cagcaaaaaa ggaaaaagta aactaaaaaa aaaaaggccg ccgtgacctt ttaccctctc540
acttcccgct tcagaaatcta aacgtgggtca ctttcgagta gagaggcccg cccgccacc600
gtgggcagtg ccaccgcgag atgacacgcg ctctccacca cccaacccaa accatgagaa660
tttgcaacag gggaggggaaa aaggaccaaa acttccaagg cctctgcttt ttcttaaaa720
gtactttaaa aaggaaaatt gtttgatgt tctatttaca ttgatagtg ttgacatat780
tgtaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcgttc840
tctggcctac ttctggaatt ttacgttggt ggggtgttga ccatgttcaa ttataatccc900
aaaaggggga aaaaaaacct tt                                     922

```

## (2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 870 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ggaagtgagg gtgcgaggcc tgcgtcacag cgagcggagc cgcggtccgg acggcagcgc 60
gtgccccgag ctctccgcct ccccccgcgc gccagccgag gcagctcgag cccagtcgcg:20
ggcccccaga gcagcgcgca gagcagccccc agtagcagcg ccatggccgg gtggaacgcc:80
tacatcgaca acctcatggc ggaaggggacc tgcaggagcg cggccatcgt gggctacaag:240
gactcgccct ccgtctgggc cgccgtcccc gggaacacgt tcgtcaacat cagccagct:300
gaggtgggtg tcctgggttg caaagaccgg tcaagttttt acgtgaatgg gctgacact:360
gggggcccaga aatgttcgt gatccgggac tcaactgtgc aggtggggga atttagcatg:420
gactctcgta ccaagagcac cgggtggggcc cccaccttca atgtcactgt caccagact:480
gacaagagcg tagtccgtct gatgggcaaa gaaggtgtcc acggtgggtt gatcaacag:540
aaatgttatg aaatggcctc ccaccttcgg cgttcccaat actgacctcg tctgtccct:600
ccccctcacc gctcccccac gctttgcacc ctttccctcc ccatacacac acaaacatt:660
tatttttttg ggccattacc ccataccctt tattgtctgc aaacccacat gggctggggg:720
ccaggggctgg atggacagac acctccccc acccatatcc ctcccgtgtg tgggtggaaa:780
acttttgttt ttgggggttt ttttttctg aataaaaaag attctactta acaaaaaaaa:840
aaaaaaaaaa aaaaaaaaaa aaaggggggg                                     870

```

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1418 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

ataaaagagg aaagagtgc caggttttca ctccactgag actgcagaac tcagagctgc 60
ttttctcttg tggccagctg gggaccagca tcatgaagt gatggtggtg gtcttggtct 120
gcctccagct cttggaggca gcagtggtca aagtgcctcc gaagaaattt aagtctatcc 180

gtgagaccat gaaggagaag ggcttgcttg gggagttcct gaggacccac aagtatgac 240
ctgcttgga aatccgcttt ggtgacctca gctgacctca cagcccatg gcctacatgg 300
atgcttgcta ctcttggtg atccagcatg ggaactccacc ccagaacttc ctggtccttt 360
ttgacaccgg ctctcccaac ttgtgggtgc cctctgtcta ctgcccagag caggcctgca 420
ccagtcactc ccgtttcaac ccagcgaggt cgtccacctc ctccaccaat gggagacct 480
tctccctgca gtagggcagt ggcagcctca ccggctcttt tggctatgac accctgacct 540
ccagagcat ccaggtcccc aaccaggagt tcggcttgag tgaagatgag cctggtacca 600
acttctgcta tgcgcagttt gatggcatca tgggcttggt ctacctgtct ctgtccgtgg 660
atgaggccac cacagctatg caggggcatgg tgcaggaggg cyccctcacc agcccgctgt 720
tcagcgctta cctcagaac cagcagggtt ccagcggggg agcggttgtc ttgggggggtg 780
tggatagcac cctgtacac ggcagatct actgggggcc tgtcacccag gaactctact 840
ggcagattgg cattgaagag ttctctatcg gcggccaggc ctccggctgg tgtctgagg 900
gttgccaggc catctggag acaggcacct ctctgctcac tgtgccccag cagtacatga 960
gtgctcttct gcaggccaca gggggccagg aggatgagta tggacagttt ctctgaactc 1020
tgaacagcat tcagaatctg cccagcttga ccttcacat caatggtgtg gacttccctc 1080
tgccaccttc cctcatatc ctccagtaac acggctactg caccgtggga gtccagccatc 1140
cctacctgtc ctccagaac ggcagcccc tgtggtacct cggggtatgc gccgcttagal 1200
cctactatct cgtctacgac ttgggcaaca acagatagag ctttgccact gcgccttagal 1260
cttctgtgct cgacagctgg gctccccctt tctcttgac cctgcacctt cttagggcat 1320
tgtatctgtc ttctccactc ggattcagcc ttctttttct ggaactctga ctttctctaa 1380
taataaatag ttcttctttt aaaaaaaaaa aaaaaaaa 1418

```

## (2) INFORMATION ON SEQ ID NO. 76:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1712 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

gtggcagaaa acctcatgac acaatctctc cgctccctcg tgttggtgga ggatgtctgc 60
agcagcattt aaattctggg agggcttggg tgtcagcagc agcaggaggg gcagagcaca 120
gcctcgtcgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca aacgccgacc 180
aaggaaaact cactaccatg agaattgcag tgatttctt ttgcctccta ggcatcact 240
gtgcctatcc agttaaaccag gctgattctg gaagtctctg ggaaaagcag ctttaacaa 300
aataccocaga tctgtgtggc acatggctaa accctgaccc atctcagaag cagaatctcc 360
tagcccccac gaatgctgtg tcctctgaag aaaccaatga ctttaaacaa gagacccttc 420
caagttaagt caacgaaagc catgaccaca tggatgatat ggatgatgaa gatgatgac 480
accatgtgga cagccaggac tccattgact cgaacgactc tgatgatga gatgacactg 540
atgattctca ccagctctga gagtctcacc attctgatga atctgatgaa ctggtcactg 600

atcttccccc ggacctgcca gcaaccggaag ttttcactcc agttgtcccc acagtacaga 660
cacatgatgg ctggagggtat agtgtgtgtt atggactgag gtcaaaatct aagaagtctt 720
gcagacctga catccagtac cctggtgcta cagaacgaga catcacctca cacatggaaa 780
gcgaggaggt gaactgggtga tacaaggcca tccccgttgc ccaggacctg aacggccctt 840
ctgatttgga cagccgttgg aaggacagtt argaaacgag tcagctggat gaccagagt 900
ctgaaaccca cagccacaag cagtcacagt tatataacgc gaaagccaat gatgagagca 960
atgagcattc cgatgtgat gatagtcagg aactttccaa agtcagccg caattccacal 1020
gccatgaatt tcacagcca gaagatatgc tgggtgtaga ccccaaaagt aagggaagag 1080
ataaacacct gaaattctgt atctctcatg aattagatag tgcattcttc gaggtcaatt 1140
aaaaaggaga aaaaatacaat ttctcacttt gcatttagtc aaaaagaaaa atgccttatal 1200
gcaaaatgaa agaaacactg aaatgcttcc ttccagttt attggttgaa tgtgtctatal 1260
tttgagctcg gaataaccta atgtgtttga taattagttt agtttgtggc ttcatggaal 1320
ctccctgtaa actaaaagct tcagggttat gtctatgttc attctataga aaaaatgcaal 1380
acctacactg tattttaata ttgtttatcc tctcatgaat acaaaattat gtagaagcaal 1440
acaaaaatct ttaccacct taaaaagaga atataacatt ttatgtcaat ataatcttt 1500
gttttttaag ttagtgtata tttgttgtg attatorttt tgtgtgtgta ataatcttt 1560
tatcttgaat gtaataagaa ttgtgtgtg tcaattgtct atttgtttc ccacgggtgt 1620
ccagcaatta ataaaacata acccttttta ctgcctaaaa aaaaaaaga gaaaagaaaa 1680
aaaaagaaag aaaaaaaggg gagggagggg ag

```

## (2) INFORMATION ON SEQ ID NO. 78:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

acgcgccccg ctgtgggtct cagcagctcg ggcggcgcca ggggtggcag cggcaaggca 60
gcccagcttc gcgaaggctg tcggcgcgcc gcggcccgca gccacccggc acgcgccttc 120
cccgcaggca ccggccaacg gccttccccg ccgccacgat gcccaagagg aaggctcagct 180
ccgcgcgaag gcggccaagg aagagcccaa gaggagatcg gcgcggttct cagctaaacc 240
tcctgcacaa gtgggaagcga accgaaaaaa gcagcagcga aggtataatc ttacagacaa 300
aaagtgcacaa caaaaggga aaggggagca agggaaaaac aggccgaagt ggctaaccac 360
gaaactaaag aagacttacc tgcgggaaac ggggaaacga agactgagga gagtccagcc 420
tctgatgaag caggagagaa agaagccaa tctgattaat aaccatatac catgtcttat 480
cagtggtccc tgtctccctt ctgtacaaat ccagaggaat atttttatca actattttgt 540
aaatgcaagt tttttagtag ctctagaac atttttaaga aggaggggaat cccacctcat 600
cccatttttt aagtgtaat gottttttt aagaggtgaa atcatgtgct ggtgtgttat 660
tttttggtag aaccagaaaa tagtggtgga tattgaatta tgggaggctc tgactgtctc 720

gggtgtcagc ttaacattcc acagatgggg ggtagtctt tatatcctat aatacaaaagc 780
atattaaaatg gcaatatgga gtacgtcctg catttaatgt ctggaacatt ttaattatcc 840
ctattatccca ctgtgttttt tagtagaatt gtttccataaa gaaaaccactc ctttgatcat 900
ggctctctct gccagaattg tgtgcactct gtaacatctt tgtggtagt cgtgtttcct 960
aataactcttg ttaactgtct gtgaaagatt acagatttga acatgtagtg tacgtgtctg 1020
tgagtgtgga actggtgggc cgtatgtaac agctgaccac cgtgaagata ctgtgtactt 1080
atagcctctt aaggaaaaat tgcctccaaa ttttaagctg gaaagtccat ggaataactt 1140
taaaaaagaa ttacaataca tggcctttta gaattccgt acgtatgtta agatttgtgt 1200
acaaattgaa atgtctgtac tgatcctcaa ccaataaaat ctacagttaa aaaaaaaa 1260
aaaaaaaaaaa aaa
1273

```

## (2) INFORMATION ON SEQ ID NO. 79:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2342 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

cctcggacga cccgactggc ctggggcggg acgtgggcgc gggggcgcg cgtcggcac 60
gctgcagggc tgaagcggcg gcggcggtgg ggaactgcac tagcccgcg ctcggcatgg 120
ctctcctggg cctcgggtctg gtgagctgta cctctcttct ggcaagtgaat ggtctgtatt 180
cctctcagtga tgaatgtgat gaattaacrc catcaaattt caaccggaaa gttattcaga 240
gtgtagattt gtggcttgta gaattctatg ctccatgggt tggctcactgt caaagattaa 300
caccaagaatg gaagaaagca gcaactgcac taagaatgtg tgtcaaaagt ggtgcagtgt 360
atgcagataa gcatcattcc ctaggagggtc agtatgggtt tcaaggattt cctaccatta 420
agattttttg attccaaacaa aacagaccag aagattacaa aggtggcaga actggtgaag 480
cgaattgtag tgcgcgcgtg agtgcctcgc gccagctcgt gaaggatcgc ctcgggggac 540
gaagcggagg atacagttct ggaacaaacag gcagaagtga tagtcaagt aagaaggatg 600
tgattgagct gacagaagac agctttgata agaattctct ggacagtga gatgtttgga 660
tggttgagtt ctatgctcct tgggtgggac aetgcacaaa cctagagcca gagtgggctg 720
ccgcagcttc agaataaaa gccctccgat acgggattag aggaattcct acaatcaga 840
ctacagtcac tcagattctg gcctcccgat atgacgggtg gcggacaaag tccgacatcg 900
tatttcagaa agcgagctct cctgtggatt atgacgggtg gcggacaaag tccgacatcg 960
tgtcccgggc ccttgatttg tttctgata acgccccacc tcttgagctg cttgagatta 1020
tcaacgagga cattgcacag aggaactgtg aggaacacca gctctgtgtt gtggctgtgc 1080
tgccccatct ccttgatact ggagctgcag gcagaaattc ttatctggaa gttctctgaa 1140
agttggcaga caaatcaaaa aagaaaatgt gggggtgggt gtggacagaa cgtggagccc 1200
agtctgaact tgggggattg gagggtttgg tagccccgc attggcgcca 1260

tcaatgcacg caagatgaaa tttgctctgc taaaaggctc cttcagttag caaggcatca 1263
acgagtttct cagggaagctc tcttttgggc gtggctccac ggcaacctga ggaggcgggg 1323
ctttccctac catcgttgag agayaagcctt gggacggcag ggaatggcag ctcctcggtg 1383
aggatgacat tgacctcagt gatgtggagc ttgatgacct agggaaaagt gactgtgag 1440
agccacaaca gaggcttcag accttttct tttctggga gccagtggat tttccaaga 1503
gtgaaggagg atctctcaca ctacagtgac tctaccagtg gccctttaac caagaaagt 1563
tacttgattg gtcatttgaa aacactgcac cagtgaactt ttgcattca caaaaaacatt 1623
gaaaaattct atgaattgtt gtgacgggtg aattgagtcg tattctgtca cataattatt 1683
tgaagaaaaa ttggctgtcg aaacattttt ctctctgact gctgttgaa tttcttgaa 1743
ggctgtttct tatgtatggg ttttttttaa tgtgatccct tcaattgaa attaatgct 1803
ttttccatta aagaataaaa tatthtgga aatgcogata aatgtatga ttagtatcc 1863
acatcataaa ttacagatga tgtttagcag taaatcaata ttttgaagt atcacagat 1923
gtctttcttc cccacaaact tttttaaaaa aaaaaaaga cctctttct ttgatgggt 1983
ccaactatgc ccaaccaaac agagatttta catggaaaac gggctcagtg agaactgat 2043
tcttgcccaa tatthtctt tgggctgtct ctagtgaata attattaa gaaatcagc 2103
gttatcacag tcaaggcttt ctatgttgtt aatgaacctc aaaaatagcc ttaagacat 2163
aaatcacgca gcaggttacc aatgcgaaca ggtagttcgc atttatgaa aacattcaga 2223
aaatgaagtt ttgaatttgt tggaaacatc aaaggactgt agagcatttt attgtaact 2283
aaaaaaataa atcaactgt cactaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2343
aa

```

2342

## (2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1959 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcagttatat aataagtttg ggagacaaaa tgatacgcac acgagagaag atgaagaaga 60
tactcaaaagt tccaaatctg aagaacatca tttgtactct aatccaatca aagaagaagt 120
gactgagttct aagttctctta agtactctga aatgagtgag gaaaaacgag ccaaaacttcg 180
tgaattttgag ctcaaaagtta tgaagttttca ggaatgaattg gaattctggg aaagaccttaa 240
aaaaaccaggc cagagttttc aggagcaagt agaacactac agagataaac ttcttcaaac 300
agagaagaag aaagagttag aaagagaacg agaagagac agaaagaata aagaaaaatt 360
ggaaatctcgc tccaaagaca agaaggaaaa agatgagtg actccgacaa ggaaggaaag 420
gaagaggcga cacagttacat cccccagccc atctcgcagt agcagtggtt gacgagtgaa 480
atccccatca ccaaaatcgg agcgatcaga gcgttcagaa agatctcata aagagagctc 540
acggtccagg tcattctaca aagattctcc tagagatggt agcaaaaaag ccaaaagatc 600
accatctggt tcaaggacac ctaaaaggtc taggcgatca cggtctagat ctctctaaaa 660

atcaggaaaag aagttccagat cccagttccag atctccacac aggtctcata aaaagtcaaa 720
gaaaaacaaa cactgacgta aatttttaaag atgctgtcac ttattggaaa tgcgatttgt 780
tttgtgcttg aacgggtctgt tttttaaaaa aacaaaaaat caaatgaaag agcattctctg 840
gggttttttg ttgttttttg tatgcattgtg taaactcatg agcaactgca tctgtagatc 900
tgctcattgtt ttatatatttg taaactactt tcattgtggc tatttctcaa gatgaaattt 960
ttattgttct aatggatttc atcagaaatg tgtataatgg atctgctgac agtagtagtal 1020
ttttgtttta ggaatgtttg acttagcaaa aataatacac atgtcttccc cctttttgtal 1080
gctttgacaa ttggaattag atttcaataa aaactctaac agaaaaactat aatgttgttt 1140
ttttgcccc aacggtgatat taagtccttt aaagtctcac tgagtttcaa actactgttg 1200
tgcttcttat acctgatgca ctttataaag cccagtggtc aagtagctta agttttatat 1260
ttactaaagt gactatccaa attaagggag ctgagactcc tatttgttgg ttgtttaacc 1320
atttgctttt gataaagttt ctttgggtta tactaatacc cagatatcaa agactaggtal 1380
gatattggat ggcgttttgt tagtggaatg cctggctaaa acattttttt cacagaagcal 1440
atatgatatt catacatcca acccatgttc tgagcaacta ctacttttta gggggaaaat 1500
aaatatcttt tcatttcttc ttctattatg aaagaagttt atttgtaaaa caaattttct 1560
aacaaggttt ggcctatagaa ttctcttgta tgattgttga ccttttataa tcttctgtag 1620
gctattcttt aaacactggc atcagaatat tttttataag ttgtgtttta aacagcttag 1680
ctgggtcccc ccccccactc caagagactt ggggttagtt atagctttta gtaaaattal 1740
aaaaataaat gtttttcagg aaacttcgta tctaattggt tgtaaaattca aggtcgcaaaa 1800
agtttgattta aaccatttgc agagttgaac tctattatga aaataaattt gctacggtat 1860
gaggaagaaa taaaacttgt gtaatgttgg tcataatact gctataaata taataaagggt 1920
ttattgtaga ttgaactgac aaaaaaaaaa aaaaaaaaaa

```

1959

## (2) INFORMATION ON SEQ ID NO. 81:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3708 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

```

gccccattta   tcacgcacgg   tagacaagct   tttttttttt   ttttttttta   cagcttataa   60
cacacactttt   attagaaaaa   ttatacataa   ctatagcatca   actattttca   agaacaatat   120
taaaccccgat   aagcaacaaa   aaccagacta   acaaaattgtg   taacaagaaa   ctaatgacct   180
ttctaaaaatc   aaacattcaa   ttatctacaa   tgtcttttta   caaacgggga   aaactcctgt   240
gtttcacaggc   acatcatatt   gaatataaag   ctgcaatagc   aattttatac   aattaccact   300
ctgaagaaac   tgaattcatta   aaacagtaat   tacgagtcca   caaatttaaa   acatttcaca   360
taatttttaa   ttattgggta   tacaactgaag   tctgagtttc   aaaagtgtat   tttttttccc   420
acaaaagcttt   caactcttaa   gctagaactt   tctggtttaa   cttgccccta   aaaagttaag   480
acatatctcg   ataatacata   cagtcacatg   attttctgatg   ctatctgtgc   tgttaataat   540

```

```

aaagctcttta   tttggatgta   tttttcttca   attaaattac   aggsaaactgg   atatatgatt   600
tcgctgcgaac   gctatataag   ttccaaacca   cggagctgtga   gcaactggaaa   agggagctaa   660
tcctaaaaact   tacaataaaat   atcagagaaag   ccgttagcttt   ttacagcatc   gctgctctaa   720
aagcttaagtt   gaccagggtag   ataattttccc   atcagctctgt   ccttctgtagt   ggcagggcaa   780
ttctctgttt   catgatcggga   ataactcaaat   agtccactcta   atcttttaa   aaactcctgt   840
tatagctctct   agaaaagttaa   gtttttttaat   agtccactcta   ctctaatcag   ctaactgttt   900
gctcatcttt   tgccctcact   aaaaataacag   atttcagtat   agccaagtt   tccagaaaga   960
ctccaaatgga   atgattttaca   aataagaaaca   ctttaaacaca   ggctcagctct   atctttttgt   1020
agctgaaggct   tactcagtcac   aacacaatttt   cggctacccc   tctgtctcat   attggaattc   1080
acttaaaagc   aatctcaaga   gggtagccatt   tgttgtttca   gataccatccc   ctaaggagaa   1140
tggtttaacag   gaagattgccc   agtgttactg   atggaaaagaa   gtgtttgttt   gttttttttt   1200
cttctgcaaa   accttacacca   tagtttttaa   ttaaacctgct   aggcattttt   ctacagaggt   1260
tttctttttc   agtcagtaaa   tgaagaacta   agataaaaaat   catgactttt   gactgcactt   1320
caacattatt   acatgcacca   atattgcaca   catctgttct   gaactgttaa   atcatcttcl   1380
tgaagtcttt   ggggtgctgt   ttctccatac   taactcaaaa   acaacccatc   taactcagtt   1440
ccctcaaaaga   tgaataatgac   aaatttaagt   tactggaaaa   aaatgaagaa   ggsaaaaggl   1500
aaagactcttg   taccagacaaa   aatctaaagt   ttctcaaaag   gttctgtgtc   cctacacact   1560
ggggggcaatt   tctaagcact   agtgaatcaa   acactagctta   taatgctctt   agctccttcl   1620
ataaatgga   accttggctc   aggtgttgcg   atgactgtac   tgtacgtgtc   ttctcgtgtc   1680
agctcaaatg   ctctgctgct   tttaagaacc   aagaagctgt   agaaactttg   ggcagctgtt   1740
ttctctgtct   taattcgaca   taactcaaac   aaactgtatg   attcagctgt   agttttagcal   1800
agagcacgct   gaagaccatg   aagcatctgc   tgagtctctt   tgttccatct   tcttttttcc   1860
tgcattctgt   cgcctcttga   tgcattctca   tctcttctct   tctctcatct   ttctttttcc   1920
ttctctctct   ccttctctct   ttctggcaga   agtctcaact   ctgggtattg   ctgacagata   1980
cttggagggt   cttctggggg   aagctctaca   ggtgtgtatt   cccatctgt   cccagtaac2   2040
ttgtccagct   ttgcctttaa   ctccctgagg   tgggtgttga   ggcatagctg   accatctcat   2100
gtttgtctct   gttgcctcca   tcaactgactc   ctggagggcg   ctggctctt   caataatggg   2160
ctcatcgata   acatcacgct   gctgatctgt   ctggagggcg   tctctcttag   gaacctctgg   2220
attttcaaat   tttttgagga   attcatccaa   ctctctctct   ttctctctct   tctctctctt   2280
tctaaggctc   tctggtacaa   gcggtgtgaag   acagcgtgta   aagagcttca   gtatctgttt   2340
attccacaaa   ggcctgagcag   gtaaaagaaa   cagtttttct   actcctcctg   tctctttcca   2400
catcatcaat   ttcttgggtg   cggtagccga   tccaaaagtag   taacaatatc   tgaataactc   2460
ctaagtgtgg   cctcaattgt   ctgtcatctc   aactctttga   cactgtcaac   aattagctc   2520
ctctctctct   tggctttgt   ttctttaaca   gttatatcaa   taggctccaa   tgcaaaactc   2580
tctctctcat   ttggaacaaag   tgttgtttga   tcaagtcatg   ttggcattct   tcaacgggga   2640
tccactgaaat   caggactatc   agggccacccc   attgatacat   tatcatctct   atccatctgc   2700
tcatgtgcag   gctgctctgt   caacatcacc   cctgcctcag   agagggcagg   gggatcatac   2760
aagatcacccg   catcattatt   actaataagt   ttgtcatctc   atattccacc   atcatttctc   2820
tctccaaaat   tatcatctct   atattgtatc   tcatatttca   aatggttaat   ttctctactc   2880
agattgtctg   tgcctgtgtc   agactcfaat   aggaagttag   aagtagtagt   gctctcaaac   2940
atctgctcat   cctccaaaagc   actgccttct   ctcatattct   cagcatcatc   actccaaa3   3000
tcacacaaat   cattttctgt   taaaatactg   atgttcccaa   ctctctctct   catggttatc   3060
tcttccactc   tactctgatt   caagctgaac   tgcgtggcca   cttcatgtct   attctagcca   3120
ggcagtggtt   gatcaaaagc   atgaaattct   ctaggtaaag   taatggcatt   ataaagctgt   3180
tcccgatctct   cctcggcgag   gtcaaccaca   cctgcggcaa   aagccattct   tatcttaact   3240
aatgcttcat   tacaactcgc   aagaaggtat   ttgctttctc   tctgtatagat   tcgaataact   3300
cccagtaaga   gatgtctctg   tgtccgtaat   gccattttta   ctttgggtga   gatgaactc   3360
ttccacgcgt   ctctctaaat   tacactcgaa   ccatggggct   tgggttagct   tcttatccca   3420
atgggcgcgt   agccaaaatt   ttgcccagagg   cactctttta   ctgagaacaa   tatgtgcta   3480
gaacattgtt   ctggtggctc   atgaaaacag   aagaaaacct   tgctctccgc   tggagattg   3540
cggggcgtct   tggcccgggg   agggggaagag   ggtcggggga   ggggggggga   aaaaggggga   3600
gccttctgca   ggtgtagctt   ccgagcagct   ccccgggccc   cagacccggc   gcctccttcc   3660
cgattcacctc   aaacacacaa   gatggctgcc   gttcaaccgc   cgactcttc   3708

```

[illegible]

- ```
(i) SEQUENCE CHARACTERISTIC:
    (A) LENGTH: 3045 base pairs
    (B) TYPE: Nucleic acid
    (C) STRAND: individual
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
                    ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
    (A) ORGANISM: HUMAN
    (C) ORGAN:

(vii) OTHER ORIGIN:
    (A) LIBRARY: cDNA library
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

gtccattgccc caaaatccgc tatgaaagct tgaccaatcc ccagtaaaat agacctctgg 60
gaaaagagct gccattattac ccattccccc aacaaccaag atcgaaacct cactatttgt 120
gatactggaa ctggaatgac caaggctgac ttgatacata accttggtag tatcgccaa 180
tctggggacca aagcgttcat ggaagctttg caggctgggt cagatattct tatgattggc 240
cagttccgtg ttggttttta ttctgcttat ttggttgcgt agaaaagtaa tggatccagc 300
aaacataaac atgatgagca gtacgcttgg gaggctctcg cagggggagc attccacagt 360
aggacagaca cagggtgaac tatggttcgt ggaacaaaag ttatcctaca cctgaaaaga 420
gaccaaaactg agtactttgga ggaacgaaga ataaaggaga ttgtgaagaa acattctcag 480
tttatttgat atccatttac ttcttttctg gagaaggaa cgtgataaga agtaacgagc 540
gatgaggctg aaaaaagga agacaaagaa gaagaaaaga aaaaagaaga gaaagagtgc 600
gaagacaaac ctgaattgga agatgttggg tctgtgagg aagaagaaaa gaaggtatgt 660
gacaaagaaa agaaagagaa gattaaggaa aagtacatcg atcaagaaga gctcaacaaa 720
acaaagccca tctggaccag aaatcccagc gatattacta atgaggagta cggagaattc 780
tataagagct tgaccaatga ctgggaagat cacttggcag tgaagcattt ttcagtgtga 840
ggacagttgg aattcagagc cctctattt gtcccacgac gtgtcctttt tgatctggtt 900
gaaaacagaa agaaaagaa caatatcaaa ttgtatgtac gcagagtttt catcatggt 960
aaactgtgag agctaatccc tgaatatctg aacttcatga gaggggtgtg agactcggag1020
gatctccctc taacataatc ccgtgagatg ttgtcaacaa gcaaaatttt gaaagtattc1080
aggaagaatt tggctcaaaa atgcttagaa ctcttttact aactggcgga gataaagag1140
aactcaaaag aattctatga gcagttctct aaaaacataa agcttggaa acacgaagac1200
ttctaaaaat ggaagaagct tcaagagctg ttaaggtact acacatctgc ctctgggtat1260
gagatggttt ctctcaagga ctactgcacc agaataaggg agaaccagaa acatatctat1320
tatatacag ctgagaccaa ggaccaggta gctaactcag cctttgtgga acgtctctgc1380
aaactgtgct tagaagtgat ctatatgatt gagccattg atgagtactg tgtccaacag1440
ctgaaggaa ctgaggggaa gactttagtg tcagtcacca aagaaggcct ggaacttccal500
gaggttgaag aagagaaaaa gaagcaggaa gagaaaaaaa caaagtttga gaacctctgc1560
aaaaatgag aagacatatt ggagaaaaaa gttgaaaagg ttggtgtgtc aaacgattgt1620
gtgacatctc catctgtgat tgtcacaaag acatatggct ggacagcaaa catggagaga1680
atcatgaag ctcaagccct aagagacaac tcaacaatgg gttacatggc agcaaaagaal1740
cacctggaga taaacccctg ccatccattt attgagacct taaggcaaaa ggacagaggt1800
gataagaacg acaagtctgt gaaggatctg gtcatctctg tttatgaac tgccgtcctg1860
tctctggct tcagctctgga agatccccag acacatgcta acaggatcta caggatgatc1920
aaacttggct tgggtattga tgaagatgac cctactgctg atgataccag tgctgctgtal980
actgaagaaa tgccacccct tgaaggagat gacgacacat cacgcatgga agaagtagac2040
taactctcgg ctgagggatg acttacctgt tcagtaactc acaatctctc tgataataa2100
tttcaagga tgtttttctt ttttttgggt aatattaaaa agtctgtatg gcatgacaac2160
tacttttaag ggaagataag atttctgtct actaaagtat actatgtatc gatggggta2280
aaagcagagc tagtaatgct ttttgagttt catgttgggt tattttcaca gattggggta2340
acgtgcactg taagactgat gtaacatgat gtaacctgt ttggtgttaa agtgtttagc2400
tgtcaagccg gatgcctaag tagaccaaat cttgttattg aagtgtctgc agtctatct2460

```

```

tgtgttttag aaaaagtatt gttacatctt gtaggatcta ctttttgaac ttttcaattcc2460
ctgtagttga caactctgca tgtactagtc cttcagaagt aggttaaaat gaagcaactc2520
gatggaagga tctctccaca gggcttgttt tccaaagaaa agttattgtt ggagcaga2580
agttaaaagc ctacctaaagc atatcgtaaa gctgtccaaa aataactcag acccaggtt2640
gtgggtgaaa atgtagtgtc cgagtccatc tctggttaaa gttgttaaaa atacagatga2700
cttaaaagat attgtgtgac agtgtcttat ttagggggaa aggggagtat ctggatgaca2760
gttagtgcca aaatgtaaaa catgaggcgc tagcaggaga ttgttaaaaa ctactgctc2820
caagggttga catggtcttc ccagcatgta ctacagaggt gtgggttgga gcaacatgag2880
gcacagaaaa caggaaatgca gacacatgc atccccgag tccatgagtt acatgtgtc2940
tcttagtgtc ccgtgtgtt tgatgttatt catggaatac cttctgtgct aaatacagc3000
acctaaatcc ttggccaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3045

```

## (2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2815 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

cagtgggcgc gcaaccagcc ttctagggcg gggaggaggt ggagtcacaa tatcaatgga 60  
 gcaagtccaca gtctgtgatg ccagcttctt ctgaaatct acccagaatg gaactcctgac 120  
 aatgatacag gacacacaaat ggggtgatcca ttcatgttc agcagctctac aaatccagca 180  
 ccaggaaatc tgggacctcc accctccctca ttcatcttg ggggaccagc agttggacca 240  
 agaggaaatc tgggtgctgg aaatggaaaac ctgcaaggac ctagacacat gcgaaaggcc 300  
 agagtggaaa ctacgagagt tgttcacatc atggattttc aacgagggaa aaacttgaga 360  
 taccagctat tacagctggt agaaccattt ggagtcattt caaatcatct gattctaaat 420  
 aaaaattaaat aggcattttat tgaatggcca accacagagg atgctcaggc cgcagtgagat 480  
 tattacacaa ccacaccagc gttagtattt ggcaagccag tgagagttca ttctctgagc 540  
 aagataaaaa gaataaagaa accctgaagg aaagccagatc agaagtttga tcaaaaagcaa 600  
 gagctgtggac gtgtgatata tctcagcaat ttgcccatt ctggctattc tgatagtgc 660  
 gttctcaagc ttgctgagcc ttatgggaaa ataaaagaatt acatattgat gaggatgaaa 720  
 agtcaggctt ttattgagat ggagacaaga gaagatgcaa tggcaatggt tgaccattgt 780  
 ttgaaaaaag cctcttgggt tcaggggaga tgtgtgaagg ttgacctgtc tgagaaatat 840  
 aaaaaactgg ttctgagat tccaaacaga ggcattgatt tactgaaaa agataaatcc 900  
 cgaaaaagat ctactctccc agatggcaca gaattccaa gtgataagaa atccaaaact 960  
 gctggttccc agaagactga gattcaacc gaagtaaga acaagaagag aagtcoggtg1020  
 aagatggtga gaaagacaca aaggatgacc agacagagca ggaacctaat atgcttctt1080  
 aatctgaaga tgagctactt gtatgtaag aagaagcagc agcactgcta gaaagtggc1140  
 gttcagtggt agacgagacc gatcttgcta attaggtga tgtggtctct gatgggaaa1200

aggaaccatc agataaagct gtgaaaaaag atggaagtgc ttacgacgca gcaagaaaa1260  
 agcttaaaaa ggtggacaag atcgaggaaac ttgatcaaga aaacgaagca gcgtggaaa1320  
 atggaattaa aaatgaggaa aacacagaac caggtgctga atcttctgag aacgtctgat1380  
 atcccaacaa agatcacaaat gaaaacgcag atgtgtcaaa tgatgagaa agggacgact1440  
 atacaatccc agatgagat agaatggac catatcagcc caatgttctc gttgtaatag1500  
 actatgtgat accctaaaaa gggttttact gtaagctgtg ttcaactctt tatatacaat1560  
 aagaagtgtc aaagaatact catgacgca gccttcccca ttatcagaaa ttaaaagaat1620  
 ttctgaataa attggcagaa gaacgcagac agaagaagga aacctaaagt gtgcaggag1680  
 atttaatgat ttcaagaaaa ataagtgttc ttgttttta atgttaacct ttttaata1740  
 caaactgat agttagaaga aaactattgt actcttttgt tttagtgag aaaaataga1800  
 tgtctgttca tgtgttaagt gttatagcaa aaaaaataca catatggtta agttaagtga1860  
 tagtttttgt ttatcagaa tggcaacaga cagaagtact ttgtagagat tgaactcta1920  
 agtactttaa gacaacttgc accctaaga aaaaaatgta gaacctttg gaaaaatgaa1980  
 attcttagt tccaagtttc aaagaatgt caacatttta ttccattcaa taagaacaa2040  
 aaccaatagt gtttttata ctttcatctg aaacattcca tgttttaac tgagccttg2100  
 agactttcat ttggagtttg aaaccgtttt ggttgcaatt catttttgga gaacttaatt2160  
 aacgtgagat tggcaattga aatgcaggtg cagttttctg ttaatgtcat gctgttgtt2220  
 aggtataaag aaatattaag taattggott tagattttgt catgttttcc cctgagttcc2280  
 tcttagattt cgtattctag tagtcaatgt attttcagtg aaatgcacaa atattcccatt2340  
 tatctttgac cagtattaat ttctgagac ttactcgttg tcaactgaat ccogtgattg2400  
 tcaatacatc ctggtataag caacatttga tttttgaagt gtgtagacca tctctcata2460  
 ttttcaagat gtaattttac atttctgcat ttttaaaaaa atcttgccaa aatccatagat2520  
 gcaagcttct aattcatgta cctgcacatg tgaaccttgt gaacagaat ttgcattgat2580  
 aattttgtgt atctgttaac ttcttggtta tatactgctt atactctgtg atccaagtta2640  
 gctgaagtga taccaataaa aagaaaaccc taggccaagt taattgtgta tacaagtgt2700  
 gaatgttaac caaaaaaaaa aacagttgtg gtttttacc gctctaacc ttgtgctgat2760  
 ctttaacaat ttatcgcttt taaatctaga gtgaattctt aaagagctgc cgcta 2815

0014579.00200

## (2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3462 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaaacga 60
cccgctctct ccgcctatct gccgctgttc cccggaagc gagttgcgac accgcaggtt 120
cccgcccgga agaagcgacc aaagcgctcg aggacccgca acatggtgcy gtcggggaa 180

aaggcagctg ttgtgctgtg tatggacgtg ggctttacca tgagtaactc cattctcgtt 240
atagatccdc catttgaaca aqcaagaagc gtgataacca tgtttgtaca gcgcagagtg 300
tttcgtgaga acaaggatga gattgcttta gtctctgttg gtacagatgg cactgcacaat 360
ccccctcttg gtggggatca gtatcagaac atcacagtgc acagacatctc gatgcctaca 420
tttttgatct ttgctggagg cattgaaagc aaaaatccac caggtttctca accgctcgac 480
tttcgtgatg cactaatcgt gagcatggat gtgattcaac atgaaaccaat aggaagaag 540
tttgagaaga ggcattatga aatattcact gacctcagca gccgattcag caaaagcag 600
ctggatatta taattcatag ctggaagaaa tgtgacatct cccgtcaatt ctctctgctt 660
tttcactctg gcaagggaaga tgggaagtgg gacagaggag atggccctct tcgctttagt 720
ggcctctggc ctctctctcc actaaaaagg attaccgaac agcaaaaaa gaagctcttag 780
atagtggaaa tgggtgatgt atctttagaa gg-gaagatg ggttgatga aattattcca 840
ttccagtga gctctgagaa actctgcgtc ttcaagaaaa ttgagaggca ttccattcac 900
tggcctctgc gactgaccaa tggctccaat ttgcttataa ggattgcagc ctataaatcg 960
attctacagg agagagttta aaagacttgg acagtgtgtg atgcaaaaac ccaaaaaaa 1020
gaagatcatac aaaaagaaac agtttattgc ttaaagtgtg atgatgaac ttgaagttaa 1080
aaagaggata ttattcaagg gttccgctat ggaagtgata tagttccttt ctctaaagt 1140
gatgaggaac aaatgaaata taaatcggag tggaaagtgt ctctctgttt gggattttgt 1200
aaaatctctc atgttctcag agaatctctc atgggaaatc aaagtctaaa ggtctttgca 1260
tcgaagatg atggcgagc tgcagttgca ctctctctcc tgattcagc ttggaagac 1320
ttagacatgg ttgcctatgt tgcgatgtct tatgacaaa gagctaatcc tcaagtcgg 1380
gtgctctctc cccatcataa gcaataacta gagtgtttag tgtatgtga cgcgctttc 1440
atggaagact tggcgcaata catgttttca tccctgaaaa acagtaagaa atagcctcc 1500
accgaggcac agttgaaatg tgttgatgct ttgattgact ccatgagctt ccgcaaa 1560
tatgagaaga cagacacccc tgaagacttg ttccaaccca ccaaaatccc aaatctcga 1620
tttcagatg tatttcagtg tctgctgcac agagctttac atccccggga ctacctccc 1680
ccaatctcgc agcatatttg gaatatgctg aatctctccc ctgaggtgac aacgaaaagt 1740
cagattccct tctctaaaat aaagaacctt ttctctctga ttgaagccaa gaaaaagat 1800
caagtgaact ctccaggaat ttccaagaac aacctgaag atggaacctc agctcaaaaa 1860
ttaaaagat tccaaggggg agcccaactc agcgtctcca gtctggctga aggcagtgt 1920
accctcgttg gaagtgtgaa tctgctgtaa aacttccgtg ttctagttaa acagaaag 1980
gcoagctttg aggaagcgag taaccaactc ataaatocaa tcgaaacagt ttggataact 2040
aatgaaacac cgtattttat gaagagcata gactgcattc gagccttccg ggaagaagcc 2100
attaatgttt cagaagagca gcgctttaac aacttctgga aagcccttca agagaaggt 2160
gaaattaaac aatataatca ttctctggaa attgtgtccc aggatggaat tactctgat 2220
accaaaagag aagcctctgg aagttctgtc acagctgagg aagccaaaaa gttctcggc 2280
cccaaaagca acccaagtgg agacacagca gctgtatttt aagaaggtgg tgatgtgac 2340
gattttatgg acatgatata ggtcgtggat gtatggggaa tctcaagagag ctgcactcgc 2400
tgtgtgctgg ggaagtctaa caaaacaagt tggatcgccg cattcaaggg gagcaaaa 2460
ctcaagaata tcccgacagg ttacctggag cgggatctct taactctctg tgaaatgaa 2520
acacacatat atattacaag ggaataatta gacccatac aagtttataa agagctcat 2580
ttattttctg ttgtgtgtat tatttttct ttgtgtttac atattacata 2640
catgctcttg agttctctga aagtagatct ttcttgacc tagtatatca gtgacagtg 2700
cagccctgtg gatgtgatta gtgtctcat tggaaacctg gcatggttat gctcattt 2760
cttaacccc tcacagctcc tcttttgct gatcctccaa cagctgtcac aactgtgtt 2820
gagcaagcag tagcatcttc tctctcccaa caagcagctg gcttaggaaa accatggct 2880
aggacgagct cacttctctt tttagttgag gcttctagt taccacatta ctctgctct 2940
gtatattgct ggttttcttt aagtgggtg ggaaggggag caacaatttc ctactaact 3000
cttttaagca gtgagttatg ttggtggtct catgaagaaa agaccttttg gcccaattc 3060
tgcoatacta gtcacacttt agaaaactcaa aaactcgaaa attactaca gtgttagaa 3120
ttatatcact tcaactgtct ctacttgcaa gctcacaaga gagaaagttt cgttatata 3180
aaaacactg gaaacttttc ggtctttccc atttccact aagtcagett tcaactttg 3240
ggatgtgttc tcttttacta aataagaaaa taacaaagcc ctatttctct tttttttct 3300
tccctacttc tgccttagt tccagttcct ctgtgtgtga cagacttctt ggtaccagct 3360
cacctctctc ttcagacccc tcatagctgc tcaataaac acagttttgt acatgataca 3420
ttaaagcat aatatgacta aaaaaaaaaa aaaaaaaaaa aa

```

## (2) INFORMATION ON SEQ ID NO. 85:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

atagggcccg  tctgcctgc  ggaagccggc  ggctgagagg  cagcgaactc  atctttgcc  60
gtacaggagc  tcgtgccgtg  gccacagcc  cacagccac  agccatgggc  tgggacctg  120
cggtagaat  gctggcgggc  aacgaattcc  aggtgtccct  gagcagctcc  atgtcgggt  180
cagagctgaa  ggcgcagatc  acccagaaga  tcggcgtgca  cgccttcag  cagcgtctg  240
ctgtccacc  gagcgggtgt  gcgctgcagg  acagggtccc  ccttgccag  caggccctg  300
gccccggcag  caggttctct  ctggtgtgtg  acaaatgcga  cgaacctctg  agcatcctg  360
tgaggataaa  caagggtccg  agcagcacct  acgaggtgag  gctgacgcag  accgtggcc  420
acctgaagca  cgaagtgcgc  gggctggagg  gtgtgcagga  cgaacctgtc  tggctgacct  480
tcgaggggaa  gcccttgagg  gaccagctcc  cgctggggga  gtaacgcttc  aagccctga  540
gcacgtgtt  catgaatctg  cgctgcggg  gaggcggcac  agagcctggc  gggcgga  600
aagggccctc  accagcatcc  gagcaggatc  aagggtccga  aataaaggct  gttgtaaa  668
gaaaaaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 86:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ggaaaccggt ctcattgaac tcgcctgcag ctcttggtt tttgtggct tcttcgtta 60
ttggagccag gcttacaccc cagcaacccat gtccaaggga cctgcagttg gtattgattc 120
tggcaccacc tactcttggtg tgggtgtttt ccagcacgga aaagtcgaga taattgccaa 180
tgatcaggga aaccgaacca ctccaagcta tctcgccttt acggacactg aacggttgat 240
cggtgatgcc gcaagaatc aagttgcaat gaacccccc aacacagttt ttgatgccaa 300
acgtctgatg ggaagcagat ttgatcatgc tgttgcacag tctgatatga aacatcgccc 360
ctttatggtg gtgaatgatg ctggcaggcc caaggtccaa gtagaataca agggagagac 420
caaaagcttc tatccagagg aggtctcttc tatggtctcg acaaaagatga aggaaattgc 480
agaaagctac ctggggaaga ctgttaccaa tgcttggtg cacagtgccg gcttacttta 540
atgactctca gcgtcaggct accaaaagat gcctggagact attgatggct tgcaatttac 600
tttaggaatt atttaatgga gccaaacttg tgcctggtaa ttcctttacg ggtttgggca 660
aaaaagggtt t

```

671

(2) INFORMATION ON SEQ ID NO. 88:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1108 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

agtggaggag ggagagacgc tggcccggga cccgaggggc gtgggcatcg gggggcgggc 60
ccgggttagg ggccgggaccg ccgcccgtgtt aaaggcgctt atttcccagg cagccgctgc 120
agtcgcacaca cctttgcccc tgctggcgtg accctgtcgc cactctctgt tcggacgtcc 180
ccacggcgccg ggtgcaggcg tcccctctgc aagcggttaga cttctttggg aatgggccc 240
cagtttaacta caagacaggc aatctatacc tgcggggggcc cctgaagaag tccaatgcac 300
cgctttgtcaa tgtgacccct tactatgaag cactgtgcgg tggctgccga gccttctcga 360
tccggggagct cttcccaaca tggctgttgg tcatggagat cctcaatgtc acgtcgggtc 420
cctacggaaa cgcacaggaa caaaatgtca gtggcaggtg ggagttcaa tggcagcatg 480
gagaagagga gtgcaaatc aacaagggtg aggcctgcgt gtggatgaa ctgacatgg 540
agctagcctt cctgaccatt gcttgcattg aagagtttga ggacatgga agaaagtctc 600
cactatgctt gcagctctac gccccagggc tgcgcgcaga cactatcatg gagtgtgcaa 660
tggggggacg cggcattgac ctcatgcaag ccaacgcccc gcggacagat gctctccagg 720
cacgcgcacga gtatgtgcc tgggttaccg tcaattggaa acccttggaa gatcaagacc 780
agctccttac ccttgcctgc cagttgtacc agggcaagaa gccggatgtc tgccttctct 840

caaccagctc cctcaggagt gtttgcctca agtgatggcc ggtgagctgc ggaagagctca 900
tgggaaggcga gtgggaaccc ggctgcctgc cttttttctt gatccagacc ctgggcacct 960
gttacttacc aactggaaaa ttttatgcat cccatgaagc ccagatacac aaaattccac 1020
cccatgatca agaattcctg tccactaaga atgggtgtta agtaaaacta gtttaataag 1080
ccccaaaaaa aaaaccgcgt cggctgcac 1108

```

## (2) INFORMATION ON SEQ ID NO. 89:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 720 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

aaagcagccg ccggcgccgg gtgcctcaca gcacgctgcc acgccgagcg agacccctct 60
ctgtacgccg gccgcgccgc acccaccatg gccacagttc agcagctgga aggaagatgg120
cgctctgggg acagcaaaag ctttgatgaa tacatgaagg agctaggaggt gggaaatagct180
ttgcgaataa tgggcgcaat ggcgaagcca gattgtatca tcacttgtga tggtaaaaaa240
ctcaccataa aaactgagag cactttgaaa acaaacacagt ttctctgtac cctgggagag300
aagttcgaag aaaccacagc tgaaggcaga aaaaactcaga ctgtctgcga ctttacagat360
gggtgcattg ttacagatca ggagtgggat ggggaaggaaa gcacaataac aagaaaaatt420
aaagtcgggg aattagtggt ggaagtgttc atgaacaatg tcacctgtac tcggatctat480
gaaaaagtag aataaaaaat ccatcatcac ttgggacagg agttaattaa gagaatgacc540
aagctcagtt caatgagcaa atctccatac tgtttctttt cttttttttt cttactgtg600
ttcaattatc ttatcataaa acatttttaca tgcagctatt tcaaaagtgt tggatataa660
taggatcacc cttttgggta ataaaaaaat gtgtttgtgc taaaaaaaaa aaaaaaaa720

```

## (2) INFORMATION ON SEQ ID NO. 90:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctctccgagc gattggctgt tagcggcggtt gtagttaagc tcgtgtaacy gggcggtgtg 60
cgccagctgc tgtagcgaag agagtgtggc gcgatgtctc acaccatttt gctggtacag120
cctacaagaa ggccagaagg cagaacttat gctgactacg aatctgtgaa tgaatgcacg180
gaaggtgttt gtaaatgta tgaagaacat ctgaaaaagaa tgaatcccaa cagtcctct240
atcacatatg acatcagcca gtgtttgat ttcatcgatg atctggcgaa cctcaggtgc300
ctgttttaccc gagctgatac ccagacatac cagccttata acaaagactg gattaaagag360
aagatctacg tgcctcttcg tcggcaggcc caacaggctg ggaataaatt gtgttggaag420
cacctggggg gttggggggg gcttggaaca caggtgtgta cagcgtgctg tactggaagt480
tttgtatcat agtaatcctg ttccacctt gtatactct agccaagatt gactgtatta540
gatgaaatgt gaggatcttg tcaactcgg taatgatatt tagatggaag ttgtctctcg600
ttctcttttt tctttttact tcaactcgg taatgatatt tagatggaag ttgtctctcg660
tcaacttaag ctggttccag tccctcaact gtccatatt acattataac attcacatac720
taacctctct tcaagatggg gtgggggggt gaaatgcagt ttagccatgt cctcaagata780
aagctctggt aaaaaataat aaatgtcttt tagttataaa aaaaaaaa aaaaaa 837

```

## (2) INFORMATION ON SEQ ID NO. 91:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

gtagggtcag cgtcggaggc ggtagtgcag gtggcggttc cttgagggaag agtgaggggt 60
ccaaacttttc tgcttatctg ggaggtgttg ggcgcgagaca gtcgagatgt cagagaaaaa120
gcagctgggtg gacttaggtc tgttagagga agacgacgag tttgaagagt tccctgccga180
agactgggtt ggcttagatg aagatgaaga tgcacatgtc tgggaggata attgggatga240
tgacaatgta gaggatgact tctcaatca gttacgagct gaactagaga aacatggtta300
taagatggag acttcaatgc atccagaaga agtggtgaag taacctaaac ttgacctgct360
taatacatctc tagggcagag aaccaggat gggacactaa aaaaatgtgt ttatttcatt420
atctgcttgg atttatctgt gtttttgaac cacaaaaaat aaatgttttg atataaaaaag480
gaaagagaaa aattgcgg                                     498

```

- (2) INFORMATION ON SEQ ID NO. 92:
- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1077 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:



(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

gggtctgagc  tggatacaaca  gggacacagt  gtttcacgtt  gacaggtttg  cttgggacgc  60
tagtaaccat  gggcttgctg  acttagccaa  agaagagtta  agaagaaaaa  acacacaagt  120
atacagactg  ttcttagttt  cttagactta  tctgcataat  ggataaaaaa  aatgcaattg  180
tgctcttcac  ttaggatgct  ttcatgtctt  ttaagatgtg  ttaggaaatg  caacagagca  240
aggagaaaaa  aggcagtcct  ggaatcacat  tcttagoaca  cctacacccc  ttgaaaaatg  300
aacaacttgc  agaattgaga  gtgattcctt  tcttaaaagt  gtaagaaagc  atagagattt  360
gttcgtattt  agaattggat  cactgaggaa  agagaaggaa  agtgattttt  ttccacaaga  420
tctgtaatgt  tatttccact  tataaaggaa  ataaaaaatg  aaaaaacatta  ttgggatatc  480
aaaaagcaat  aaaaacccaa  ttcagtctct  tctaagcaaa  attgctaaag  agagatgaac  540
cacattataa  agtaatcttt  ggctgtaagg  cattttcacc  ttctcttcgg  gtgggcaaaa  600
tattttaaag  gtaaaacatg  ctggtgaacc  aggggtgttg  atggtgataa  gggaggataa  660
tagaatgaaa  gactgaatct  tcccttgttg  cacaataaga  gtttggaaaa  agcctgtgaa  720
agggtgtctc  tttagactta  tgcctttaaa  agtatccaga  gatactacaa  tattaacata  780
agaaaaagatt  atatatatt  tctgaatcga  gatgtccata  gtcaaatgtg  taatatctta  840
tcttttgttaa  tatttattta  tatttattta  tgacagtga  catctctgatt  ttacatgtaa  900
aacaagaaaa  gttgaagaa  atctgtgaag  aaaaatgtat  ttttccataa  tagaaataaa  960
tgatcccat  ttttggtaaa  aaaaagtatg  tgagatttat  tcgtaaacgt  gactactttaa  1020
tttctaaaa  agagattccc  taccgtcgct  ctacaagcag  ttcagaatgc  catgctt  1077

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1755 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

cgccgggctg cttgtgatct ggtacgagga ttatgcaagt tttttgaggg acctgtgaca 60
ggaaatctct ctgggttatgt taattccatg ctgcagggaat acgcacaaaaa tccatctgtc 120
aactggaaaac acaaaagatgc agccatctac ctagtgcacat ctttggcatc aaaagcccaa 180
acacagaaagc atggaattac aacagcaaat gaacttgtaa acctaactga gttctttgtg 240
aatcacatcc tccctgattt aaaatcagct aatgtgaatg aatttcctgt ccttaaagct 300
gacggtaata aatatattat gatttttaga aatcaagtcg caaaagaaca tcttttagtc 360
tcgatctctc tcttgattaa tcaatctcaa gctgaaagta ttgtgttca tactttacga 420
gctcatgctc ttgaacggct ctttactatg cgagggccca acaatgccac tctctttaca 480
cttcagaaaa tgcacccgtt tgttgagatt ctgctaacaa acottttcaa agctctcaca 540
cttcctggct ctccagaaaa tgaatatatt atgaaagcta tcatgagaag ttttctctc 600
ctacagaaga ccataatccc ctacatccct acctctatca ctacgcttac acagaagcta 660
ttagctgtta gtaagaaccc aagcaaacct cactttaatc actacatggt tgaagcaata 720
tgtttatcca taagaataac ttgcaaaagt aacctgtctg ctgttgtaaa ttttgaggag 780
gctttgtttt tgggtgtttac tgaatcttta caaatgatg tgcagaagtt tattccatca 840
gtctttcaaa tgaatgtctt gctctgggaa acacacaaaa atgacatccc gtcttcttat 900
atggccttat ttctccatct ccttcaagca gtgctttggg aaagaacagg aaatattctc 960
gtcttagtga ggccttctca agcatcttta gaacggggtt caaacacaa atgcaagtgct 1020
gcagctgaca aaattcctgg gttactagggt gtctttcaga agctgattgc atccaaagca 1080
aargacaccc aagggttttta tctctaaaac agtataaag agcacatgcc tctcgaaatca 1140
gttgaccaat ttatcaagag ttttttagtc ttattaat ttgattgcat aaatatgggg 1200
gcactagcac tacaagaaat atttgatggt atacaacca aaatgtttgg aatggtttgg 1320
gaaaaaatta ttattcctga aattcagaag gtatctggaa atgtagagaa aaagatctgt 1380
ggggttgcca taaccaaatt actaacagaa tgtcccccaa tgatgggaca tgaatattcc 1440
aaactctgga ctccattatt acagctcttg attggtcttt ttgagttacc cgaagatgat 1500
accattcttg atgaggaaac ttttattgac atagaagata caccaggata tcagactgcc 1560
ttctcacagt tggcattttg tgggaaaaaa gagcatgac ctgtagggtc aatggtgaat 1620
aaccacaaaa ttcacctggc acagtcaact cacaagtgtg ctaccggctg tccagggaag 1680
gttccatcaa tggcacaaga ctctgtgata aatggagact ttaatggagg ggcacaaagg 1740
tagtagtagt cctggg

```

1755

## (2) INFORMATION ON SEQ ID NO. 94:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

gttcgcccag cagacacctt cgaacgcttc cggggacccc tcgtcgtgt cctccogaag 60
cggacccggg gccccaggct cgcgctgccc ggacgggtgc tcgtgtccca ccccgggcgc 120
acgcctcccg cgagtcccgg gccctcccg cgcctctctt ctcgcccggc gcgcagatag 180
gcgccccccg aggtccctgc gtctgggctt ctgcttgccg cggcgacggc gacttttgcc 240
gcagctcagg aagaatgtgt ctgtgaaaac tacaagctgg ccgtaaaactg ctttgtgaat 300
aataatcgtc aatgccagtgt tacttcagtt ggtgcacaaa atactgtcat ttgctcaaa 360
ctggctgcca aatgttttgt gatgaaggca gaaatgaatg gctcaaaact tgggagaaga 420
gcaaaacctg aagggggcct ccagaacaat gatgggcttt atgactctga ctgcatgag 480
agcgggctct ttaaggccaa cagctgcaac ggcacctcca tgtgctgggt tgtgaacct 540
gctggggcca gaagaacaga caaggacact gaaataacct gctctgagcg agtgagaacc 600
tactggatca tcattgaaat aaaaacaaaa gcaagagaaa aaccttatga tagtaaaagt 660
ttcgggactg cacttcagaa ggagatcaca acgcgtttatc aactggatcc aaaaatttatc 720
acgagatttt tgtatgagaa taatgtttatc actattgatc tgggtcaaaa ttcttctcaa 780
aaaaactcaga atgatgtgga catagctgat gtggtttatt attttgaaaa agatgttaaa 840
ggtgaatcct tgtttcattc taagaaaaatg gacctgacag taaaagggga acaactggat 900
ctggatctgt gtcaaaactt aattttattt gttgatgaaa aagcacctga attctcaag 960
cagggtcttaa aagctgggtg tattgtctgtt atgtggtttg tgggtgtagc agttgttgct 1020
ggagattgtt tgctggttat ttccagaaag aagagaattgg caaagtatga gaaggctgag 1080
ataaaggaga tgggtgagat gcatagggaa ctcaatgcata aactatataa ttggaagatt 1140
atagaagaag ggaataagca aatggacaca aattacaagt gtgtgtgcgt gggcgaagat 1200
catctttgaa ggtcatgagt ttgttagttt aacatcatat atttgtaata gtgaaacctg 1260
tactcaaaat atagacagct tgaactggc ttaccaatc ttgaaatttg accacaagt 1320
tcttatatat gcagatctaa tgtaaaatcc agaacttgga ctccatcgct aaaattatt 1380
atgtgtacaa ttcaaatgtg tgcatttaat atgcttcac agtaaaatct gaaaaactga 1440
tttgtgattg aaagctgccc ttctatttac ttgagctctg tacatacata cttttttatg 1500
agctatgaaa taaaacattt taaactgaaa aaaaaaaaaa aaggc 1545

```

## (2) INFORMATION ON SEQ ID NO: 95:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

gcgcggtatt atcgggtaga catctcgac cgcgtctcgg aaacgggtag cgcttcgacg 60
atggcgtagc aactgactga agagcgagatt gcagaattca aagaagcttt ttcactattt 120
gacaaagatg gtgatggaac tataacaaca aaggaaattgg gaactgtaat gagatctctt 180
gggcagaatc ccacagaagc agagttagac gacatgatta atgaagttaga tgcgtgatgt 240
aatggcacaa ttgaacttcc ctgaatttct ggacaaggat ggcaagaaaa atgaagaca 300
cagacagtga agaagaaatg agagaagcat tccgtgtgtt tgataaggat ggcaagggtc 360
atctgagtgc tgcagaactt cgccatgtga tgacaaacct tggagagaaq ttaacagatg 420
aagaagttaga tgaatgatac aggggaagcag atattgatgg tgatgggtcaa gtaaacatag 480
aagagtttgt acaaatgatg acagcaaatg gaagaccttg tacagaatgt gttaaatttc 540
ttgtacaaaa ttgttttatt gccttttctt tgtttgtaac ttatctgtaa aaggtttctc 600
cctactgtca aaaaaaatatg catgtatagt aattaggact tcattctctc atgttttctt 660
cccttatctt actgtcattg tcttaaaacc ttattttaga aaagttagatc aaggttaacat 720
gttgcatgtg gcttactctg gggaaatatc taagcccttc tgcacatcta aacttagatg 780
gagtggtgca aatgagggaa catctgggtt atgccttttt taaagttagt ttcttttagga 840
actgtcagca tgttgttgtt gaagtgtgga gttgtaactc tgcgtggact atggacagtc 900
aacaatatgt acttaaaagt tgcactattg caaaacgggt gtattatcca ggtactcgta 960
cactattttt ttgtactgct ggtcctgtac cagaaacatt tctttttatt gttactgtct 1020
ttttaaaact ggttttagcca cttaaaatct gcttatggca caatttggcc caaaatccat 1080
tccaagtgtg atatttgttt tccaataaaa aaattacaat ttcccaaaaa aaa 1133

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 791 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

gcgcgccgcg cggaccgcgc gagagcgccg gccgggagcg gcggtgatgg accgggtccgg 60
ggagcagccc agaggcgggg gcccccacag cctcgagcag atcatgaaga cagggggccct120
tttgcctcag ggtttcattc aggatcgagc agggcggaatg ccccgagct180
ggccctcgac cccggcgctc aggatcgctc caccagaagc ctgagcgagc gtctcaagcg240
catcggggac gaactggaca gtaacatgga gctgcagagg atgattgcgc ccgtggacac300
agactcccc cagagaggtct tttcccgagt gccagctgac atgttttctg acggcaact360
caactggggc cgggttgctg ccttttctta ctttgccagc aaactgggtg tcaaggccct420
gtgcaccaag gtgccgggaa tgatcagaac catcatggcg tggacattgg acttccctcg480
ggagcgcgct ttgggctgga tccaagacca ggggtggttg gacggccctc tctcctact540
tgggacgccc acgtggcaga ccgtgacbat ctttgtggcg ggaagtgtca ccgcctcact600
caccatctgg aagaagatgg gctgaggccc ccagctgcct tggactgtgt tttccctca660
taaatctatg catttttctg ggaggggtgg ggaattgggg acatgggcgt tttcttact720
ttgttaatta ttgggggggtg tgggggaagag tggctcttgag gggggaataa acctcctctg780
ggacacaaaa a

```

791

## (2) INFORMATION ON SEQ ID NO. 97:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 599 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

tctcgcttc accatgaagt ccagcgccct cttcccttc ctggtgctgc ttgccctggg 60
aacctctggca ccttgggctg tggaggctc tggaaagtcc ttcaagctg gagtctgtct120
tccaaagaaa tctgccagc gcttagata caagaaacct gactgccaga gtgactggca180
gtctccaggg aagaagagat gttgctccta caactgtggc atcaaatgcc ttgatcctgt240
tgacacccca aacccaacaa ggaggaaagc ttggaaagtgc ccagtgcact atggccaatg300
tttgatgctt aaacccccca atttctctga gatggatggc cagtgcacag gtgacttgaa360
gtgttgatg ggoatgtgtg ggaatccctg cgtttccctt gtgaaagctt gattcctgcc420
atctggagga ggctctggag tctctgctctg tgtggtccag gtcccttcca cctcgagact480
tggctccacc actgatatcc tcttttgggg aaaggcttgg cacacagcag gctttcaaga540
agtgcacgtt gatcaatgaa taataaacg agcctatttc tctttgcaaa aaaaaaaaa 599

```

## (2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 643 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

gggcccgcgg ctcgggcgta ggaggcggtg cctctgcagc aagcgtgggg cgcgggaacc 60
cgagcaggac tctccagtc ctagtcacct tggacaaaga agtggtgac ctcagattcc120
atcttttcca actccaaggt gccatggcag agaaggtgct ggtaacaggt ggggctggct180
acattggcag ccacacgggtg ctggagctgc tggaggctgg ctacttgctt gtggtcatcg240
ataacttcca taatgccttc cgtggagggg gctccctgcc tgagagcctg cggcgggtcc300
aggagctgac aggcgcctct gtggagtttg aggagatgga cattttggac caggggagccc360
tacagcgtct cttcaaaaag tacagcttta tggcggtcat ccactttgag gggctcaagg420
ccgtgggcga gtcggtgcag aagcctctgg attattacag agttaacctg accgggacca480
tccagctctt ggagatcatg aaggcccacg gggtgaagaa cctggtgttc agcagctcag540
ccactgtgta cgggaacccc cagtacctgc ccccttgaat gaggggccacc ccacggggtg600
ggatgtaaca accttacgga agtccaaatt tctttatctt ttc 643

```

- (2) INFORMATION ON SEQ ID NO. 99:
- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 860 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ctcgagccgc tcgagccgat tcggctcgag tgcctccaga ggactggcca cattttgcct 60
agataaagat gcacttagag atgaatatga tgatctctca gatttgaatg cagracaaaat120
ggagagtggt cgagaatggg aaatgcagtt taaagaaaaa tatgattatg taggcagact180
cctaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaacttctg aaacacacaa agtcaggggc cttcagaact gcaattctta300
ctccctttca cagactgtcc ggagtctttg ggtttgattc acctgctgcg aaaaacattc360
aacaatttct gtacaagata aattaatctc actatgaaga ttgtaataac tagacattat420
ttatgctgcc aaactcattt gttgcagttg ttgtaatgt ctagtggggc ttcatcatcc480
tgaagaagaag gagacaggga tttttttaa gacgaagaaa gtacacaatat tacttctttc540
cttctttttt tctcttttcc cttctcttct tctcttttct tcttttttaa atatatattgaa600
gacaaccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagttg ttcaaggctac tgaaacatta aaatgtgaat780
tcccaaaactt tcttttttgg cattgttcgg gggataggga aatatcgttt ttaaggagat840
ctcgggaatt ggggtgtggg 860

```

## (2) INFORMATION ON SEQ ID NO. 100:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

gggggtctgg cgaagcctggg cgggggagag gactgggtgg gcaggggggc cggcccgccg 65
gggggagagg gggccggggcg gggtctgggg tatctgaggg tcggagccac cggcccgccg 120
ggggcccgag caacctcctcg cgaagcagcg tcgggagcca gccacagagc ggaaataggc 180
agacaatttt tcgctccatg atgcgttatc tgggtctgga aacccaaacc ctcaaggatg 240
gcctggcgga tggggggaacc agcctgctgg ggcagggggg taccacgggg ctccctatcc 300
tggggcctac cccgggcacgg cacccccagg gcttatcct ggaagggcac ctccaggcgc 360
ctactctgga gcacctggag ctatcccggg gcaacctgca cctggagctc acccaggggc 420
accacaggcg ctcggggcct acccatcttc tggacagcca agtggccacg gagcctaccg 480
tgccacctgg cctataggcg ccccgctgg gccaactgat gtgctttata acctggcctc 540
gcctggggga gtgttgcctc gcatgctgat acaattctg ggcacgggtg agcccaatgc 600
aaaagagatt gtcttgatg tccaaaaggg gaatgatgtt gccttccact ttaaccccacg 660
cttcaatgag aacaataggg gagtcattgt ttgcaataca aagctgggata ataacctggg 720
aaggggagaa agacagctgg ttctccattt tgaagtgagg aaaccattca aaatacaagt 780
actggttgaa cctgaccact tcaaggcttg agtgaatgat gctcacttgt tgcagtacaa 840
tcctcgggtt aaaaaactca atgaatcag caaactggga tttctgggtg acatagacct 900
taccagtgct tcaataacca tgatataatc tgaagggggc agattaaaaa aaaaaaaga 960
atctaaagct taactgtgta aaggttcat gttcactgtg agtgaaaatt tttaattca 1020
tcaactcccc tctgtgaagt catctactta ataatatta cagtgaaaaa aaaaaaaa 1080
aaaaaaaagg gtcgaaaaag gagggggaag gagagagagg gaagaagaga gaggagaagg 1140
aggggggggg tgggg

```

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aaaaatattt gctggaaatt gctgtgtagg attacaggcg tgaccactgc gcccgccac 60
attcagttct tatcaaaagaa ataacccaga cttaactctg aatgatacga ttatgccaa 120
tattaaagtaa aaaaataaag aaaaggttat cttaaataga tcttaggcaa aataccagct 180
ga:gaaggca tctgatgctt tcactctgtc agtcactccc aaaaacagta aaataaacca 240
ctttttgttg ggcaatatga aattttttaa ggagtagaat accaaatgat agaacaagac 300
tgccctgaatt gagaattttg atttcttaaa gtgtgtttct tctaaattg ctgttctcta 360

```



```

atttgactaa ttttaattcat gtattatgat taaattctgag gcagatgagc ttacaaagtat420
tgaataaatt actaattaat cacaaatctg aagttatgca tgatgtaaaa astacaaaca480
tttcaattaa agggctttgca acacaaaaaa aagaaaaaaa aa 522

```

## (2) INFORMATION ON SEQ ID NO. 102:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ccagctcgcc ctgcctagcc aggggcgccc cgccccctgc ctgccccgcc accttcggga 60
gcgccttcca ataggcgctt gccattggct ctggcgacct cgcgcgcttg ggaggtgtag 120
cgcggtctct aacgcgctga gggcgcttga gtgtcgcagg cgcgcgagggc gcgagtgagg 180
agcagaccaca ggcacgcgcg gccagagaagg ccggcgctcc ccacactgaa ggtccggaaa 240
ggcgacttcc gggggctttg gcaacctggcg gacctcccg gagcgtcggc acctgaacgc 300
gaggcgctcc attcgcgctg cgcgttgagg ggcttcccg acctgatcgc gagaccocaa 360
cgcgctggtg cgtcgccctg cgcgtctcggc tgagctggcc atggcgcaat gtgcgggctg 420
aggcgagagc ggcgtttctc gccctgctgg gatcgctgct cctctctggg gtctctggcg 480
cgcaccgaga acgcagcacc cagcacttct gcctggtgtc gaagggtggt ggcagatgcc 540
ggcgctccat gcctagggtg tggtaacaat tcaactgacg atctctgccag ctgttttgtg 600
atgggggctg tgacgggaaac agcaataatt acctgaccaa ggaggagtgc ctcaagaagt 660
gtgcgaactgt cacagagaat gccacgggtg acctggccac cagcaggagt gcagcggatt 720
cctctgtccc aagtctctcc agaaggcagg attctgaaga ccactccagc gatattgtca 780
actatgaaga actctgcacc gccaacgcag tcaactggcc ttgcctgtca tcttcccacc 840
cctggtaact tgacgtggag aggaactcct gcaataactt catctatgga ggctgcggcg 900
gcaataagaa cagctaccgc tctgaggagg cctgcgatgt ccgctgcttc cgcacgagg 960
agaactcctc cctgcccttt gctcacaagg tggctggtct ggccgggctg ttctgattg 1020
tgttgatcct cttcctggga gctccaatgg tctacctgat ccgggtggca cggaggaacc 1080
aggagcgtgc cctgcgcacc gtctggagct ccggagatga caaggagcag ctggtgaaga 1140
acacatatgt cctgtgaccg cctgtgcgcc aagaggactg gggaaggagg gggagactat 1200
gtgtgagctt tttttaaata gagggattga ctcgatttg agtgatcatt agggctgagg 1260
tctgtttctc tgggaggtag gacggctgct tctctggtctg gcagggatgg gtttctgtt 1320
gaaatctctt aggaggtctc tctctgcgat gcctgcagtc tggcagcagc ccgagttgt 1380
ttcctcgctg atcgatttct tctctccagg tagagtttct tttgcttatg ttgaattcca 1440
tctcctcttt tctcatcaca aagtgatgt tggaaatggt tcttttgttt gtctgattta 1500
tgcttttttt aagataaaa aaaaagtgtt tattagcatt ctgaaagaa gaaagtaaaa 1560
tgtacaagtt taataaaaag gggccttccc ctttagaata aaaaaaaa 1620
aaaaaaaaa 1628

```

## (2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 605 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cctggcagct  gtcggctgga  aggaactggc  ctgctcacac  ttgctggctt  ggcgatcagg  60
actggcctta  tctcctgact  cacggtgcaa  aggtgcacto  tgcgaacgctt  aagtcctcc120
ccagcgcttg  gaatcctacg  gcccccacag  ccggtacccc  tcagccttcc  aggtcctcaa180
ctccccgga  cgctgaacaa  tggcctccat  gggctacag  gtaatgggca  tcgcctggc240
cgtcctgggc  tggctggccg  tcactgcttg  ctgcgcgctg  cccatgtggc  gcgtgacggc300
cttcactggc  agcaacattg  tcactcgca  gaccatctgg  gagggcctat  ggaatgaact360
cgtgggtgag  agcaacggcc  agatgcagtg  caaggtgtac  gaactcgctg  tggcaactgc420
gcaggacctg  caggcggccc  gccccctcgt  catcatcagc  atcatcgtgg  ctgcctctgg480
cgtgctgctg  tccgtgggtg  ggggcgaagt  gtaacaaact  tgcctggagg  attaaaagcg540
ccaagggcaa  gaacatgatt  cgttggcggg  cgtgggtgtt  tctgtttggg  ccggccta600
gggtg   605

```

## (2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2731 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agggggggcg acagacacag actatgcaga tgggagtga gacaaagtag taagaatgac 60
agagggagaa gaagtggctg aggtggagga cgatgaggat ggtgatgagg tagaggaaga 120
ggctggaggaa cccatcgaag aagccacaga gacacacaga gtctgtcgaa gaggtgggtc 180
gagtgagtgt ctctgaacaa gccgagacgg ggccgtgccg agcaatgato tccgctggt 240
acctgagtgt gactgaaggg aagtggccc cattcttta cgccggaagt gggcgcaacc 300
ggacaactct tgacacagaa gactactgca tggcgtgtgt tggcagcgcc attcctaaca 360
cagcagccag tacccctgat gccgttgaca agtatctga gacacctggg gatgagaagt 420
aaccatgcaca ttccagaaaa gccaaagaga ggcttgaggc caagcacagg gagagaatgt 480
cccaggtctat gagagaatgg gaagaggcag aacgtcaagc aaagaacttg cctaaagtgt 540
ataagaaagg agttatccag catttccagg agaaagtgga atotttggaa caggaagcag 600
ccaacgaagg acagagcgtg gtggagacac acatgccca agtggaagcc atgtcaatg 660
acccgcgcgg cctggccctg gagaactaca tcaaccctct gcaggctgtt cctcctcggc 720
ctcgtcacgt gtccaatatg ctaaaagaag ttctccgcgc agacacagaa gagacagcag 780
acacccctaaa gcatttcgag catgtgcgca tgggtggatcc caaagaagcc cctcagatcc 840
ggtcccaagt tatgacacac ctccgtgtga ttatgagcg catgaatcag tctctctccc 900
tgctctacaa cgtggcctgca gtggccgagg agatccaggg tgaagttagt gagctgtctc 960
agaaaagagca aaactatcca gatgacgctt tggccaacat gattagtga ccaaggatca 1020
gttacgggaa agatgctctc atgccacttt tgaaccgaac gaaaaccacc gtggagctcc 1080
ttcccgtgaa tggagagttc agccctggag atctccagcc ttggcattct tttgggctgt 1140
actctgtgcc agccaaacaca gaaaacgaa ttgagcctgt tgatgcccg cctgtgcgcg 1200
accgaggact gaccactcga cccggttctg ggttgacaaa tatcaagag catcagatct 1260
ctgaagtga gatggaatga gaattccgac atgactcagg atatgaagt ggactatgt 1320
aattgggtgt ctctgcagaa gatgtgggtt caaaccaagg tgcaatcatt ggcactatgt 1380
tggcggtgtg tgcatacgag acagtgatcg tcatcacctt ggtgatgctg aagaagaac 1440
agtacacatc catttcacat ggtgtggtgg aggttgagcg cgtctgcaac ccagagagag 1500
gccacctgtc caagatgcag cagaacggct acgaaaatcc aaacctaca agcttgagc 1560
agatgcagaa ctgaccccc gccacggcag cctctgaagt tggacagcaa aacctgtgt 1620
tcaactacca tcggtgtcca ttatagaaat aatgtgggaa gaaacaaacc cgtttatga 1680
tttactcatt atcgcctttt gacagctgtg ctgtaaacac gttagatgoc tgaacttga 1740
ttaatccaca catcagtaat gtattctatc tctctttaca ttttggttc tatatacat 1800
taataatggg ttttgtgtac tgraaagaat ttagctgtat caaactagt catgaataga 1860
ttctctctgt attatttacc acatagcccc gtatatatt gtatatatt cttgtggtt 1920
gtgacccaat taagtctcat ttacatatg ctttaagaat cgatggggga tgcttcatgt 1980
gaacgtggga tgcagctgc ttctcttgc taagtattcc ttctctgac tatcatcgt 2040
ctaaagttaa acatttttaa gtatttcaga tgcttttag agatttttt tccatgaet 2100
cattttactg tacagatgct tgcttctgct atatttgtg tataggaaat aagaggatac 2160
acagctttgt ttctctgtgc ctgttttatg tgcaacacat aggcattgag acctcaagct 2220
ttctcttttt ttgtccagta tctttgggtc ttgtataaag aaaagaatcc ctgttcatgt 2280
taagcaacttt tgcggggcgg gtggggaggg gtgctctgtc ggtcttcaat tgcagaagt 2340
ttctcaaaac atttttctgc aggatgattg tacagaatca ctgcttatga catgatcgt 2400
ttctacactc tattacataa ataaataaac taaaataacc ccgggcagaa cttttcttg 2460
agagatgact agagacatta aataatcgaa gtaattttgt gtggggagaa gaggcagatt 2520
caattttctt taaccagctc gaagtttcat ttatgatata aagaagatg aaaaatgga 2580
tgcaatatata aggggatgag gaagcatgc ctggacaac cctcttcta agatgtgtc 2640
tcaatttgtta taaaatgggt ttttcatgta aataaatata ttcttgagg agccaaaaaa 2700
aactatatata ctggcaggtt tataatatg c

```

2731

## (2) INFORMATION ON SEQ ID NO. 106:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2194 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gaattcagaa gttaatgatg ttgggttaaga gaacaatggt aagagagcaa tctaagaata 60
tatcacctac tttaatttta tatgagagta catggaggta gctgtgatgt ggaaattgtag 120
cactctctct acccagcgag atttatctcca gtgaacaac aactggaaact tcaagtaact 180
cctccagagag tacttccaac ttgggtgtgg ccccaaatcc aactaatgcc accaccaagg 240
tggctgggtgg ttgctctgag toaacagacca gtctctctgt ggtctcactc tctctctctg 300
atctctactc ttaagagact caggccaaga aacgtctctt aaatttcccc atctctctaa 360
cccaattccaa atggcgctct gaagtccaat gtggcaagga aaaacagggtc ttcactgaat 420
ctactaattc cacacctttt attgacacag aaaaatgtga gaatcccaaa ttgattgta 480
ttgaagaaca tgtgagaggt ttgactagat gatggatgcc aatattaaat ctgctggagt 540
ttcatgtaca agatgaagga gaggcaacat ccaaaatagt taagacatga ttctcttgaa 600
tgtgggttga gaaatatgga cacttaatac taccttgaaa ataagaatag aaataaagga 660
tgggattctg gaatggagat tcagttttca ttgtgttcat taattctata agggccataaa 720
acaggtaata taaaaagctt ccatgattct atttatatgt acatgagaag gaacttccag 780
gtgttactgt aatttctcaa cgtattgttt cgacagcact aatttaatgc cgataactc 840
tagatgaagt ttacattgtt tgagctattg ctgttctctt ggggaactgaa ctcaacttcc 900
tcttgaggct ttgattttga cattgcattt gaccttttat gtatgaattg acatgtgcc 960
gggcaatgat gaatgagaat ctacccccaag atccaagcat cctgagcaac tcttgattat 1020
ccattattgag tcaaatggta ggcatttctt atcacctgtt tccattcaac aagagcacta 1080
cattcattta gctaaacgga ttccaaagag agtctcaact tgtcccgccg cccggaagtgc 1200
aatgcttttt attattatta tttttagac agtctccagg gctcaagcga tcttctgccc 1260
agtggtggca ttccagatca gtgtaccatt tgctctccgg acctgccacc atgcccgcc 1320
tcagcctccc aagtactctg gattacaggc atttctgcat atgttgaata ctttttacaa 1500
atgtttagtag agacagggtt toaccatggt gcccgagctg gtttctgaat cctgacctca 1380
gggtgctcac ccgctccggc ctcccaaat gctgggatta caggcttgag ccccgccgcc 1440
cagcactcaa aatgcttttt atttctgcat atgttgaata ctttttacaa 1500
tgatctgttt tgaaggcaaa attgcaaatc ttgaatttaa gaaggcaaaa atgtaaagg 1560
gtcaaaacta taaactcaagt atttgggaag tgaagactgg aagctaaatt gcattaaat 1620
cacaaaactt tatactcttt ctgtatatac atttttttct tttaaaaaac aactatgga 1680
cagaatagct acatttagaa cactttttgt tatcagtcaa tatttttaga tagttagaac 1740
ctggtctctaa gcctaaaggt gggcttgatt ctgcagtaaa tcttttacaa ctgctcgac 1800
acacataaac ctttttaaaa atagacactc ccggaagtct ttgtttcgca tggctcacac 1860
ctgactgata gatgtttccg taacttaata tggccacagt atgcttgatg accaaagct 1920
tttttttcca tcttttagaaa actacatggg aacaaacaga tcgaacagatt tgaagctac 1980
tgtgtgtgtg aatgaacact cttgctttat tccagatgc tgcatactta tttgtgattg 2040
tatattgtgt ttgtgtattt acgctttgat tcatagtaac tcttatgga attgatttgc 2100
attgaacaca aactgttaaa aaaaagaaat ggctgaaaga gcaaaaaaaa aggaagaaa 2160
aaaagaaaaa aaaagaaaaa aaaaaggggg agggc

```

2194

## (2) INFORMATION ON SEQ ID NO. 107:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

cggaagggtg accctggatg aattttgacg agaacaagtt cgtggaccga agaagatggg 60  
ggccgcacgc ccaggcccg gcccgcagca gcccgcaggtg gacacctgcc ccttcgcgcaa 120  
aggaacacgt aaacagaccg tacaggcagc tctgaagaac cccctcatca acaccaagag 180  
tcaggcgagtg aaggaccggg caggcagcat tgtcttgaag gtgctcatct cttttaaagc 240  
taagtataata gaaaaggcag ttcaatctct ggacaagaat ggtgtggatc tcctaatgaa 300  
gtataattat aaaggatttg agagcccgct tgacaatagc agtgctatgt tactgcaatg 360  
gcatgaaaaa gcaactgtct cggaggaggt agggctccat gtctgtgtct tgactgcaag 420  
aaaaactgtg tagtctggca ggaagtggat tatctgcctc gggagtgga attgctggta 480  
caaaagccaa aacaacaaaa tggccacgct gccctgtggg tagcatctgt ttctctcagc 540  
tttgccttct tgctttttca tatctgtaaa gaaaaaaatt acatatcagt tgccttttaa 600  
tgaaaaattg gataatatag aagaatttgt gtaaaaatag aagtgtttca tcctttcaaa 660  
accatttcag tgatgtttat accaatctgt atatatata atttacattc aagtttaatt 720  
gtgcaacttt taacccctgt tggctgtgtt ttgtttctgt tttgttttgt attattttta 780  
actaatactg agagatttgg tcagaatttg aggcagattt cctagctcat tgctagtcag 840  
gaaatgatat ttataaaaaa tatgagagac tggcgagcat taacattgca aaactggacc 900  
atatttccct taattataaa gcaaaaatag tttttggaat aagtgtgtgg tgataccac 960  
tgccaaagtta tagctttgtt ttgcttgccc tccgatttat ctgtactgtg ggtttaagta1020  
tgctactttc ttcagcatc caataatcat ggccctcctaa tttatttgtg gtaacccag1080  
tttcagagca agaagctctt cttatatacaa atgtatccat aaaaatcag agctgtgtgg1140  
gcatgaacat caaacttttg ttccactaat atggctctgt ttggaaaaaa ctgcaaaatc1200  
gaaagaatga ttgcagaaa gaaagaaaaa ctatgtgtga atttaaacct tgggcagcct1260  
ctgaatgaaa tgcacttttc tttagaataa taatagctgc cttagacatt atgaggtata1320  
caactagtat tttaagatacc atttaatatg ccccgtaaat gtcttcagtg ttcttcagg1380  
tagttgggat ctcaaaagat ttggttcaga tccaaaacaa tacacattct gtgttttag1440  
tcagttgttt ctaaaaaaag aaactgccac acagcaaaaa attgtttact ttgttgagac1500  
aaccaaatca gttctcaaaa atgacacggg gcttataaaa agttataaat atcgagtac1560  
tctaaaacaa accacctgac caagagggaa gtgagttgt gcttagtatt tacattggat1620  
gccagctttt taatcatgca cttatgtgca aactggtgca gaaattctat aaactctttg1680  
ctgttttttg taacctgttt ttgtttcatt ttgttttgt ttgtaaaaat gataaaact1740  
cagaaaaata aatgtcagtg ttgaataaaa taaaaaaca aattgaagaa gaggatgga1800  
atttcgactt gg 1812

## (2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 890 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

aacgactcct ggtaccttgc tcccattact tcccggtttc tggatctgct gctcgtctca 60
ggctcgtagt tgccttccaa catgcgggaa ccagcggaagt cgcctcccg ccccaagaag120
ggctcgaaga aagccgtgac taaggcgagc aagaaggagcg gcaagaagcg caaggcagcc180
gcaagcgagag ctactccgta tacgtgtaca aggtgctgaa gcagggtccac cccgacaccc240
gcactctctc taaggccatg ggaatcatga actcctctgt caacgacatc ttcgacgca300
tcgagggtga ggcttcccg cttggcgatt acaacaagcg ctgcaccatc accctcagg360
agatccagac ggccgtgcgc ctgctgctgc ccggggagtt ggccaagcac gccgtgtccg420
agggacacaa ggccgtcaccc aagtacacca gcgctaagta aacttgccaa ggagggactt480
tctctggaaat tctctgatat gaccaagaaga gcttcttatt aaaaagaagca caattgcctt540
cggttaccct attatctact gcagaaaaaga agacgagaat gcaaccatac ctatagtgac600
ttttccacaa gctaaagctg gcctcttgat ctcatccaga ttccaaagag aatcatttac660
aagtaatttt ctgtctcctt ggtccattcc ttctctctaa taatcattta ctgttctcca720
aagaattgtc tacattaccc atctcctctt ttgcctctga gaaagagtat ataagcttct780
gtaccccaact ggggggttgg ggtaatattc tgtggtcttc agccctgtac cttaataaat840
ttgtatgcct ttctctctaa aaaaaaaaaa aagaagaagg aaggagatgc 890

```

## (2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2627 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ggcaccgagat gtgaaaggt ttgtgtgaca coacctccaa aataaaaaa tggaaaaaac 60
accttttagtg aagtagaagt atttgagtat ctgtatgcag taacttatag ttgtgatcct 120
gcacotcgac cagatccatt ttocattatt ggagagagca cgattttatg tggtagacaa 180
tcagtttgga gtcgtgctgc tccagagtg: aaagtggtea aatgtcgatt tccagtagtc 240
gaaaaatgaa aacagatatc aggtattgga aaaaaatttt actacaaagc aacagttatg 300
tttgaattcg ataaaggttt ttacctcgat gccagcgaca caattgtctg tcacagtaac 360
agtaactggg atcccccaag tccaaaagtg cttaaagtgt cgacttcttc cactacaaaa 420
ttctccaggt ccagtgcttc aggtcctagg cctacttaca agcctccagt ctcaaaattat 480
ccaggataac ctasaactga ggaaggaata ctggacagtt tggatgtttg ggtcattgct 540
gtgattgtta ttgccatagt tgttggagtt gcagtaattt tgtttgtccc gtacagatat 600
cttcaagaga ggaagaaaga agggaaagca gatgggtggag ctgaatatgc cactaccag 660
actaaatcaa ccactccagc agagcagaga ggctgaatag attccacaac ctggtttgcc 720
agttcatctt ttgactctat taaaaatttc aatagttggt attctgtagt ttcaactcca 780
tgaagtcaac tgtggcttag ctaatatgac aatgtggcct gaatgtaggt agcactcttt 840
gatgctcttt tgaaacttgt atgaattggc gtatgaacag attgctgctt ttcccttaaa 900
taacacttag atttatgga ccagtcagca cagcatgcct ggttgtatta aagcagggat 960
atgctgtatt ttataaaatt gccaaaaata gagaatatata gttcacaatg aaactatat 1020
ttctttgtaa agaaagtggc ttgaaatctt ttttgttcaa agattaatgc caactttaal 1080
gattattctt tcaccaacta tagaatgtat tttatatac gttcattgta aaaagccctt 1140
aaaaatatgt gtatactact ttggctcttg tgcataaaaa caagaacact gaaaattggg 1200
aatatgcaca aacttggctt ctttaaccaa gaatatattt ggaaaaattc ctaaaaattal 1260
atagggtaaa ttctctattt ttgttaagt gtccgggtgat ttocagaagc tagaaagt 1320
atgtgtggca ttgtttttca ctttttaaaa catccctaac tgatcgaata tatcagtaa 1380
tcagaatcca gatgcacctt ttcataagaa gtgagaggac tctgacagcc ataacaggag 1440
tgccacttca tgggtgcgaag tgaacactgt agtcctgttg ttttccaaa gagaactccg 1500
tatgtttctt taggttgagt aacccactct gaattctggt tacatgtgtt ttctctccc 1560
tccttaataa aagagagggg ttaaacatgc cctctaaaaa taggtgggtt tgaagagaa 1620
aaattcatca gataacctca agtcacatga gaattctagt ccaattacat tgccctggc 1680
agtaaaaagc attctatgat atgtcttacc tcaattctca aaaggcagag tacaagtaa 1740
gccatgtatc tcaggaaagt aacttcattt tgtctatttg ctgttgattg tcccaaggga 1800
tggaaagaag aaatatagct caggtagcac ttatactca ggcagatctc agccctctac 1860
tgagtccttt agccaaagcag ttctttcaa agaaagcagc aggcgaaaaa cagggaactg 1920
cactgcattt catatcacac tgttaaaagt tgtgttttga aatttatgt ttagtgtcac 1980
aaattggggc aaagaacaat tgcccttgagg aagatatgat tggaaaaatc agagtgtaga 2040
agaataaata ctgttttact tgcctaaagac agttcttatg tgctctgtaa atgttctt 2100
cctttgtagt ctctgggaag atgctttagg aagataaaa tttgaggaga acaaacagg 2160
attctgaatt aagcacagag ttgaagttta taccogtttc acatgctttt caagaaatg 2220
gcaattacta agaagcagat aatggtgttt tttagaacc taattgaagt atattcaac 2280
aaataactta atgtataaaa taatatatt caataatac tgtatagcac ttctgtctc 2340
acatttgtatt ttctcaaat taatattat attagagatc tatatatgta taatatgta 2400
ttttgcaaa ttgtttactt aaatatatag agacagattt tctctggaag ttgttttaa 2460
tgacagaagc gtatatgaat toaagaaaaa ttaagctgca aaaaattgat tgcataaaa 2520
tgagaagctc cactgataga ggttctttat ttcaaaaaatg gactcttga 2580
atctgttata aaaaaattgt acatttggaa aaaaaaaaaa gccaaaaa 2627

```

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 976 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ctcgagccgc gagattcccc cgaagttctc catgaagcgc ctcaccgcgc gcctcatcgc 60
cgtcatcgig gtggtcgtgg tggccctcgt cgcggcgatg gccgtcctgg tgatcaccaa120
ccggagaaag tcgggggaagt acaagaaggt ggagatcaag gaactggggg agttgagaa180
ggaaccgcgag ttgtaggcac ccggcggggc aggggatggg gtggggtacc ggatttcgg240
atcgtcccaag acccaagtga gtcacgcctc ctgattcctc gccgcaagg agacgtttat300
cctttcaaat tctcgccttc cccctccctt ttgcgcacac accaggttta atagatcctg360
gcctcagggt ctctctttct tctcacttct gtcttgaagg aagcatttct aaaatgtatc420
ccctttcgtt ccaacaacag gaaacctgac tggggcagtg aaggaaagga tggcatagcg480
ttatgtgtaa aaaacaagta tctgtatgac aaccgggat cgtttgcaag taactgaatc540
cattgcgaca ttgtgaaggc ttaaatgagt ttgatggga aatagcgttg ttatcgccct600
gggtttaaat tatttgatga gttccacttg tatcatggcc tacccgagga gaagaggagt660
ttgttaactg ggctatgta gtagcctcat ttaccatcgt ttgtattact gaccacatat720
gtttgtcact gggaaagaag cctgtttcag ctgcctgaac gcagtttgga tgtctttgag780
gacagacatt gcccggaaac tcatgtctat tattcttcag ctgcccctta ctgccactga840
tattggtaat gttctttttt gtaaaatgtt tgtacatatg ttgtctttga taatgttctg900
gtaatttttt aaaataaaaac acgaatttaa taaatatatg gaaaggcaca caaaaaaaaa960
aaaaaaaaaa aaaaac

```

976

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing



- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cttcgggggt gactgectct tccagggcgg ggggtgtggt gcacgcattg ctgtgctcca 60
actccctcag ggcctgtgtt gccgcactct gctgctatga gcttccctaa aagtttcccg 120
cgcctcgggc cagcggaggg gctcctcgcg cagcagccag acactgaggc tgtgctgaac 180
gggaaggggc tcggcactcg taccctttac atcgctgaga gccgcctctg ttggttagat 240
ggctcctggat taggattctc actggaatac cccaccatta gtttaccatgc attatccagg 300
gaccgaagtg actgctcagg agagcatttg tatgttatgg tgaatgccaa atttgaagaa 360
gaatcaaaag aacctgttgc tgatgaagaa gaggaagaca gtgatgatga tgttgaacct 420
attactgaat tttagattgt gcctagtgtat aaatcagcgt tggaggcaat gttcactgca 480
atgtgcgaat gccaggcctt gcatccagat cctgaggatg aggattcaga tgactacgat 540
ggagaagaat atgagtggga agcacatgaa caaggcacagg gggacatccc tacattttac 600
acctatgaag aaggattatc coactaaca gcagaaggcc aagccacact ggagagatta 660
gaaggaatgc ttctcaagtc tgtgagcagc cagtataata tggctggggg caggacagaa 720
gattcaataa gagattatga agatgggatg gaggtggata ccacaccaac agttgctgga 780
cagtttgagg atcgagatgt tgatcactga aaatgattta tgcaagttta agattctgct 840
cctaagtgtg ggagagaact tggctcctct tccactctgg agtgaagtta atgaaagtct 900
ttttcctttt ccaaaaccca acctgaacca gtctcttctt gagacagact atactgagac 960
aacaagtgtg caccagcaga agatagataa tatgaccttt attaaactga tgaattaactt 1020
taaccaagag ggtattttga gtttactatt taccttaaaa ctttctgtgt ctgggtaccc 1080
tctgagttagg cctataattc ctaccttgac tgtgtgcac c atttgaagc tagcagatct 1140
atgtgggtgaa aagtcacagg agcttggtag actgcggggg aaagagagag ctctcttcgc 1200
catgttttac cagctctgct ttataacctc ttagggttga tcctttaatt ccagccttt 1260
taggttagtt tctgtaacag aacaagttag tctgggatga agtctctcaa gtactccaal 1320
tggttaattgt ttgttttttg taatagctta acaataaac ctagggtttc tatattaaaa 1380
aaaaaaaaa aaaaaaaaaa aaggtacctg ccctaataat attctgc 1427

```

(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2639 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ccccatatt accctcccg attctcttt ttctttttt tttttatat ggctttcttc 60
ttctttctt ttctttttt tcccccttt tatttgacca gtgaaataa caaacattta 120
tttgtgtcac ttatggtaga aaaaactccc tacaccagat gcacatgacc cagttgttaa 180
atagaacatt ttgaaggtag acacacaccc taacccaggc tttttaccog cttttaaaga 240
tgggccattc ttctctcccc ccccacccaa agacatgtga gcaacgccta atgaaagcca 300
gtaaacagcc gcttaggcta tagcagtttc aactccactc tgaggtgaag attccaatt 360
cattcgagac ttatgtcttt tcaatttttt cctaaccaaa gtccctgagt ccagatttta 420
caataattaca gcactagcac atcagtgctc acaactcctc tttttctgct gtacccctct 480
cacagttggg gggagggcct gcacttccat agagtttgct gataattggt tgaacaattt 540
cttccagctc ctctctctta gctttgaagt ctccaatgic agcatcttgg tggctttcca 600
gccattcaat ctctttcttc acagcttttt ccatggtctc ctattctcca gaggaaagt 660
tactctccag ctctttctta tctccaatct gatcttttag agaattagcca tagctttcca 720
actcaattct agtatacaat cgtctcttga gctttttgtc tctctcagca aactctcag 780
catcaattac catctcttgg atttcttga gtgtcaggcg attctgttca ttgggtattg 840
tgattctatt ttgttccct gtacccctgt ctccagctgt cactcgaaga ataccattca 900
catctatctc aaaggtgact tcaatctgtg ggaacccacg agggacagga ggaattccag 960
tccagtcaaa tgaaccaga agatgattgt ctttgtcag ggttcttcca ccttcataga 1020
ccttgattgt aacagtttgt tgattatcag aagctgtaga aaagatctga gactcttgg 1080
taaggccac tggttctctt ggaatcagtt tggctatgac acctccacca gttccaatt 1140
caagtgtgag gggacataca tcaagcagta ccaggtcacc tgaatcttga cccacagaga 1200
gcacccacgc ctggacagca gcaccatacg ctacagcttc atctgggttt atgccacggg 1260
atggttctct gcaattgaag aactctttaa caagttgctg aatctttgga attcgagctc 1320
agcccacac aagaacaatt tcatcaatat cacagctctt caaatcgaaa tcttccaac 1380
ctttctggac gggcttcaata gtgacccgga acagatccat gttgagctct tcaattttg 1440
cccgtctcag ggtctcagaa aagtcttctc ctctcataga ggaactcaat tcaattctg 1500
cttgatctg agaagacagg gcccgtttgg ccttttctac ctccgcccgg agttctgca 1560
cagctctatt gtctttctcg acatctttgc ccgtctcttt ttgtacagt ttgatgaag 1620
gttccatgac acgctggtga aagtcttctc caccacagat agtatctcca ttagtggcca 1680
caccttcgaa gacaccattg tcaatggtga gaagagacac atcggaagtt ccgccacca 1740
ggctcaaacac caggatgttc ttctccccct cctcttacc caggccataa gcaatagca 1800
cgcgcgtagg ctgcttgatg atcctcataa catttaggcc agcaatagtt ccagcgtct 1860
tggtgtctgt cgtttgggca tcatataaat aggcctggtac agtaacaact gcatgggta 1920
ctttctttcc caataaagcc tcagcggttt ctctcaattt agtgagaacc atggcagaa 1980
tttcttcagg agcaaatgtc ttgttttgcc cacttccaat atcaacttga atgtatggt 2040
tagttcttgt ttcaaccacc ttgaacggca agaacttgat gtctctgtgc acagaagg 2100
catctccagt gcggccgatg agccgcttgg cgtcaaaagc cgtgttctcg ggttggag 2160
tgagctgggt ctggccggca tcgccaatca gacgttcccc ttccaggagt asggcgaca 2220
aggacgggt gatccggttg cctgatcgt tgccgatgt cctccagcgg cgttcttga 2280
acacgcgcac gcaaggatag gtggtccccc ggtcgtatgcc gaccaccgtg cccagctct 2340
ctctctgtgc ctctctctcg gcccgccgcg cgtctgagcag cagcagcctc cggccacca 2400
gggagagctt catcttgcca gccagttggg cagcagcagg cagctccagc acagcgcta 2460
gcacaggagc acagcgcaat ttccgacttg gggccggcag gggccggggg tcacaagg 2520
ccacgaccca ggcgaaaggg aggtctagaa atacagggcg cggcgcttcc ctctcaact 2580
cgcgaaacac cccaataggt caatctgtct gtctgtctct ggcggcctc gaccttag 2639

```

## (2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 634 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

ctccccgcgcg cgcggttaaa tccccgcacc tgagcagcgg ctcacacctg caccocgcgc 60
gggcatagca ccatgcctgc ttgtcgccta ggcocgctag ccgcgcgcct cctcctaagc120
ctgctcgtgt tcggcttcac cctagctcca ggcacaggag cagagaagac tggcgtgtgc180
cccgagctcc aggcctgacca gaactgcacg caagagtgcg tctcgacag cgaatgcgc240
gacaaacctca agtgcctcag ccgggctgt gccaccttct gctctctgcc caatgataag300
gaggggttcct gcccccagggt gaacattaac ttctggccag atgaatgtct gccgcaatgg ctgtgggaag420
tgccaggctgg acagccagtg tctctggccag atgaatgtct gccgcaatgg ctgtgggaag420
gtgtcctctg tcactcccaa ttctctgagct ccagccacca ccaggctgag cagtgaaggag480
agaaaagtct tcgctggccc tgcatactgt tccagccacc ctgccctccc ctttttcggg540
actctgtatt cctctctggg ctgaccacag cttctccctt tcccaaccac taaagtaacc600
actttcagca aaaaaaaaaa aaaaaaaaaa aaaa

```

## (2) INFORMATION ON SEQ ID NO. 115:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 719 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN

## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gtcgactttt tttttttt tttaaacatgg aaagtattt ttaaaaaatcg aataatccta 60
ttcaagtcaa ccagtgttaa ccccggtgtg ctctctgcca gtctgttccct ccccatggga120
gtcacacaaa atgaaaaatct cctagaaaaga gaagacaaaag acccgcaaaa gatgtatgcc180
acctatctatg agctgaaaaga agacaagagc tacaatgtca cctccgtcctt gtttagggaa240
aagaagtgtg actactggat caggactttt gtccagggtt gccagcccggt cgagttcacg300
ctgggcaaca ttaagagtta cctcggatta acgagttacc tegtccgagt ggtgagcacc360
aactacaacc agcatgctat ggtgttcttc aagaaaagtt ctcaaaacag ggagtacttc420
aagatcaccc tctacgggag aaccaaggag ctgacttcgg aactaaaagg gaacttcac480
cgcttctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt cccaatcgac540
cagtgtatcg acgggtgagt gcacaggtgc gcccagctgc cgcaccagcc cgaacccac600
tgaggggagct gggagacctt ccccacagtg ccaccatgc agctgctccc caggccaccc660
cgctgatgga gccccacctt gtctgctaaa taaacatgtg cctcaaaaaa aaaaaaaaaa 719

```

(2) INFORMATION ON SEQ ID NO. 116:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 494 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

gtcgataacg ccagacgcaa gacgcccggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgctgttcca aggcattctgt gagccccggg agtatcaccc atgagcacaag ctacacctcc120
cgagttgaaa aaattttatgg acaagaagtt atcattgaaa ttaaatgggt gcagacatgt180
ccaagggaata ttgcccggat ttgatccctt tatgaacctt gtgatagatg aatgtgtgga240
gatggcgact agtggacaac agacaataa tggaaatggg gtaatacgag gaaatagat300
catcatgtta gaagccttgg aacgagtata aataatggct gttcagcaga gaaacccatg360
tccctctctc atagggcctg ttttactatg atgtaaaaaa taggtctatg acattttcat420
attagacttt ttgttaaaaa aacttttgta atagtcaaaa aaaagttttg tctcatctac480
cttataatat ctgc

```

494

## (2) INFORMATION ON SEQ ID NO. 117:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

accgggtcga ctacgctcaa agctccattg ttgatctctt ttgtctctcc ttcttggtctc 60
ctctctctct cccacccctc taataggctc ataagtgggc tcaggcctct ctgcggggcct 120
cactctggcg ttacaccatgg ctttcattgc caagtccttc tatgacctca gtgccatcag 180
ccgggatggg gagaaggtag atttcaatac gttccggggc agggcgctgc tgattgagaa 240
tgtggcttcg ctctgaggca caaccacccg ggaacttcacc cagctcaacg agctgcaatg 300
ccgctttccc aggcgcctgg ttgtctcttg cttcccttgc aaccaatttg gacatcagga 360
gaactgtcag aatgaggaga tcttgaacag tctcaagtat gtcctgtctg ggggtggata 420
ccagcccaac ttacaccttg tccaaaaatg tgaggtagat ggggcagaacg agcatcctgt 480
cttcgcctac ctgaaggaca agctccacct cctctatgat gacccatttt cctcatgac 540
cgaatcccaag ctcatcattt ggagccctgt gcgcgcctca gatgtggcct ggaactttga 600
gaagtctctc taggggcggg agggagagcc cttccgacgc tacagccgca ccttcccaac 660
ctcaacatt agccttgaca tcaagcgctt ccttaagt gccatataga tgtgaactgc 720
tcaacacaca gatctctac tccatccagt cctgaggagc cttaggtgc agcatcctt 780
ccagagacac tgcctgacct cagcattccc ttgatctac tcccttcac tgcagagcct 840
tgccctttcc cttgcctgt tctcttttcc tctcccaacc cttctggttg tgattcaact 900
tgggttccaa gacttgggta agctctgggc ctccacagaa tgatggcaac ttctaaacc 960
ctcatgggtg gtgtctgaga ggcgtgaagg gcctggagcc actctgctag aagagaccaa1020
taaggggcag gtatggaaaa aaaaaaaaaa aaaaaa

```

1065

## (2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 648 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggactgcggt cggtagtctc cggcgagttg ttgcctgggc tggacgtggt tttgctgct 60
gcgcccgctc ttgcgcgtct cggttcattt tctgcagcgc gccagcagga tggcccaaal20
gcagatctac tactcggaca agtacttcga cgaacactac gagtaccggc atgttatgtt180
accagagaaa ctttccaaac aagtacctaa aactcactcg atgtctgaag aggagtggag240
gagacttggg gtcccaacaga gtctaggctg gggttcattac atgattcatg agccagaaacc300
acatatctct cttcttagac gacctctctcc aaaaagatcaa caaaaatgaa gtttatctgg360
ggatcgtcaa atctttttca aatttaagt atattgtgtat ataaggtagt attcagtgaa420
tacttgagaa atgtacaaat ctttcatcca tacctgtgca tgagctgtat tcttcacaga480
aacagagctc agttaaaatgc aactgcaagt aggttactgt aagatgttta agataaaagt540
tcttccagtc agttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaag tttgtatgtt gcatttaaaa aaaaaaaaaa aaagtcga 648

```

(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1842 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcgagccgc tcgagccgct gctctctgga gggggtagag atcaaaaggcg gctccttcgg 60
acctctccaa gagggccagg cactggagta cgtgtgtcct tcttgcttct acccgtatcc 120
tgtgcagaca cgtacctgca gatctacggg gtccctggagc accctgaaga ctcaagacca 180
aaagactgtc aggaagggcag agtgcaagagc aatccactgt ccaagaccac acgacttcga 240
gaacggggaa tactggcccc ggtctcccta ctacaatgtg agtgatgaga tctctttcca 300
ctgctatgac ggttacactc tccggggctc tgccaatcgc acctgccaa gtaatggccc 360
gtggagtggg cagacagcga tctgtgacaa oggagcgggg tactgtcca accgggcat 420
ccccattggc acaaggaagg tgggcagcca gtaccgcctt gaagacagcg tcacctacca 480
ctgcagcggg gggcttaccc tgcgtggctc ccagcggcga acgtgtcagg aaggtggctc 540
ttggagcggg acggagccct cctgccaa ga ctcttcattg tacgacaccc ctcaagaggt 600

ggccgaagct tccctgtctt cctgcagaca gaccatagaa ggagtgcag ctgaggatgg 660
gcacggccca ggggaacaa acagaagcgaa gatcgtcctg gacccttcag gctccatgaa 720
catctacctg gtgcagatg gatcagacag catitggggcc agcaacttca caggagccaa 780
aaagtgtcta gtcaacttaa ttgagaaggt ggcaagttat ggtgtgaagc caagatatgg 840
tctaagtaca tatgccact accccaaaat ttgggtcaaa gtgtctgaag cagacagcag 900
taatgcagac tgggtcacga agcagctcaa tgaatacaat tatgaagacc acaagttgaa 960
gtcaggggact aacaccaaga agggcctcca ggcaagtgtac agcatgatga gctggccaga1020
tgcagctcct cctgaaggct ggaacccgac ccgccatgtc atcatcctca tgactgatgg1080
attgcacaa acatgggcgggg acccaattac tgcattatga gagatccggg acctgctatal140
cgggcctttg gtgaaccaa ggaacatcaa tgcattatga gagatccggg acctgctatal140
catitggcaa gatcgcaaaa acccaaggga ggaattatcg gatgtctatg tgtttgggg1200
cgggcctttg gtgaaccaa ggaacatcaa tgcattatga gagatccggg acctgctatal140
acatgtgttc aaagtcaagg atatggaaaa cctggaagat gttttctacc aaatgatcga1320
tgaaaagccag tctctgagtc tctgtggcat ggtttgggaa cacaggaagg gtaccgattal380
ccacaagcaa catatggcagg ccagaatctc agtcattcgc ccttcaaaag gacacgagag1440
ctgatatggg gctgtgtgtgt ctgagtaact tgtgtctgaca gcagcacatt gtttcaactgt1500
ggatgacaaa gaacactcaa ccaaggtcag ctatggaggg gagaaagcgg acctggagat1560
agaagtatgc ctatttcacc ccaactcaaa catataatggg aaaaagaagg cagggaattcc1620
gactatcagg cccatttgtc ttgcccctga caagctcaag aataagctga aatatggccal680
tccaaactacc acttgcacgc tccocctgca caggggaaca actcgagctt tgaggcttcc1740
gctgtgtttg tccggggggg aaaaaaaacc gcccccgggg gg 1842

```

## (2) INFORMATION ON SEQ ID NO. 122:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

gggggggtata aaagcccccac ccaggccagc cggtctctgct cagcatttgg ggcagctctc 60
agctctcggc gcacgggcccac gcttccttca aaatgtctac tgttcacgaa atcctgtgca 120
agctcagctt ggagggtgat cactctacac ccccaagtgc atatgggtct gtccaaagct 180
atactaactt tgatgctgag cgggatgctt tgaacattga aacagccatc aagaccaaag 240
gtgtggatga ggtcacatt gtcaacattt tgaccaaccg cagcaatgca cagagacagg 300
atattgcctt cgcctaccag agaaggacca aaaaggaaat tgcctcagca ctgaaagctag 360
ccttatctgg ccacctggag acggtgattt tgggctcatt gaagacacct gctcagtatg 420
acgttcttga gctaaaaagt tccatgaagg ggctgggaac cgacgaggac tctctcattg 480
agatcatctg ctccagaacc aaccaggagc tgcaggaaat taacagagtc tacaaggaaa 540

tgtacaagac tgatctggag aaggacatta ttctggacac atctggtgac ttccgcaagc 600
tgatgtgtgc cctggccaaag ggtagaagag cagaggatgg ctctgctatt gattatgaac 660
tgatttgacca agatgctcgg gatctctatg acgttgagat gaagaggaaa ggaactgatg 720
ttcccaagtg gatcagcatc atgaccgagc ggagggggccc caccctcaga aagtatttga 780
taggtacaag agttacagcc cttatgacat gttggaaaagc atcaggaaaag aggttaaaag 840
agacccgtgaa aatgctttcc tgaacctggt tcatgtcatt cagaacaagc cctctgattt 900
tgctgatcgg ctgtatgact ccatgaaggc caaggggagc cgagataaag tctctgatcg 960
aatcatggtc tcccgcagtg aagtggacat gttgaaaaat aggtctgaat tcaagagaaa 1020
gtacggcgaag tcccgtactc attatatcca gcaagacact aagggcgcat accagaaaagc 1080
ggtgcgtgac ctgtgtggtg gagatgactg aagcccgcac cggcctgagc gtccagaaat 1140
gggtgctcacc atgcttccag ctaacaggtc tagaaaaaca gcttgcgaat aacagtcccc 1200
gtggccatcc ctgtgagggc gacgttagca ttacccccaa cctcatttta gttgcttaag 1260
cattgctctg ccttctctgc tagtctctcc ttgaagccaa agaaatgaac atttccagga 1320
gttggaaagt gaagtctatg tgtgaaacac ttgctctcct gtgtactgtg tcataaacag 1380
atgaataaac tgaatttcta ctttagaatac acgtactttg tggccctgct tccaactgaa 1440
ttgtttgaaa attaaacgtg cttgggggtc agctggtgag gctgtccctg taggaagaaa 1500
gctctgggac tgagctgtac agtatggttg cccctatcca agtctcgcta ttttaagtaa 1560
attttaaata aataaaataa aataaaatca aaaaaa

```

1596



## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gtcgagctg accctcgctc ccgccccgc ctggagtcg acgtggaaagt tgcctggctga 60
ctgggcttgc gaggaaccgc cctcggagct gcagccgaag gcaaggaaac actgaagatc 120
ggcggaggag gacagggggt tcatcatggg tggctttttc tcaagtatat ttccagctct 180
gtttggaact cgggaaatga gaattttaat ttggggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tggggagaagt tgttactact atacctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaacaca gatgcagtc tttatgtagt 420
agacagtgtg gaccgagacc gaattggcat ttccaaatca gagttagtgt ccattgttga 480
gggaagaagag ctgagaaaaa ccattttagt ggtgtttgca aataaacagg acatggaaca 540
ggccatgact tcctcagaga tggcaaatcc acttgggtta cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaacaa aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acatttaaaa gcagacagta attcagtcac ttctctccc ctgaaatgaa 720
gactacatca cctctctccc ttggaaaca gtcaagtgtg cttcacacta ctgatgtta 780

aaactatatg attattggca tatactgact gactgcaata ttgtagtaa atagggaaaa 840
taagtattta gttggaggga taatttgatc gaatcacctg aatgttctat gtaatgtaaa 900
atatcttttt ctgtctttct tgtgttaagg tatatatctt attgtatgg aattcttatt 960
caaatcacag tctattaaag agtatactcc tattggatga aaaaaacctt aaaaaaaaaa 1020
aaaaaaaaaa aaa                                     1033

```

## (2) INFORMATION ON SEQ ID NO. 124:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ICLLVHFVSR AKTVNLTFYSY WWVITENKDL FSCSLKSHK NNQIGSCLLS CVSWFLTCVH60  
TPVCL 65

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 64 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ISVFRLEFKYL TRFQTCTMFY KPLDFQQHTI ENTCYSKHNH SVSSIAVVRD NIAISGMLQA60  
FKIA 64

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 61 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

KANLLPATPE GTQIWVGPVF QLGKRMGKPG DGFHKFSSGL WHSFQEIPLG KGLLANMHFQ60  
T 61

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

LKNTNEVKAL NWYTLFTPIF QVWKCIFASR PLPRGISWKE CHNPLENLWK PSPGFFIRLP60  
 SWKTGPTHIW VPSGVAGRRF AF 82

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

HTWDVYPLGI SPRTIRPVQK PKVAFGMLNF PLSSKKVHLEN EVTIRLNPCK SLDFVFKNS60  
 TFPKLSLVIK ISTLPKCDST AWFLANKNPI 90

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

MVADYGCTIL ILGPETHRNH TKWPDITYFTE QFKYYTLAKS TYSTHPGEGG EKTHYKTTTS60  
LDTMCLPTIS SLNNFHLRC LV 82

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

RNLVTQMKSG IEDPWTWQVN ADYSLAFFLY LCKEGYTELI LFQAYNFKFY HLNSSTFAAE60  
EWNQKNVSW 70

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 60 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AIQCEAYFIA TLVDCQGDSA TVLDKLMFFP SLAANRRATY SAGSRARSWG SRGYTSSLIIE60

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 181 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

IPNMAAPLGG MFSGQPPGPP QAPPGLFGQA SLLQAAPGAP RFSSTLVDE LESSFEACFA 60  
 SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFLLQ KRLQLSVQKP EQVIKEDVSEL20  
 LRNELQRKDA LVQKHLTKLR HWQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180  
 T 181

## (2) INFORMATION ON SEQ ID NO. 133:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 423 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

LSSEDEIRTLK QKKIDETSEQ EQKHKETNNS NAQNFSEEEG EGQDEIDILPL TLEEKENKEY 60  
 LKSLFETIIL MGKQNIPLDG HEADEIPEGL FTFDNFQALL ECRINSGEV LKRFETTAV120  
 NTLFCSKTQQ ROMLEICESC IREETLREVR DSHFTSIITD DVVDIAGEEH LPVLVRFVDE180  
 SHNLRDEFIG FLPYEADAET LAVKFHTMIT EKWGLNMEYC RGQAYIVSSG FSSKMKVVAS240  
 ALLEKYPQAI YTLGSSCAEN MWLAKSVFVM GVSVALGTIE EVCSFFHRSP QLLLELDNVI300  
 AVLFQNSKER GKELKEICHS QWTGRHDAFE ILVELLQALV LCLDGINSDT NIRWNNYIAG360  
 RAFVCSAVS DFDFVITIVV LKNVLSFTRA FGKNLQGQTS DVFFAAGSLT AVLHSLNEVS420  
 GRY 423

## (2) INFORMATION ON SEQ ID NO. 134:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

VENIEVYHEF WFEATNLAT KLDIQMKLPG KFRRAHQGNL ESQLTSESYY KETLSVPTVE 60  
 HIIQELKDF SEQHLKALKC LSLVPSVMGQ LKFNTESEHH ADMYRSDLPN PDTLSAELHC120  
 WRIKWKHRGK DIELPSTIYE ALHLPOIKFF PNVYALLKVL CILPVMKVEN ERYENGRKRL180  
 KAYLRNTLTD QRSSNLALLN INFDIKHOLD LMDVTYIKLY TSKSELPDTON SETVENT 237

## (2) INFORMATION ON SEQ ID NO. 135:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRINGSLCP QTKNNLYFHI VELSIGASV GERWYMGES ILPARGESQG LLCLYFYKE160  
 LPLFLVNKLR GTDVGLEQGL SSGEGSWTA 89

## (2) INFORMATION ON SEQ ID NO. 136:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

FEERAKREEL ERILEENNRK IAAQAQKLA EQLRIVEEQR KIHEERMKLE QERQRQQKEE60  
QKTIILGKGS RPKLSFSLKT QD 82

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 71 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

SALKVEYLLS CPVSCRVCSS AAIRASFLFK MICTVSLAIP ASAAQPFIKK QHTRKAEELRN60  
ADVYGKKEQK M 71

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

SSAQRKYFNL FVEILVMERC QTVLNGRTSK SEATVPTTRG LLYCSTFSAL YFLAEASPWS60  
AMYKLG 67

## (2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

RAEKVEQYKS PRVVGTVASL LLVLFFKTVW HLSMTRISTG RLKYFLCAE

49

## (2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

SCERRGFIMA DDLKRFLYKK LPSVEGLHAI VVSDRDGVFV IKVANDNAPE HALRPGFLST 60  
 PALATDQGSK LGLSRNKSII CYYNTYQVVQ FNRLPLVVSF IAASSANTGL IVSLEKELAP120

LFEELRQVVE VS

132

## (2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF



- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

QMIILLFLESP SLLPWSVARA KVDKKPKGRKA CSGALSFATL ITGTPSLSDT TMAWSPSTLG 60  
 :FLYKNRFRS SAMMNPILLSQ QQSRLGFLG CLVLSAVTSG TALKTGSSSS HRHMIHDLVCI20  
 APGSTF 126

(2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGLAGATA NKASHNRTRA LQSHSSPEGK 60  
 EEPEPLSPEL EYIPRKRGKN PMKAVGLAWA IGFP CGILLF ILTKREVDDK RVKQMKARQN120  
 MRLSNTGEYE SQRFRASSQS APSPDVGSQV QT 152

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

EGRSAPQVCT PDPTSGDGL WEEALNLWLS YSPVLNRMF CRAFTCFTRS LSTSLVRMK 60  
 BRIPQKGKMA QASPTAFMGF LPLFLGMYSS SGRDGSGLL PSSELWLCRA RVLL 114

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 267 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

EDEVEEESTA LQTKDKKEIL KKSEKDTNSK VKPKGKVRWT GSRTGRWKY SSNDESEGG 60
SEKSSAASEE EEEKSEEEAI LADDEPCCK CGLPNHPCLI LLCDSDCSGY HTACLRPPLM120
IIPDGWFCE PCQHKLLCEK LEEQLQDLGV ALKKKRAER RKERLVVYGI SIENIRPPPE180
PDFSEDEEEK KDKSKKSKAN LLERRSTRTR KCISYRFDEF DEADEAIED DIKEADGGGV240
GRGKDISTIT GHRGKDISTI LDEKIIT                                     267

```

## (2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

SSEKSGSCGG MMFSILIPY TKRSFLRSAR SFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RQAVWYPLS QESHRRISGG WFGRPFLHG SSSSARMASS LSFSSSSSEAL20
ADDFSLPDPS LSSILLEYFHL PRVREPVRHT LPLGFTLEFV SFSDFFKISF LSVFCKAVDS180
SSTSS   185

```

## (2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

KRQPTSAMKD PRRSSTSPSI INEDVIINGH SHEDDNPF AE YMMWNEEEF NRQIEEELWE 60  
SEFTIERCFQE MLEEEHEHW FIPARDLPQT MDQIQDQFND LVISDGSSE DLVVKSNLNP120  
NAKEFVPGVK YGNI 134

(2) INFORMATION ON SEQ ID NO. 149:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 135 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

HSDKRAFTIK SSNTAFTVWK LCYIHQKRAP STQIFPYFTP GTNSFAFGFR LLLTTRSSRE 60  
EPLITRSLN WSWIWSIVCG RSRAGINHSC SSSSSISWK QRSINSSSHN SSSICLLNSS120  
SFSIHMYSAN GLSSS 135

(2) INFORMATION ON SEQ ID NO. 150:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 58 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

LVSGANQCGS CNSKSFLTKA WYVRVGFRFF RGGLDFDFDF FFYVIFGKTH SELYLVT 58

## (2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

FFVLKSLLVG ACYWEQVFVQ KLQSESLCIT ETLFITSLLS LPQKTVGLNK IICILIVLKC60  
L 61

## (2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SACKFLRLDP LLTVQQLMYT CIKALNKSL WLITAKMGTR HLLCVLVTAV ALRAVRPCL160

## (2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

KRDIIINVES QRSHKRKKNQ NQINHHREKNE TPHGNTKLWL GSSYYYSSHI GWRKPF 56

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

IPVHRLHGRA DPLGWSIVSD LITSGLGAGV LRGLPARRLH SLGRRVLGRP GWWLERLGHG 60  
 RRDALGANSA AQRPRTPGRP ACVCAPRRGP ESPSADPVPP PGRAGDPSPP DASASGPRGG120  
 AATKACPAHD PQQLRPELRV LPPFPRGDRE 150

(2) INFORMATION ON SEQ ID NO. 156:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 81 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

LPVAAGGRGQ DAQLRFELSG VVSRPRLLGG APSRSRGRI GVARVSSPAG RRDVCGGGL60  
GASAGRAHAG GAARGAGPLR G 81

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 214 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

PGSQSVTPPM AEPLQPDPGA AEDAAAQAVE TPGWKAPEDA GPQPGSYEIR HYGPAKWVST 60  
SVESMDWDSA IQTGFTKLNS YIQGKNEKEM KIKMTAPVTS YVERGSGPFS ESTITISLYI120  
PSEQQDFDPR PLESDVFIED RAEMTVFVRS FDGFSSAQKN QEQLLTASI LREDGKVFDE180  
KVYYTAGYNS PVKLLNRNNE VWLIQKNEPT KENE 214

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PNFYRGFIEN LTMCGGLSCL NLFRAVCSVH QMGRSGMGHL RPFSGLNRM LEPRLDSDTL60  
RF 62

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 104 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

IHLPKKLISF YLRGEVQFSF GSSESKHLIC WVKWTPFLAF YVLSHNNSIK QEGKQKTKKK 60  
 KGKKKNLHGL VSLTKHVGAV CLGGAGYRTC QCLGFSINLA RDIK 104

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

SLLSIRKIKQ NTSPARLTCV YIIYKQRATP TSQQLGEISA VHAVVCQFGE ITPWKNWKNL60  
 LAGKNSFICI KSVLQKNPCG 80

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

PSIDLEAEES QRLKVVMMWF SFKKLLFLES RIYGVNCSL FVHKIKPFKK LKKKKRGEK60  
 KREKKGKGRK RRGEE 75

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 68 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

KYLTLPYKLL VPFCIPPSIT LTKGIFYCKE YFILIYTSHE FLPLVTIQML PSIIQIAQP60  
 FYVHNSLL 68

## (2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

LFFLFRYHTV PLPPKGRVLI HWMTCQTM KLMAIPLVFQ IMFGILNGLY HYAVFEETLE60  
 KTIHEE 66

## (2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 159 amino acids



- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

TRLKGDGRGGV HFLKALRRGG LRASLLYLLK KYRLVFLLSI CVRGMVSSVK SFLVGEQLLS 60
ISEPRFRKMSV CKCSFLSTTS TFVPISSDSK KVSSYFSLCS ESLAEQNLFM MPEVFCSEQK120
FDEPLNDLSF FFTRLFSSLV TLRVSPHAPA SEMQTVLSS                               159

```

(2) INFORMATION ON SEQ ID NO. 167:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 439 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

KSLLTSSKF FLISFSSPQG LKFRSKSSLA NYLHKNGETS LKPEDFDFTV LSKRGIKSY 60
KDCSMAALTS HLQNQSNNSN WNLRTSKCK KDVFMPPSSS SELQESRGLS NPTSTHLLK120
EDEGVDDVNF KRVKPKPGKV TILKGIPIKK TKKGCRKSCS GFVQSDSKRE SVCNKADAES180

```

```

EPVAQKSQLD RTVCISDAGA CGETLSVTSE ENSLVKKKER SLSSGSNFCS EQKTSGIINK240
PCSAKDSSEHN EKYEDTFLES EEIGTKVEVV ERKEHLHTDI LKRGSEMDNN CSPTRKDFTE300
DTIPRTQIER RKTSLYFSSK YNKEALSPPR RKAFKKWTPP RSPFNLVQET LFHDPWKLLI360
ATIFLNRTSG KMAIPVLWKF LEKYPSSAEVA RTADWRDVSE LLKPLGLYDL RAKTIVKFS420
EYLTKQWKYP TELRGIGAP

```

439

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

DCGKVQTQMQ FALTNFLGLI SLCKTPVLSE LPQDRVQSFL KHALRCPHLR HCFVDTLKGV60  
 HKAKKSDQML RASNLVLTW TWHWQKSLQH 90

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

SDFCQCHQVQ VRYKLLALSI WSDFFALWTP LRVSTKQCLR CGHLRACFRK LCTLSCGRKE60  
 RTGVLHKEIS PRKLVNANCI CVCTLQSQYI VF 92

## (2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ADSHQNYIPW PFACVLLARP WLASLTREKD LQKIRLWDHF VCALGMTFFP TPGKPLGLSE60  
TLWLAKHMVS LKVERLSNPP IPREFQSVDV I 91

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

NGGLNAHLAS ASEFDHSGVQ LIEREEIEICI FYEKINIQEK MKLNGEIEIH LEEKIQFLK60  
MKIAEKQRQI CVTQKLLPAK RSLDADLAVL QIQFS 95

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 90 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

KTEFGAQLGR HPGTSLAVI SSSHKFVFAS QSSFSGIGS FLPVDVFQFL HLVSSSLGYL60  
FEHKKCIFLL PALSAERHYG QIQRQLSCH 90

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AVRSRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60  
 SPFHDIPIYA DKVRHPCFWT QSLYSDQLVL HMNFLICLST SA 102

(2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

VKRLCPKTRM PYLICINWNI MKWRYILSFL IFEDSVLQG EGRGALLGAE AAHSAGVLP60  
 PLFQSHQPAR GAD 73

(2) INFORMATION ON SEQ ID NO. 175:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RRQRKAEPGA CALGRVSGEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60  
 CRSEMEVDAP GVDGRDGLRE RRGFSEGGRO NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120  
 VVFLFVYFLP 130

## (2) INFORMATION ON SEQ ID NO. 176:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 62 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ILKMATNFLN KEDRTLNRRI SHLQGTLPFI LHFVTNLQNS INWVGFPFL AKFLKLNPLV60  
 RV 62

## (2) INFORMATION ON SEQ ID NO. 177:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 174 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AVYCIHQOK VLRLYKRALR HLESWCVORD KYRVFACLMR ARFEHKNKNEK DMAKATQLLK 60  
 GAESEFWYRQ HPQYIIFDS PGGTSYERYD CYKVPEWCLO DWHPSEKANY PDYFAKREQW120  
 KKLARRESWER EVKQLQEETP PGGPLTEALP PARREGDLPP LWWYIVTRPR ERM 174

## (2) INFORMATION ON SEQ ID NO. 178:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRMAV 60
DADGTRILPR PPSAAGWSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120
TPFADVVNCI R                                     131
```

(2) INFORMATION ON SEQ ID NO. 179:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```
LMMTIYALSN EFAFKINEEQ LSFFPLLVSQ LWHAQRFLD SWSGVIPFF FSCSCLFFLY60
PPKWRQIHDL KDTQYLLNSS                                     80
```

(2) INFORMATION ON SEQ ID NO. 180:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 140 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

KVLRFKLPQPE EASGQMAGAG PTMLLREENG CCSRRQSSSS AGSDSDGERED SAAERARQQL 60  
EALLNKTMR I RMTDGRILVG CFLCTDROCN VILGSAQEFL KPSDSFSAGE PRVLGLAMVP120  
GHHIVSIEVQ RESLTGPPYL 140

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 114 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SLKGRHRGQ RYGGPVRSL CTSMETMWCPT GTMARFPSTRG SPAEKESDGL RNSCAEPRMT 60  
LQSRVQRKQ PTVSRPFSVMR MRIVLLSSAS SCCRARSAAE SSRSPSESFA LELL 114

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RLSRLTEPKE DPMAGISTAE HHLOPTAALP TQLSRSRHSP QVISTOGGET RGCGRQERKA60  
ERRVCKNAKV TFPVGGKQZ RHWFOCHROS EHLEL 95

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 131 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

RRVQHPPFFS QLIRDAAKRT FRITRLQAFS KYLVVYVYLN GSMLPVPSPC PLCQPPVALV 60  
 LVSPSSAKR PWNLNGGCFA LGGSCWWDQS FDKPPAPWWH LSWKDVTFG AQTACGSRSTS120  
 AFGIFLPQWG R 131

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 128 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TAPCCRCFAP VPSVNPLSLW CWFRSRLQON DLGTSMGAAL LWEVLVGGTR ALTNLLLLGG 60  
 TSPGRTSLOLQ VLRLPVAAEP VPLAFSSHNG EGDFGILTNS SLGLSLLPST ASRFSSICAY120  
 YLRTVSAP 128

(2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 75 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

DSRVYCFSGN YRKLVLPRKT GAIKNGSNIS KLRKQDVLSF AHLGFLLPF SLFSLRSLFQ60  
FFSDLPLVPL ESQRL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

LGDSSEMPLL ALKCPVRLLG TLEPSEILII LGSSPYQMF SAQHWVLSST TENPEEKGR60  
FP 62

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 89 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

PHPSRRLTQG RMYRKSRYAM EKIPVSAFLR LVALSYNLAR DSTVKPGAKK DAKESRAKLR60  
QTLRSRWGEQ LIWTQTYEEA LYKSLRATN 89

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GNFELPWRKF QCQHSICALWR SPTIWPGIAQ SNLEPKRTGR SLEPNCARPS PEVGVNNSG60  
 LRRMKKLYIN RD 72

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SLGHRPRNGG HSRGCDLGGI HAHSPPRLQ GAGLQQAANA AYSVSLPPGC VGHLPPLRL 60  
 HHRTGREHRA HTLLPLWDPL FHLLLPAGS CCQSDQARPG EEAFFEVGDS GSGRGLQSP120  
 GCYRY 125

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 200 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

RGDRSCPRSP PALRSSPAAL LRAGSSTKFT ANALALGSRM ATTVPDGCGRN GLKSKYYRLC 60  
 DKAEAWGIVL ETVATAGVVT SVAFMLTLPI LVCKVQDSNR RRMLPTQFLF LLGVLGIFGL120  
 TFAFIIGLDG STGPRRFFLF GILFSICFSC LLAHAVSLTK LVRGRKPLSR LVILGLAVGF180  
 SLVQDQVIAIE YIVLTMRNTK 200

## (2) INFORMATION ON SEQ ID NO. 191:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AEAHGQTQNH QPGKGLPPFD ELGQTDMSMQ QAGEADGKED PKEEEACGFC APVQSDDEGE 60  
 GEAKDAQHTQ EEEKLSRQHF SPVGVLHLAD EDRESEHEGH RGHNPCCGHR F 111

## (2) INFORMATION ON SEQ ID NO. 192:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

EIYWETOYNH SGTIDAHMR TALRKAGFTL NSQVQQTIAL RYACSKLGIN FDSFVACMIR60  
 LETLFKLFSL LDEDKDGMVQ LSLAEWLCCV LV 92

## (2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ESLIAFLFLH DQCAQDSIVL TMKDVVRIQ WTRNECKGGL EQRGCPGK ESYQILLNLQ60  
 PERLEFHRPQ SAFFHCSRHI K 81

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

KTTIHGPCQN HLPFPHCFK RPTLSKGGP IDSSQEGFRA SIRAWPVLAP LLSEQQGFQG60  
 SGWHESLSLP SCSFMTNVER TQ 82

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RPPFSSRSSL AGQTNTQHS SARES

25

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 71 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TMPSLSSRR LNSLKRVSRR IIQATKLSKL MPSLLHAYRR AMVCCTWLLR VKPAFLRAVL60  
 ISWASMVPEW L 71

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 86 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

IRRNISRAISV HTWRRTPPYD SPACFSCSIV SLESGGFFSC VSVFFSFDLS NFSISAISGL60  
 SDMVAEKQS EAHEYERQFL ASRRSG 86

## (2) INFORMATION ON SEQ ID NO. 198:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

HPFSTFPTLP PQAGKFDATL LASQCILGGA RLLTIRLLAS PVQSFLMKAV DFSLASLSSS 60  
 VSTYRISR SQ PYRVQQTWLR RKSKARRST SDSSSRLLAAV A 101

## (2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TPFPFSQLYP LKQVNSTQHF SHLSAYLAAH ASLRFACLLL LENRFFGRQW IFLLRLCLLQ 60  
 FRLIEFLDLS HIGFVRHGCG GKAKRGARVR ATVPRVSPQW 100

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GLTDQYLELN ALQEEELGPFQ LVILGFPSNQ FGKQEPGENS EILPSLKYVR PGGGFVFNQ 60  
LFEKGDVNGE KEQKFYTFPK NSCPPTAELL GSPGALFEP MKIHDIRWNF EKFLVPGDGI120  
PVMRWYHRTT VSNVKMDILS YMRRQAALSA RGK 153

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 249 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

LMPPFFYPYPL PIMQGPGRGS SGRKPHSQSF YPHPRFSLL HKRQAWHNCV SEPLWTRDNC 60  
PSVCMATQPR ICLLETQGWS ICVYGLAHP HIFFSFLFOM SPKETQVLGP MVLKPEHHS120  
WGQHLPHANT THQPPSSFL KDPPEPPSPS HSAPETSQDN CERDGRVPOV RGVSMKEGFI80  
EALVGGPPLS PSVVPALSAF RLRLPGROTT PAPLEDMLSS HSVHWYLNTP ICPVKVFLQQ240  
KKKKKKKKKK 249

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGLSAPFPAP LLCRAQAPLA LGPNFSYRHG VRFSSSPGAH LPEARCGGGP RGRSQAQSPQ 60  
 SSGPVGGRRR SGSKARTPQL FRLQQQLCRF GHGCEVPRCW LQAAREHPGQ GQEAQSEEEG120  
 EGQEGEGQEE GGSPLKGPQ GSLNPLCLR VPTTWS 136

## (2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

DPTSLTAMEF DLGAALPTS QKPGVGAGHG GPKLSPHKV QGRSEAGAGP GPKQGRHSSS 60  
 DSSSSSSSDS TDVKSAAAGS QKHESIPGKA KKPVKVKKKE GKKEKGKKKE APH 113

## (2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

GGFPPPKHLS SRNLVLVGRE EGLMSPVQGP SVGSLLLLAL LLLALLLLH FGLLGLARDA 60  
 LVLLGASSVG LHIRVRIAGA AAGVGRAVVS LLWTRTCPL RPALNFVGTG LGISPVARPH120  
 TGLLGGGLQG CSQVELHGKG RSWVLRPRAP GPCRGAEQGE ER 162

## (2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 145 amino acids
  - (B) TYPE: Protein



(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

VEPWTCRAA GAVMADYWKS QPKKFCDYCK CWIADNRPSV EFHERGKNHK ENVAKRISEI 60  
KQKSLDKAKE EEKASKEFAA MEAAALKAYQ EDLKRGLGES EILEPSITFV TSTIFPTSTS120  
NQKKEKKEKK KKRSFRGQMG RRHNL 145

(2) INFORMATION ON SEQ ID NO. 206:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 262 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PALSHLRHQ INRKKRKRKR KKDPSKGRWV EGITSEGYHY YYDLISGASQ WEKPEGFQGD 60  
LKKTAVKTVW VEGLSGDGFT YYNTETGES RWEKPDDFIP HTSCLPSSKV NENSLGTLDE120  
SKSSDSHSDS DGEQAEDEGG VSTETEKPKI KFKEKNKNSD GGSDPETQKE KSIQKNSLGL180  
SNEEKSKTLK KSNPFGEWQE IKQEVESHEE VDLELPSTEN EYVSTSEADG GGEKPVVFE240

KTVTSLGVMA DGVAPVFKKR RT

262

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 73 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GKGRRGKIGK VCCNGGSCPE SIPRGFEKTW LRVNFGAKH NISNQHYPTY LDIKSTERKE60  
 REEEKILQR ADG 73

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

IWNFQALKMS MYQLQKLMVA ENPKWYLKKK QSLLELWQM EWPQSSKREE LENGKILGKF60  
 KGNEVMIQ 68

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 194 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SVHCFREDKM KFTIVFAGLL GVFLAPALAN YNINVNDNN NAGSGQGSVS VNNEHNVANV 60  
 DNNNGWDSWN SIWDYNGGFA ATRLFOKKTC IVHKMNKEVM PSIQSLDALV KEKKLQKGKGP120  
 GGPPPKGLMY SVNPNKVDDL SKFGKNIANM CRGIPTYMAE EMQEASLFFY SGTCYTTSVL180  
 WIVDISFCGD TVEN 194

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VHQALGRWSS WSLTLKLLFL DQCIKGLNGG HDFLVHFVHN ACLLLKESGC SKAISIIIPDG60  
 IPGVPSVVIV NIGHIVFIVD TH 82

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

EEGLNHLWLR VWLEPTAQVP DVLFFPEFMER SEKAVSLLLW FNVKEPQLPP LPGREAFGFL 60  
 LLLALVAGE VLQHRLLAQ LVLAGLRARA GLRFRKALT KASARCAPEG WTSESASF 119

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 136 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

IICGCVSGLS PLHRSIMYCF QSSWRGRKRL YLCCSGLMSK SRSSLLCLAE KPLAFFFFSL 60  
RLWRVKYSRT TALRCSWSSR ACGLMRGVCA SGRPSRRPRP AVLLKAGHRS HSPLSETMHG120  
RSHSSFSDFR RRLMT 136

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TLETVHQGFV QWAQARHAAT DDSGQALKGR SSRGYFSDK IQMPLLCGY Y RNPSTGNKAH 60  
FQNYHQRRPP ESYQAKLRV HCGNRWLYFL HLEQIPASV K 101

(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 204 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LRCFAFRSTA GRGLREGPLPE AQTPRMSPQA REDQLQRKAV VLEYFTRHKK KEKKKKKAGF 60  
 SARQRRELRL FDIKPEQQRY SLFLPLHELW KQYIRDLCSG LKPDTPQPMI QAKLLKADLH120  
 GAIISVTKSK CPSYVGITGI LLQETKHIFK IITKEDRLKV IPKLNCFVTV ETDFGISYV180  
 GSKTQLRSSE RSAKKFKAGK TIDL 204

## (2) INFORMATION ON SEQ ID NO. 216:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 645 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PTRPVAAGSE QQQQSAFIQE RQPVALMRLL SFNVPHIKNS TGEPIWKVLI YDRFGQDIIS 60  
 PLLSVKELRD MGITLHLLH SDRDPIDVP AVYFVMPTEE NIDRMCDLR NQLYESYYLN120  
 FISAIRSKL EDIANAALAA SAVTQVAKVF QCYLNIFITL DDMFVLNQN KELVSYRAIN180  
 RPDITOTEME TVMTIVDSL PCFFVTLGAV PIIRCSRGTA AEMVAVKLDK KLRENLRDAR240  
 NSLPTGDTLG AGQFSFORPL LVLVDNRIDL ATPLHHTWTY QALVHDVLDF HLNRVNLEES300  
 SGVENSPPAGA RPKRKNKXSY DLTPODKFWQ KHKGSFPPEV AESVQGELES YRAQEDVKR360  
 LKSMGLEGE DEGAISMLSD NTAKLTSASV SLPALLEKKR LIDLHTNVAI AVLEHKKR420  
 LDVYFYEK IMSKTTLDKS LLDIISDPDA GTPEDKMRLF LIYYISTQQA PSEADLEQYK480  
 KALTDAGCNL NPLQYIKQWK AFTKMASARA SYGSGTTTKFM GLLSRVMNTG SQFVMEGVKN540  
 LVLKQQLPV TRILDNLMM KSNPETDDYR YFDPKMLRGN DSSVPRNKNP FQEAIIVVVG600  
 GGNIEYQNL VDYIKGKQSK HILYGCSELF NATQFIKQLS QLQSK 645

## (2) INFORMATION ON SEQ ID NO. 217:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGSQSLRLH YPRISMAVRQ WVIALALAA LVVDREVPVA AGKLPSRMP ICEHMVESPT 60  
 CSQMNSLVCG TDGLTYTNEC QLCLARIKTK QDIQIMKGK C 101

## (2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

QLGWIFYFMS YPLHAHHCSP ADTSWLEVLL WDQHLPSFMI WMSCLVFIRA QSMWHSFVYV 60  
 SPSVPQTRLD IWEQVGDSMT CSQMGIKLG SFFPAATGTL SITRRAAKAR AITHWRTAML120  
 ILG 123

## (2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

IKAKFNINAF FFFLLRSEI GTVILSTERQ IIKWAMKGGG KVLIVIRGIQ PEIKPIYKHV60  
 CSSK 64

## (2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

SFAIPFPWHC TISPIIGQSL GFLGFTMVAT TIRLIDGNSL KKKVMVMDKI SRSREVCYHK60  
ITVASTS 67

## (2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

TIISSTDSQ LQEVAEQLEI FAALHEVLHI INDRKNLKGQ LQEVAEQLEL ERIGPQHAG 60  
SDSLLTGMAF FKMREMFED HIDDARYCGH LYGLSGSSY VQNGTGNAYE EEANKQS 117

## (2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 196 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

PTCPIQHFM MKLWVPSRSL PNSPNHYRSF LSHTLHIRYN NSLFISNTHL SRRKLAVTNP 60  
IYTRKRLNI FYLLIPSCRT RLILWIIYIY RNLKHWSTST VRSRSHSIYR LRPSMRTNII120  
LRCHSYXKPP ISHPHYWNNP SRMNLRLGLS RQSHLDPLR FPLHLTIYYR GPSNRSPPLP180  
PRNRKIQPNR IKLRCR 196

## (2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

LPSAIEGPTP VSALLHSSTI VVAGIFLLVR FHPLTTNNNF ILTILCLGA LTTLFETAICA 60  
 LTQNDIKKII AFSTSSQLGL IIVTLGINQP HLAFLHICTH AFFKAILFIC SGSIIHSLAD120  
 EQDIRKIGNI TKIIPFTSSC LVIGSLALTG IPFLTGFYSK DLIIEAINTC NTNA 174

## (2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

FLKTTALIIIS VLGLIALEL NNLTIKLSIN KANPYSSFST LIGFFPSIIM RITPIKSLNL 60  
 SLKTSLSLTD LKWEKTIPK STSTLHTNIT TLTNQKGLI KLYFISFLIN IILIIILYSI120  
 NLE 123

## (2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

NMLLAEVRIIS MVIIRNSVRYL MNRLMFGSEC IYHEENCIID HVTKRATDVN RIEKKSVLKL 60  
 ILSSIEFMVT QQQVVIYISI LLWKNINRGK RLIMKENLID VVVYSGKLMC LIRFDIEIRI120  
 GDSRRMKIK 129

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

FFFFFFFAIQ MNVYFLNPHR VRAELRDANH SISHPGSLPR SFFFAQSILD LYHFLQRQYP60  
 EWQSQVYFKV GVFSGSRGDW IPS 83

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

SMMLFKVLVI TVFGTLTVAF FLSELVSINK ELQNSIIDLL NSVFDQLGSY RGTAKPLEDY 60  
 TODDLSTOSE QIMDFTPAAN KQNSEFTDV STVSSGFLEE FTENTDITVK IFLAGNPFVSP120  
 TS 122

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TSTTVFFFFF HSLFPVGCTV CSHALCINIL EIYRSVLYFL YCWILIITF TRVLNKSSLT60  
 RK 62

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ARPCWNSTKA LPHGREHTRL KMSLYLKNKM CKSSGWHKTK VNASWGTFLR GLAECVNIID60  
 FCLCYMTSVT SLKICTIQFQ LWTISVDLCE GFYLCRMGV 99

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GELQKSSHYH PPELFEMIFF VHFSGSIGGR IYYNMDHLYF CIYLFITRPQ PQSSFSPTS60  
LCL 63

(2) INFORMATION ON SEQ ID NO. 231:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 64 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

INKYRSRDDP YYSIFYHQYC SQNVQKKSFD ITQEDDNGWT FVHKLKDCGR ANSTHCIVCA60  
YGGL 64

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 88 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

PLFCAILKTC TFYFSDSLTF LIECVLYHAV MLWYYSYRVL PILKTCHEFPK RSFDSALEVL60  
HKLKLSNIN MRGGTGCONIY SQVTSLYI 88

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 161 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIAD IKKMAKQGQM 60
DAVRIMAKDL VRTRRYVRKF VLMRANIQAV SLKIQTLSN NSMAQAMKGV TKAMGTMNRQ120
LKLPQIQKIM MEFERQAEIM DMKEERIELL HLMIPVWLKG F 161

```

## (2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

RRVRTKSFAM MRTASIWPC L AIFLMSAMIF FSWVSSFCRS RSSSRMARFR ALWFCRSSSS 60
GVFERPNNRS MMVEAHWQAG AGTDTRFRFR VTLLFLGSPT CPPTKAPRSC RRRRRFRGRV120

```

## (2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

KLPQNPRDHQ MQQFNPLLLH IHDLCPLKL HHDLDLGQL QLSVHGAGL GDTLHGLCHR 60  
 VVGLECLDLE GHSLDVGPQH YKLAHIAPGA HQVFCHDANS IHLALLGHLL NVCNDFLLGL120  
 L 121

(2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 180 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

KTKRSVKDAA KKGQKDVCI V LAKEMIRSRK AVSKLYASKA HMNSVLMGMK NQLAVLRVAG 60  
 SLQKSTEVMM AMQSLVKIPE IQATMRELSK EMMKAGIIEE MLEDTFESMD DQEEEMEEAE120  
 MEIDRILFEI TAGALGKAPS KVTDALPEPE PFGAMAASED EGEEEEEALEA MQSRLATLRS180

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

LMPFQSQNLQ ERWLPQRMAG RKRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60  
 ALHLCCEDYH FEGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRKKKKK K 111

## (2) INFORMATION ON SEQ ID NO. 238:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

KICERCCQEG PEGCLHSSGQ GDDQVKEGCE QAVCIQSTHE LSAHGDEEPA RGLASGWFFA 60  
 EEHRSDGEGA KSCEDSRDSG HHEGVVQRND EGWDHRGDVR GHF 103

## (2) INFORMATION ON SEQ ID NO. 239:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 351 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TWCTTMLAA RLVCLRTLPS RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60  
 RGRGTQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120  
 IWFOYVKDRI HSTYMYLAGS IGLTALSIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180  
 MLVRSIPYDQ SPGPKHLAWL LHSQVMGAVV AFLTILGGPL LIRAAMYTAG IVGGLSTVAM240  
 CAPSEKFLNM GAPLGVGLGL VFVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFMSFLLYD300  
 TQKVIKRAEV SPMYGVQKYD FINSMLSIYM DTLNIFMRVA TMLATSGNRK K 351

## (2) INFORMATION ON SEQ ID NO. 240:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

RVAPATVVG RNIIDPNEDTK TRPRPTPRGA PMFRNFSLGA HMAVERPPT MPVYHAALM 60  
RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120  
MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 241:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 196 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

KARRRGTMAA AADERSPEDG EDEEEEEQLV LVELSGIIDS DFLSKCENKC KVLGIDTERP 60  
ILQVDSCVFA GEYEDTLGTC VIFEENVEHA DTEGNNKTVL KYKCHTMKKL SMTRILLTEK120  
KEGEENIGGV EWLQIKDNDF SYRPNMICNF LHENEDEEVV ASAPDKSLEL EEEEIQMNR180  
FKPGFVEPGE PIAPWE 196

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PPAPALRHRE TRRPVASLHV GTGALGARSH PFAGSRHLEF WQKQFARRGA DGQEPNKLRL 60  
LGAEARTQDG GSGRAWPVTR RRGAGPWRR RRTSGVQRTS KTRKRRSSWF WWNYQELLIQ:20  
TSSQNVKINA RFWALTLRGP FCKWTAVSLL GSMKTL 156

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 132 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

RRLEVSRYQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60  
IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPSI:120  
PELDGKTAKM YR 132

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 159 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

LFASISVSLP VHLCCLSIQL RNCNFWGSSR ICDRNVKLDV KLIFQEVMDI PAFSKPPSSF 60  
LVGLQSEPIV VSLVLVHIP DKGLIFLLQS LHPQLTISGS GVSLQHRDLR HNTSRGFIRH:120  
LGPGRKRNAE VVLPVAYLKA PSSLLWEDET LGCKTSFE 159



## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATLPDALPPA TKFFLKAFDD SLSPFIQSYL YIFAVFPSSS GTAISGAVVG YVIGMSNSMS 60  
 NSYFRRSWIY QHFFNHRVPS LLDSSRNQSL SAFLLFSTYR IRD 103

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 285 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKQYI 60  
 SPFHDIPIYA OKDVFMVVE VPRWSNAKME IATKDP LNPI KQDVKKGKLR YVANLFPPYKGL20  
 YIWNYGAIPO TWEDPGHNDK HTGCCGDNDF IDVCEIGSKV CARGEIIGVK VLGLAMIDE180  
 GETDQKVIAT NVDDPDAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240  
 FKDKDFAIDI IKSTHDHAWKA LVTKKTNGKR IMLIVQLFVG PLKVC 285

## (2) INFORMATION ON SEQ ID NO. 247:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TKGLRIAQAQ LCPGSPRCRS QSISRACAL CLRPSQPNT TYLRKPGGRK RAVGHKSPA60  
TRVPASVQRS QPPRAHRKSC LASLGLCKNN KCLS 94

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 113 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DPRPSRIQHI SGNPAGASER LAIRAQLKRE YLLQYNDPNR RGLIENPALL RWAYARTINV 60  
YPNFRPTPKN SLMGALCGFG PLIFIYYIHK TEADRKEKLI QEGKLDRTFH LSY 113

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 98 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VFRSGSEIRI DIYCSCIGPT KQGRIFDEPS AVGIIVLKVQV LSFQLGSYGQ PLACARRVSG60  
DMLYSAGSRV SGRVRRDLGL YFGNDILANQ GTIAPARF 98

## (2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 158 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TQVMVQSMFA PTOTSDMEAV WKEAKPEDLM DSKLRVVFEL PAENDKPHDV EINKIISTTA 60  
 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LMRKRTVQSN120  
 SPISALAPTG KEGLSTRLL ALVVLFFIVG VIIGKIAL 158

## (2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSOGADGL DRATEDTESSL 60  
 GREWATWGLL CGADRTQPHA GLQLFKGQHQ QARKGVILRE VIQHHVFRPT NV 112

## (2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

SKGCSITETV TVDPGSIPL LGLTQYRRGA VVFTLKHTFL SDGFRNLRFV VTTSVKGPLN 60  
LRSVGGSRTR ICSSSPWPLR RTPSERQRRR GGGLLAGGGG RWREGRGSEF ASLLFLVRLC120  
STTFLCWQIC FQIDF 135

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 189 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

SMQSAVSFFF FSLDQKKICL PTISLVVWPT VTIFLCVQRH IGFAFNDLLR LENTIKTNCS 60  
ATGQOVVYQI ITSRCQLHIE SFMKFINKEL FFLOGFNKSS RIVQSLVNVI LIIPNFICCI20  
CYLLKYDLFR LLIPLIQEMP RGIPWNGAS YSVNFSSFTF ANIMAEFFLS LVRQLLTEFF180  
ILTILSHGI 189

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 300 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

KSIKQKICQH KNVVEQSLTR KRRDANSPL PSRHRPPPPA SKPPPALRCL SDGVRLRGHG 60  
EDEQILVLDP PTDLKFKEGF TDVVTTNLKL RNPDRKVCVF KVKTAPRRY CVRPNSGIID120  
PGSTVTVSVM LQPFYDYPNE KSKHKFMVQT IFAPNTSDM EAVWKEAKPD ELMDSKLRVC180  
FEMPENNDKL NDMEPSKAVP LNASKQDQGM PKPHSVSLND TETRKLMEEC KRLQEMMKL240  
SEENRHLADE GLRLRKVAHS DKPGSTSTAS FRDNVTSPLP SLLVVIAAIF IGFFLGKFL300

## (2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 247 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GSSGSRFEVY VVLEERRGGR GRGMGRGDGF DSRGKRETD R HSGSDRSLK NEDKRGSGS 60  
 HNWGIVKDEL TESPKYIQKQ ISYNYSDLDQ SNVTEETEG EEHHPVADTE NKENEVEEVK120  
 EEGKENTLD EKAIAQNKDR AKVEFNIRKP NEGADGQKKK GFVLHKSKE EAAEDSVMD180  
 HHFRKANDI TSQLEINFGD LGAPGRGGRG GRGGRGRGGR PNRGSRDKS SASAPDVPDP240  
 EAFPALA 247

## (2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

FVFDSSPVVR SATSTFVLVL QARSITSTMP IKFTFATRIK SISSAHSTST APSTLFQDHH60  
 DLESRAARA 69

## (2) INFORMATION ON SEQ ID NO. 257:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 220 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
PGRGSMYDRM  RRGGDGYDGG  YGGFDDYGGY  NNYGYGNDGF  DDMRDGRGM  GGRGYGGAGD  60
ASSGFHGGHF  VHMRLPFRA  TENDIANFFS  PLNPIRVHID  IGADGRATGE  ADVEFVTHED120
AVAAHAKDKN  NMQHRYIELF  LNSTFGGGSG  MGGSGMGYGG  RDGMDNQGGY  GSVGRHMGQN180
NYSGGYGTPO  GLGGYGRGGG  GSGGYGQGG  MSGGGWRGMY  220
```

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1105 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AATGAGCCTG  GTGTTAGATG  AGTTTTACAG  CTCACCTCAGG  GTGGTGGGTG  TCTCTGCTGT  60
TCTGGGTACT  GGATTAGATG  AACTCTTTGT  GCAAGTTACC  ATGTGCTGCCG  AAGAATATGA  120
AAGGGAGTAT  CGTCCTGAAT  ATGAACGTCT  GAAAGAAATCA  CTGGCCAACG  CAGAGAGCCA  180
ACAGCAGAGA  GAACAACCTG  AACGCCTTCG  AAAAGATATG  GTTCTGTAG  CCTTGGATGC  240
AGGGACTCCC  AAAGACAGCT  TATCTCCTGT  GCTGCACCCCT  TCTGATTTGA  TCCTGACTCG  300
ACCAACATTG  GAAGCAGACA  GCGATACTGA  TGACATTGAC  CACAGAGTTA  CAGAGGAAAG  360
CCATGAAGAG  CCAGCATTC  AGAATTTTAT  GCAAGAATCG  ATGGCACAAT  ACTGGAAGAG  420
AAACAATAAA  TAGSAGACTT  TAGCACACTT  CACTTGTTTC  TAGAAGTCCA  GAATTTTGA  480
CTCCACGTG  AAAGAACTGT  TCTTACCTCT  GAACCTGGGG  CTCCCAATAG  GGATATTTT  540
CCTCAGAGTA  GCAAAGTTTC  TCTTATTAGA  GAAATCTTGT  GACTCAGATG  AAGTCAGGGA  600
TAGAAGACCC  TTGGACCTGG  CAGGTTAATG  CTGATTATTC  CTGGCCCTTT  CCCTGTGATT  660
TATGCAAGGA  AGGATATACT  GAGCTGATAC  TCTTCCAAGC  CTACAACCTC  AAGTTTTATC  720
ATTGTAACCT  AAGTACTTTT  GCTGCTGAGG  AATGGAATCA  AAAGAACGTA  GTCTCTGGT  780
AACCACTTCA  GATCTCTATT  ATTAGGCTAG  ATGTATAGCC  TCTACTCCCC  CAGCTTCTTG  840
CTCTTGACCC  TGCAGCTGAA  GTTGCCCTTC  TATTAGCAGC  CAAGGAAAAG  GGAACATGA  900
GCTTATCCAG  AACGGTGGCA  GAGTCTCCTT  GGCAATCAAC  CAACGTTGCT  ATGAAATATG  960
CCTCACACTG  TATAGCTCAT  TATAGGAGCT  CAGGTTTGT  GAAAAAAGTG  GGCAAGACAT  1020
GATTAATGAA  TCAGAACTCT  GTTTCATTGG  TGACTTGGAT  AAAGACTTTT  TAATTTTAA  1080
AAAAAAAAAA  AAAAAAAAAA  AAAAA  1105
```

## (2) INFORMATION ON SEQ ID NO. 259:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

ATTCCAAACA TGGCGGCTCC ACTAGGGGGT ATGTTTTCTG GGCAGCCACC CGGTCCCCCT 60
CAGGCCCCGC CGGGCCTTCC GGGCCAAGCT TCGTTCTTC AGGCAGCTCC AGGCGCTCCT 120
AGACCTTCCA GCAGTACTTT GGTGGACGAG TTGGAGTCAT CTTTCGAGGC TTGCTTTGCA 180
TCTCTGTTGA GTCAGGACTA TGTCGAATGG ACCGATCAGG AAGAAATTGC AACCGGTGTT 240
GATCAGTGTG TCCAGAAGTT TCTGGATATT GCAAGCAGA CAGAAATGTT TTTCTTACAA 300
AAAAGATTGC AGTTATCTGT CCAGAACCAC GAGCAAGTTA TCAAGAGGGA TGTGTCAGAA 360
CTAAGGAATG AATTACAGCG GAAGATGCA CTAGTCCAGA AGCACTTGAC AAAGCTGAGG 420
CATTGGCAGC AGTGCTGGA GGACATCAAC GTGCAGCACA AAAAGCCCGC CGACATCCCT 480
CAGGSCCTCT TGGCTACCT GGAGCAGGCA TCTGCCAACA TCCCTGCACC TCTGAAGCCA 540
ACGTGAGCAA AGGCGAGAGG CAGTTGGCCT ATGAGTGGGC TGATGCGTGA GGTGCGCCAC 600
ACATTCTCTC CTCTGGACTT GACATTTTGG AAGAACTCTT TGCCAGATAA TGAGTTCAAT 660
TTAGTTTTAT GCTCCCATTT AAAAAATTTT CACTATTTTT ATAAGCTGTT AATTTCTTGA 720
TGACTTTTAT ACATGTCTGT AGCTTGGATA AACCAAGTAA GTATTTTTTT TTTGCTTTA 780
GCCAAGTTTA GACTGTGAAT ATGATGACAC AGATTCTTTT TTATGGTGGC TTTGCTTGT 840
TTAAATTTTT GCATGACTTT TCATCTTTTT ATGTGTGTTT CCTGTAGTTT GATCCGAAGG 900
AAAAAGATAT AATAGCTGGA GAATCAGGAG ATGGGAGTTT TAGTCGTAGG CCTTATGATA 960
ATTAGCCCGC GGTGCTGTGT AGAAAAGTAT GTAAATTGTC TCTGTTTTAA GACTTTGAAC1020
TAGCTCAGGA AGAGGAATCT AATACAATAT TTGTAATGTT AAAAAAAAAA AAAAAAAAAA1080
AAAAAAAAA

```

## (2) INFORMATION ON SEQ ID NO. 260:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3292 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

|             |              |             |             |            |                 |      |
|-------------|--------------|-------------|-------------|------------|-----------------|------|
| ATCCGGAAGT  | TCTGGCGTGC   | CCCACATGCG  | ACGCGSAGAA  | GCACGAGTGC | GCAGTTGGCC      | 60   |
| TTCTTCAGGT  | TCCCGCGGGG   | CCCTGCGAGA  | TGCCAGAAAT  | GGTGGAGAA  | CTGTAGGAGA      | 120  |
| SCAGACTTAG  | AAGATAAAAC   | ACCTGATCAG  | CTAAATAAAC  | ATTATCGATT | CTGTGCCAAA      | 180  |
| CATTCTTGAGA | CTCTCTATGAT  | CTGTAGAAGT  | AGTCCTTTATA | GGACAGTTCT | TCGAGATAAAT     | 240  |
| GCAATACCAA  | CAATATTGGA   | TCTTACCAGT  | CATTTTGAACA | ACCCACATAG | TAGACACAGA      | 300  |
| AAACCGAATAA | AAGAACTGAG   | TGAAGATGAA  | ATCAGGACAC  | TGAACAGAA  | AAAAATTGAT      | 360  |
| GAAACTTCTG  | AGCAGGAAACA  | AAACCATAAA  | GAACCAACA   | ATAGCAATGC | TCAGAACCCC      | 420  |
| AGGAGAGAA   | AGGCTGAAGG   | GCAGATGAG   | GACATTTTAC  | CTCTAACCTC | TGAGAGAAAG      | 480  |
| AACCAACAAG  | AATACCTAAA   | ATCTCTATT   | GAATCTTTGA  | TCTGTATGGG | AAGACAAAAC      | 540  |
| ATACCTCTGG  | ATGGACATGA   | GGCTGATGAA  | ATCCCAGAAG  | GTCTCTTTAC | TCCAGATAAC      | 600  |
| TTTCAGGCAC  | TGCTGGAGTG   | TGGSATAAAT  | TCTGTGAAG   | AGGTCTTGAG | AAAGCGGTTT      | 660  |
| GAGACACAG   | CAGTTAACAC   | GTTGTTTTGT  | TCAAAAACAC  | ACGACAGGCA | GATGCTAGAG      | 720  |
| ATCTGTGAGA  | GCTGTATTCT   | AGAAGAAACT  | CTCAGGGAAG  | TGAGAGACTC | ACACTCTCTT      | 780  |
| TCCATTATCA  | CTGACGATGT   | AGTGGACATA  | GCAGGGGAAG  | AGCACTTACC | TGTGTTGGTG      | 840  |
| AGGTTTGTG   | ATAAATCTCA   | TAACCTAAGA  | GAGGAATTTA  | TAGGCTTCCT | GCCTTATGAA      | 900  |
| CGCGATGCAG  | AAATTTTGGC   | TGTGAAATTT  | CACACTATGA  | TAACTAGAGA | TGGGGGATTA      | 960  |
| AATATGGAGT  | ATTGTCGTGG   | CCAGGCTTAC  | ATTGTCCTTA  | TGCGATTTTC | TTCCAAAAATG     | 1020 |
| AAAGTTGTTG  | CTTCTAGACT   | TTTAGAGAAA  | TATCCCAAG   | CTATCTACAC | ACCTCTGCTCT     | 1080 |
| TCCTGTGCTC  | TAAATATGTG   | GTGGGCAAAA  | TCAGTACCTG  | TTATGGGAGT | ATCTGTTGCA14    | 1140 |
| TAGGAAACAA  | TGGAGGAAGT   | TGTGTTCTTT  | TTCCATCNGA  | TCACCAACA  | TGCTTTTGA210    | 1200 |
| ACTTGACAC   | GTAATTGCTG   | TCTTTTTTCA  | GAAACAGTAA  | GAAAGGGGTA | AAGAACTGAA1260  | 1260 |
| GGAATATCTG  | CATTCTCAGT   | GGACAGGCAG  | GATGATGCT   | TTTGAATTTT | TAGTGAACAT1320  | 1320 |
| CTCGCAAGCA  | CTTGTGTTTTAT | GTTTAGATGG  | TATAAATAGT  | GACACAAATA | TAGNATGGG1380   | 1380 |
| AATAACTATA  | TAGCTGGCCG   | AGCAATTTNGT | ACTCTGCACT  | GCAGTGTGAG | TTTGTGATTT1440  | 1440 |
| CATTGTCTACT | ATGTTGTGTC   | TTAAAAATGT  | CCTATCTTTT  | ACAAGAGGCT | TTGGGAAAAA1500  | 1500 |
| CCTNCCANG   | GCCAAACCTC   | GTGATGTCTT  | CTTTGCGGCC  | GGTAGCTTGA | CTNCGAGTAC1560  | 1560 |
| TGNNCATTCA  | CNTCAACGAA   | GTGAGTGGGA  | AAATATTNGA  | AGTTTATCAT | GAATTTTGGT1620  | 1620 |
| TTGAGGAAGC  | CACAAATTTG   | GCAACCAAC   | TTGATATTCA  | AATGAACTC  | CCTGGGAAAT1680  | 1680 |
| TCCGCGAGGC  | TCACCNNAGG   | GTAACCTTGA  | ATCTCAGCTA  | ACNCTCTGAG | AGTTACTATA1740  | 1740 |
| AAGAAACCCN  | TAAGTGTCCC   | AACAGTGGAG  | CACATTATTC  | AGGAACITAA | AGAATATATTC1800 | 1800 |
| TCAGAACAGC  | ACCTCAAAGC   | TCTTAAATGC  | TTATCTCTGG  | TACCCTCAGT | CATGGGACAA1860  | 1860 |
| CTCAAAATCA  | ATACGNTCNG   | GAGGAACACC  | ATGCTGACAT  | GTATAGAAGT | GACTTACCCA1920  | 1920 |
| ATCCTGACAC  | GCTGTACAGT   | GAGCTTCATT  | GTGGAGAAAT  | CAATGGAATA | CACAGGGGGA1980  | 1980 |
| AAGATATAGA  | GCTCCGTCC    | ACCATCTATG  | AAGCCCTCCA  | CCTGCTGAC  | ATCAAGTTT2040   | 2040 |
| TTCTTAATGT  | GTATGCAATG   | CTGAAGTCC   | TGTGTATTCT  | TCTGTGATG  | AAGGTTGAGA2100  | 2100 |
| ATGAGCGGTA  | TGAAAAATGN   | ACGAAAGCGT  | CTTTAAAGCA  | TATTTGAGGG | AACACTTTGA2160  | 2160 |
| CAGACCCAAA  | GCTCAAGTAA   | CTTGGCTTTT  | GCTTTAAACAT | AAATTTTGA  | TATTAACCA2220   | 2220 |
| CGACCTGGAT  | TAAATGGTGG   | ACACATATAT  | TAACCTCTAT  | ACAAGTAAAT | CAGAGCTTCC2280  | 2280 |
| TACAGATAAT  | TCCGAACACT   | TGNNAAAATA  | CCTAAGAGAC  | TTTTAAAAAT | AGGCTTTCTT2340  | 2340 |
| ATATTTGATA  | TTTGGAAAGAA  | AAAGCCGTAA  | GGTGTATGTA  | GACCACITAA | TCACATAATA2400  | 2400 |
| TGTTTGCTTA  | TAGGACTCCA   | TTGAATACAT  | TAGGCATTGA  | TAATCTACCT | GTTTAAATGG2460  | 2460 |
| CCCTCTGTTG  | AACTCTCAAG   | CTTTGAAGAC  | CTACCTGTTC  | TCCAGAGA   | GAACTGTTGA2520  | 2520 |
| AGTGCCATGT  | TTCCNTTTTG   | CGTGATCTCT  | GTGATGGCA   | CTCTGGAAT  | TCTTCAGTTA2580  | 2580 |
| AGTCATTTTA  | GACATAGCAT   | TTATTATCAT  | TGTGNAATCT  | CTACTTGTG  | GGGTGTATGA2640  | 2640 |
| ATTCTTTGNA  | AGNAAATATA   | TTTTNGAAGA  | GGTGTGGGNA  | GNAAAGGAAT | ACNATTTTAT2700  | 2700 |
| NAAAATGTTG  | TAGTGNAAAG   | CCACAAATN   | GACCTTTNGA  | CTAATANGGA | GTTTAAAGTA2760  | 2760 |
| TNGTTTAAAA  | TACTATACCT   | GNNACAGNT   | ACAAGAAAT   | ACGCGAGAAA | AGCTTTGTGAG2820 | 2820 |
| CTACCCNAAA  | CAAGGNATTT   | NCAGTGTAGA  | TTTTGTCTNT  | TCTTGAACNT | TNAAAGAAAN2880  | 2880 |
| CAATGTANCA  | AAAGTTTGAT   | NGGAAAAGCC  | TGCTGTGTTG  | CNACATCTC  | NGTTGCTGTT2940  | 2940 |
| NNTACANTTC  | CNNNTTTGTG   | GAGNCCTACN  | ATCTTNCCTA  | AGCTTTTINA | GCANGGTATA3000  | 3000 |
|             |              |             |             |            |                 |      |
| TNGTTGAACA  | CTTCTNGTTT   | CATGGTTGAG  | ACAGAATCAG  | AGGCCATGGA | TACTGACAA3060   | 3060 |
| TGATTTGTCT  | GTTTTTTTCT   | TCTGTCTTIN  | TTCCATGACT  | CTTATATACT | GCCTCATCT3120   | 3120 |
| GATTTTATAG  | CNAAAACCT    | GGNAAAACCT  | ANCAAAATAA  | GTGTTGTGGT | TTATCTAGAA3180  | 3180 |
| AAATATGGAA  | AAATTTGCTG   | TTATTTTGGG  | TGAAGAAAAA  | CNAATTTTGT | GATTTTATTT3240  | 3240 |
| TCAATCTAAA  | TAAATGTGTA   | ATTTTGTGTA  | AAAAAATAAA  | AAAAAATAAA | AA              | 3292 |

## (2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1196 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

GGTAGAAAAAT  GCAATAAATT  CTGGGACAAT  GCCCAGACCT  CTGGCATAGA  GGAGCCTTCT  60
GAGACAAAGG  GTTCTATGCA  AAAAAGCAAA  TTCAAATATA  AGTTGGTTCC  TGAAGAAGAA  120
ACCACTGCCT  CAGAAAATAC  AGAGATAACC  TCTGAAAGGC  AGAAGAGGGG  CATCAAATTA  180
ACAATCAGGA  TATCAAGTCG  GAAAAGAAG  CCGGATTCTC  CCCCAGAACT  TCTAGAACCA  240
GAAAACAGC  AAGAGAAGAC  AGAAAAGGAA  GAGGAGAAAA  CAAATGTGGG  TCGTACTTTA  300
AGAAGATCTC  CAAGAATATC  TAGACCCACT  GCAAAAGTGG  CTGAGATCAG  AGATCAGRAA  360
GCTGATAAAA  AAGAGGGGGA  AGGAGAAGAT  GAGGTGGAAG  AAGAGTCAAC  AGCTTTGCAA  420
AAAACCTGACA  AAAAGGAAAT  TTTGAAAAAA  TCAGAGAAAG  ATACAAATTC  TAAAGTAAGC  480
AAGGTAAAAA  CCAAGGCCAA  AGTTCGATGG  ACTGTTCTCT  GGACACGTGG  CAGATGGRAA  540
TATTCAGCA  ATGATGAAAG  TGAAGGGTCT  GGCAGTGAAT  AATCATCTGC  AGCTTCAGAA  600
GAGGAGGAAG  AAGAGGAAAG  TGAAGAGGCC  ATCCTAGCAG  ATGATGTAGA  ACCATGCAAA  660
AAATGTGCC  TTCCAAACCA  CCTGAGCTA  ATTCTTCTGT  GTGACTCTTG  CGATAGTGA  720
TACCATACTG  CCTGCCTTCG  CCCTCCTCTG  ATGATCATCC  CAGATGGAGA  ATGTTCTCG  780
CCACCTTGCC  AACATAAACT  GCTCTGTGAA  AAATTAGAGG  AACAGTTGCA  GGATTGGAT  840
GTTGCCTTAA  AAGAGAAAGA  GCGTGCCGAA  CGAAGAAAG  AACGCTTGGT  GTATGTTGGT  900
ATCAGTATTG  AAAACATCAT  TCCTCCACAA  GACCCAGACT  TTCTGAAGA  TCAAGAGAA  960
AAGAAAAAG  ATTCAAAAAA  ATCCAAAGCA  AACTTGCTTG  AAAGGAGGTC  AACAGAACAA  1020
AGGAAATGTA  TAAGCTACAG  ATTTGATGAG  TTTGATGAAG  CAATTGATGA  AGCTATTGAA  1080
GATGACATCA  AAGAGGCCGA  TGGAGGAGGA  GTTGGCCGAG  GAAAAGATAT  CTCACCATTCA  1140
ACAGGTGATC  GTGGGAAAGA  CATCTCTACT  ATTTTGGATG  AAAAAATAAT  AACGGC      1196

```

## (2) INFORMATION ON SEQ ID NO. 262:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1467 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

AAGGACGCTT GCCTTTTTC GGTCGGGGAA GGGGGAAGAA GGTAACTTCC GGTGACGGGG 60
TTGCATCACT TCCTCTCAAG CTGCGGCGTT TGTTTGGTGG GGTTACACGC GGGTTCAACA 120
TGGGTATCGA AAAGTGTTAT TTCTGTCGCG GGCCCATCTA TCCTGGACAC GGCATGATGT 180
TCSTCCGCAA CGATTGCAAG GTGTTAGAT TTTGCAATC TAAATGTCAT AAAAAGTTTA 240
AAAAAGAGCG CAATCCCTCGC AAAGTTAGGT GGACCAAAAGC ATTCGGGAAA CGAGCTGGTA 300
AAGAGCTTAC AGTGGATAAT TCATTGGAAT TTGAAAAACG TAGAAATGAA CCTATCAAAAT 360
ACCAGCGAGA GCTATGGAAT AAAACTATTG ATGCGATGAA GAGAGTTGAA GAAATCAAAAC 420
AGAAAGCGCA AGCTAAATTT ATAATGAACA GATTGAAGAA AAATAAAGAG CTACAGAAAG 480
TTCAGGATAT CAAAGAAGTC AAGCAAAACA TCCATCTTAT CCGAGCCCCT CTTCAGGCA 540
AAGGGAACA GTTGAAGAG AAAATGGTAC AGCAGTTACA AGAGGATGTG GACATGGAAG 600
ATGCTCCTTA AAAATCTCTG TAACCATTTC TTTTATGTAC ATTTGAAAAAT GCCCTTTGGA 660
TACTTTGAAAC TGCTAAATTA TTTTATTTT TACATAAGGT CACTTAAATG AAAAGCGATT 720
AAAAGACATC TTTCTGCAT TGCCATCTAC ATAATATCAG ATATTACGGA TGTTAGATTG 780
CATCTCAGTG TTAATCTTTT ACTGATAGAT GTACTTAAGT AAATCATGAA AATTCTACTT 840
GTAACATATG AAGTGAATTG TGGACGTAAA ATGTTGTGTC TATTTTGGATA ATGGCAGTGA 900
GCAGCATTTG TATAGTAACT AATGGCAAAA ATTCATGGCT AGTGATGTAT AAAATAAAAT 960
ATTCTTTGCA GTAAAAATTT CCTTTTGTTA ATGTTATAGA AGGGGGGATA CAAAAGGAAL1020
CTAACAAATTT GTATGGCAGT GTCAGATATT TTTATTTTAG TATTTCCTGT TTTGGTTTAT1080
TTGCATCTTA GAAGAGCAT ATGACATTGT TTGATGAAGC CTAATTATGC TGGACTGTTT1140
TGACCTGGTT TAACCCCTCT GATAGTAGT TGTGGATGCT GGGGATGAGA ACTGAATAAT1200
CTTTGCGCTG AGTGACACTA CACTCTAGAA TTTCCACTTT GGAGAAATAC ACTGTCCAAC1260
TTGATGATTC TGATAGAACA GACTTTACTT TTCTAGCCCA GCATTGATCT AGAAGCAGAG1320
GAATCCGAGC GCCTTTTAAA AGTTGTTATG TGGTTTTCTT TTAAGAAAGCT CCTGTTTTG1380
GAAAGTAGAA TTTATGGGTA CAACGTATGT TCATTATTG TACATAAAAT AAAACCAATT1440
AAAAAGTAAA AAAAAAAAAA AAAAAAC

```

1467

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 739 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

CGGCTCGAGC CCCGCTCAGT CACCCGCGAG AGGCGTGCAG TTTCGGCGCT CTCGCGCGG 60
CCGGGGAGAG TCAGCGCGCT AATGCGCTTC TTGGCGTCGG GACCCCTACCT GACCCATCAG120
CAAAAGGTGT TCGGGCTTIA TAAGSGGGCG CTACGCCACC TCGAGTCGTG GTGCGTCCAG180
AGAGACAAAT ACCGATACCT TGCTTGTTTG ATGAGAGCCC GGTTTGAAGA ACATAAGAA1240
GAAAAGGATA TGGCGAAGGC CACCCAGCTG CTGAAGGAGG CCGAGGAAGA ATCTGTG1AC300
CGTCAGCATC CACAGCCATA CATCTTCCT GACTCTCCTG GGGGCACCTC CTATGAGAGA360
TAGGATTGCT ACAAGGTCCC AGAATGCTG TTAGATGACT GGCATCCTTC TGAGAGGGA420
ATGTATCTCT ATTACTTTGC CAGAGAGAGAA CAGTGGAAAG AACTGCGGAG GGAAGAGCT540
GAACGAGAGG TTAAGCAGCT GCAGGAGGAA ACCGCCACCTG GTGTCCTTTT AACTGAAGCT540
TTGCCCCCTG CCGGAAAGGA AGGTGATTG CCCCCACTGT GGTGGTATAT TGTGACCAGA600
CCCCGGGAGC GGCCCATGTA GAAAGAGAGA GACCTCATCT TTCATGCTTG CAAGTGAAT660
ATGTTACAGA ACATGCACCT GCCCTAATAA AAAATCAGTG AAATGGAAGA AAAAAA720
AAAAAAAAA AAAAAAAAAA

```

739

(2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2146 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

TTTTTTTTT TTTTTTTTT TCCCAGGCC TCTTTTATT TACAGTGATA CCAAACCATC 60
CACTTGCAAA TCTTTGGTC TCCCATCAGC TGGAAATTAAG TAGGTACTGT GTATCTTTGA 120
GATCATGTAT TTGCTCCAC CTGTGGTGAAT ACAGAAAGG AAGGCACGAA CAGCTGAAA 180
AGRAGGGTAT CACACCGCTC CAGCTGGAAT CCAGCAGGAA CCTCTGAGAT TGCCACAGCT 240
GAACACTTAA AAGAGGAAAG AAGGCACGCT GCTCTTCAAT TATTTTGAAA GCAATTTAT 300
TTGAAAGTGC ATAAATGGTC ATCATAAGTC AAACGTATCA ATTAGACCTT CAACCTAGGC 360
TATTTAATAA TACACCACAC TGAATTAAT TTGCCAATGAA TCCCAAGAT TTGGTACAAA 420
TAGTACAAAT CGTATTTGCT TTCTCTTTT CTTCCTTCAG ACAAACACCA AATAAAATGC 480
AGGTGAAAGA GATGAACAC GACTAGAGGC TGACTTAGAA ATTTATGCTG ACTCGATCTA 540
AAAAAAATTA TGTGGTTAA CGTTAACCTA TCTAAAATCG GGCCCTTTCC GCAAGCCTTT 600
CAAGGAGGAT CAAGTCACAG TCATACAGCT AGAAAAATCC CTGAAAAAAA GAATTTGTA 660
GAAGTATAAT AACCTTTTCA AAACCCACAA CGCAGCTTAG TTTTCTTTA TTTATTTG 720
GTCA7GAAGA CTATCCCCAT TTCTCCATAA AATCCTCCCT CCACTACTGT GCATTATG 780
ACAAAAAGACT CTAAGTGCCA CCAGACAGAA GGACCCAGAT TTCCGATTAT AAACAATGAT 840
GCTGGGTAAAT GTTTAAATGA GAACATTGGA TATGGATGGT CAGATGAAAG CTCGAGCGGA 900
ATTTCGGCTCG AGCTTTCATC TGACCATCCA TATCCAAATGT TCTCATTTAA ACATTACCCA 960
GGATCATTGT TTAATAATCAG AAATCTCTGT CTTCCTGTCT GGTGGCAGTT AGAGTCTTTT 1020
GTGCCATAAT GCAGCAGTAT GGAGGGAGGA TTTTATGGAG AAATGGGGAT AGTCTTCATG 1080
ACCAACAATA AATAAAGGAA AACTAAGCTG CATTGGGGT TTTGAAAAGG TTATTATCT 1140
TCTTAAACAAT TTTTTTTTCA GGGACTTTTT TAGCTGTATG ACTGTTACTT AAACATATCT 1200
AAATAGAGCA TTTTGGTATC TTTTATCTGA CCATCCATAT CCAATGTCTT CATTTAAACA 1260
TTACCCAGCA TCATTGTTTA TAATCAGAAA CTCTGGTCTT TCTGTCTGGT GGCATTTAGA 1320
GTCTTTTGTG CCAATAATGCA GCAGTATGGA GGGAGGATTT TATGGAGAAA TGGGGTAGT 1380
CTTCATGACC ACCAAATAAAT AAAGGAAAAAC TAAGCTGCAT TGTGGGTTTT GAAAAGGTTA 1440
TTATACTTCT TAACAATTTCT TTTTTCAGG GACTTTTCTA GCTGTATGAC TGTACTTTGA 1500
CCTTCTTTGA AAAGCATTCC CAAAATGCTC TATTTAGAT AGATTAAACAT TAACCAACAT 1560
AATTTTTTTT AGATCGAGTC AGCATAAATT TCTAAGTCAG CCTCTAGTCG TGGTTCACTT 1620
CTTCACTGCT CATTTTATTT GGTGTTTGTG TAGTGTGAAG GTCTAATTGA TACGTTTGA 1680
ATTGCACTAT TTGTACCAAA TCTTTGGGAT TCATTGGCAA ATAATTTTCA TGTGGTGTAT 1740
TATTAAATAG AAAAAAATAA TTTTGTATCC TAGTGTGAAG GTCTAATTGA TACGTTTGA 1800
TTATGATGAC CATTATGCA CTTCATAAGT AATTGCTTT CAAAAATAA GAAGAGCAGC 1860
TGTCTCTCTT TCTCTTTTA AGTGTCTAGC TGTGGCATGC TCAGAGGTTT CTGCTGGATT 1920
CCAGCTTGAG CGGTGTGATA CCTCTCTTT TCAGATGTTT GTCGCTTCTT TCTCTGATC 1980
CAGCAAGCTG GAGACAAATA CATGATCTCA GAGCTTACTT AATTCAGCT 2040
GATGGAGAC CAAAGAAATT CCAAGTGGAT GGTTTGGTAT CACTGTAAAT AAAAGAGGG 2100
CCTGGGAATT CTTGCGATTC CATCTCTAAA AAAAAAATA AAAAAA 2146

```

0615773.050000

## (2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1020 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

CAAGTAAATG CAGCACTAGT GGGTGGGATT GAGGCTATGC CCTGGTGCAT AAATAGAGAC 60
TCAGCTGTGC TGGCACACTC AGCGGCTCTG GACCCGATCC TAGCCGCCGA CTCACACAAG 120
GCAGGTGGGT GAGGAAATCC AGAGTTGCCA TGGAGAAAAT TCCAGTGTCA GCATTCTTGC 180
TCCTTGTGGC CCTCTCTTAC ACTCTGGCCA GAGATACCAC AGTCAAAACCT GGAGCCAAAA 240
AGGACACAAA GGACTCTCGA CCCAACTGCG CCCAGCCCTC CTCCAGAGGT TGGGGTGACC 300
AACTCATCTG GACTCAGACA TATGAAGAAG CTCATATATA ATCCAAGACA AGCAACAAC 360
CCTTGATGAT TATTCATCAC TTGATGAGT GCCCACACAG TCAAGCTTTA AAGAAAGTGT 420
TTGCTGAAAA TAAAGAAATC CAGAAATTGG CAGAGCAGTT TGTCCTCCTC AATCTGGTTT 480
ATGAACAACG TGACAAACAC CTTTCTCTG ATGGCCAGTA TGTCCTCCAG ATTATGTTTG 540
TTGACCCATC TCTGACAGTT AGAGCCGATA TCACTGGAAG ATATTCAAAC CGTCTCTATG 600
CTTACGAACC TGCAGATACA GCTCTGTTGC TTGACAACAT GAAGAAAGCT CTCAGATTGC 660
TGAAGACTGA ATTGTAAGA AAAAAAATCT CCAAGCCCTT CTGCTGTGCA GGCCTTGAGA 720
CTTGAACCCA GAAGAAGTGT GAGAAAGACT GCTAGTGTGG AAGCATAGTG AACACACTGA 780
TTAGGTTATG GTTTAATGTT ACAACAACATA TTTTTTAAGA AAAACAAGTT TTAGAAATTT 840
GGTTTCAAGT GTACATGTGT GAAACAATA TTGTATACTA CCATAGTGAG CCATGATTTT 900
CTAAAAAATA AAAATAATGT TTTGGGGGTG TTCTSTTTTC TCCAAAAAAA AAAAAAATA 960
AAAAAATAAA AAAAAAATA AAAAATTGCC CCCAAGGGGA CGGGTTACAA TTGGGGGGCG1020

```

## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1652 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

AATTCGGATC CATGGGCCAC AGTGGATGGC TTGAAATGTG GCTGAGCGCT TCGGACAATT 60
CGGATCCATG NNNNGTGGCC ACCCCAAGAC GCGCCCCAGC CCGCCATGGC CCGGATCCTN 120
NCCGGGNNTC CTGCTTCTG TCCCTGCTCC TGGCCGGNGT TTGTTCCGCC GGGCCGGGGA 180
CAAGAGAAGT CTAAGACAGA CTGCCATGGC GGTNATGAGT GGTACCATCT ACGAGTATGG 240
AGCCCTCACC ATCGATGGGG AGGAATACAT TCCTTTTAAG CAGTATGCAG GCAAAATATAT 300
CCTCTTTGTC AACGTAGCCA GCTACTGAGG TCTGACAGAC CAATACCTTG AACTGAATGC 360
ACTACAGAA GAACTTGGGC CATTGGCTN TGGTCATTCT GGGCTTCCCT TCCAACCAAT 420
TTGGCAACA GAGGCCAGGC GAGAACTCG AGATACTCCC CAGTCTCAAG TATGTTGNN 480
ACCAGGTNNG GGGGCTTTGT GNCCTAATTN NNNTCCAGNC TCNTTTGAGA AANNGGANGA 540

TNGTNGAACN GGGGAGNAAA GAGCNAGAAA TTCTACACTT TCCTGAAGAA CTCCTGCCCT 600
CCCACTGCAG NAACCTCCTGG GNCCTANCTT GCGCCGNCCT TTTTGGGAAC CCATGAAGAT 660
CCATGACATN CCGCTGGAAAC TTTGAGAAGT TCCTGGTNGG GGCCNAGANT GGCATACCGG 720
TTATGCGCTG GTACACACGG ACCACAGTCN AGCAACGTCN AAGATGGACA TCCTGNTCNT 780
TACATGAGCG GGCAGGCRNG CCGTGANGCG CCNAGGGGGN AAGTAACCTGA NTGCCCNNNC 840
CACCTTACCC CTACCCCTCG CCGTCATNG CAAGGGGCGGA NGGAGGGGCT CTNNCAGGAA 900
GGAAGCCACG TTCCCACTCA TTCTNANCCG CCACCCGAGA TTCTCTTINC TTNATTACAT 960
AAAAGACACG CCGTGGCACA ACTGTGTGTC TGAACCACTG TNGGACACGT GACAAATTGTN1020
CCCACTGTGT GCATGGCTAC ACAGNCCAGC TATCTGCGCTG CNTTGAACCC CANGGGNATG1080
GTCCATCNTG TNGTTTACGG NCTTGGCACA ACACCCNNCT ATATTTTTTT CAGCNTTTCT1140
GTCCCAAAAN TGAANNCCCA AANNGGAAAC ACNAANGTTC TNAGGTCCNA ATNGTTCCTG1200
CTCAAAANCN TGAACATATN ATTCTNTGGG GNCCANGCAT CNTCCACAT NGCCACACN1260
TACACACCCAC CAGGCTCTCT TCTTCTTNC CTGNAAGGAC CCNTCCNNNN TGAGCCCCCA1320
AGCCNCATCC CACAGTGCNT CCGTAGACCA GCCAAGACAA CTGTGAGCGC GATGGCCGTG1380
TANCCCGAGG TNCAGGGGNT GGTGTCTCTA TGAAGGANNG GGNCCCGNA AGCCCTTGTN1440
GGGNGCGNGC CTCCCTTGAG CCGNGTCTGT GGTGCGNAGC CCTTAGTGCA TTCAGGCTTA1500
GGCTCCCNAG GCAGGGGACA CTACCCCGC GCGTCTGGAG GACATGCTAT CCTCTCACTC1560
TGTCCTCTGG TATCTCAACA CCGCATCTG CCCAGTAAAG GTCTTTCTGC AGCAAAAAAA1620
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA GG
1652

```

## (2) INFORMATION ON SEQ ID NO. 267:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

GGAGTGGCCC TCTGTGAGGG GCTCAAATGG TTGCAATTCA TGGCGCGTTA CGACTTGGCT 60
CACTTAATCA AATCCCTACC AACTCTAACT TGCCGAAGGA AGAACTTGAC CTCTTGAGA 120
ACCCCTCGATT GGTGTTTCCCT GCCATTAGA TGTGAAGTA CCCCATGAAG AGCTGCAAAA 180
ATTCTCAAGG GTGGATTACA GGAGGTGGCA GAACAGTTAG AGCTGGAACG GATAGGACCA 240
CAACATCAGG CAGGATCTGA TTCATTGCTC ACAGGAATGG CCTTTTCAA AATGAGAGAA 300
ATGTTCTTTG AAGATCATAT TGATGTGCC AAATATTGTG GTCATTGTGA TGGCCTTGGT 360
TCTGGTTCAT CCTATGTACA GAATGGCACA GGAATGCAT ATGAAGAGGA AGCCAACAA 420
CAGTCATGAC ATGAATAGT CCTTTTATT TTTATTCGAG CTACACACAT GCTTGTATAT 480
AGGTTTTATC TCTGTTTGA TCCCTCGAAC AATAGACAGT ACCTTTCCCC CCGCTTTTCAT 540
GGCCCATTTT ATTGCTCGCC TTTCAGTACT AAGTATGACC GTTCCTATCT CAGATCTTAA 600
TAAAAAGAAA AAAAAAACG CATTCAAGTT AAATTTGGCC TTAATTTAAT ATACTTGTA 660
GCAAGCGTGT GTGACAGAGA GTGGGGAAG CTACATCATT GAATTTTGTG ATAAACTTTA 720
CCGACTTGAG TTTGGTTTAT TTTTCCCTTT TCCTAAATTA ACTAGCACTG ACTGTAATTT 780

ATTTCCTCGT TTCACGCTC TCCCTTCCAT TCTSCAGGAG TTTTAGCTAT TTGAGATCGT 840
GGACCATCAG TTTTGCACCT TAGAGAGTGT TCTGACTCT AAACCTGTTT TATCAGAAAA 900
TTTGACCCAC AGAATATAGC ACGTTGTGCA AACTGTCGAT TCACAGAAAC TTAATTTGTT 960
CAAGAACTA CTGAGGAGCT TAGTAACATGCG TGTTCCTGTA CTGATGTTT TAAAAAAGAA 1020
GCACATCTAG TGCTGTGCTG TTTCTAATTG GCATGTGTAG CTTCTCTCTG TACTGAAGAA 1080
TTTCTAAACC AGCTTTACAC CCTTCAGGAA AAATCCCTGT GATTTGATG TTAATCTCG 1140
CCAGGAACCT GTACCCAGAT GTGAAGCACA GTTATTATGA TAGACACTTC CTGAGTGTG 1200
TTGTATCCAC ACCATTACCT TTTTCTTAA ATTTGAGCCA TCTATGAGCC TGATTTGCT 1260
GCAACCCATT GTAAAAACCA GAAAGCCTAG GGATTGGCCA ATAATTGGGG AAATGCTGCA 1320
GTGCCAAGGA AATGGGATGG CAAAAGAAG

```



## (2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 900 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

CCCACGCGTC CCGGAAACGG CGCGGGCGGC GACAGGACCG AGGGGCCTTA GTTGGTGGGC 60  
 AAGTCGGGGG TCCCAGAAAG AGAAGCGTGA CCCGGAAGCG GAAACGGGTG TCCGTCCCAG120  
 CTCGCGGCTG CCAGTGAGCT TCTACCATCA TGGACCTATT GTTCGGGCGC CGGAAGACGC180  
 CAGAGGAGCT ACTGCGGCAG AACCAGAGGG CCTGAACCG TGCCATGCGG GAGCTGGACC240  
 GCGAGCGACA GAACTAGAG ACCCAGAGGA AGAAATCAT TGCAGACATT AAGAAGATGG300  
 CCAAGCAAGG CCAGATGGAT GCTGTTCCGA TCATGGCAAA AGACTTGGTG CGCACCCGGC360  
 GCTATGTGCG CAAGTTTGTG TTGATGCGGG CCAACATCCA GGCTGTGTCC CTCAGATCC420  
 AGACACTCAA GTCCACACAC TCGATGGCAC AAGCCATGAA GGGTGTCAAC AAGGCCATGG480  
 GRCACATGAA CAGACAGCTG AAGTTGCCCC AGATCCAGAA GATCATGATG GAGTTTGGC540  
 GGCAGGCAGA GATCATGGAT ATGAAGGAGG AGATGATGAA TGATGCCATT GATGATCCCA600  
 TGGGTGATGA GGAAGATGAA GAGGAGAGTG ATGCTGTGGT GTCCAGGTT CTGGATGAGC660  
 TGGGACTTAG CGTAACAGAT GAGCTGTGCA ACCTCCCTC AACTGGGGGC TCGCTTAGTG720  
 TGGCTGCTGG TGGGAAAAAA GCAGAGGCCG CAGCCTCAGC CCTAGCTGAT GCTGATGCAG780  
 ACCTGGAGGA ACGGCTTAAG AACCTGCGGA GGGACTGAGT GCCCCTGCCA CTCGAGAT840  
 ACCAGTGGAT GCCAGGATC TTTTACCACA ACCCCTCTGT AATAAAGAG ATTTGACACT900

## (2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1145 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

GGGCCCCGCC CAGGCGGCTG CCGTGACCT GCCTGGGCGC GGGGAAGTGA AAGCCGGAAG 60
GGGCAAGACG GGTTCAGTTC GTCATGGGCG TGTTTGGAAA GACCCAGGAG AAGCCGCCCCA 120
AAGAACTGGT CAATGAGTGG TCATTGAAGA TAAGAAAGGA AATGAGAGTT GTTGACAGGC 180
AAATAAGGGA TATCCAAAGA GAAGAAGAAA AAGTGAAACG ATCTGTGAAA GATGCTGCCA 240
AGAAGGGCCA GAAGGATGTC TGCATAGTTC TGGCCAAGGA GATGATCAGG TCAAGGAAGG 300
CTGTGAGCAA GCTGATGCA TCCAAAGCAC ACATGAACTC AGTGCTCATG GGGATGAAGA 360
ACCAGCTCGC GGTCTTGCGA GTGGCTGTT CCCTGCAGAA GAGCACAGAA GTGATGAAGG 420
CCATGCAAAAG TCTGTGAAG ATTCCAGAGA TTCAGGCCAC CATGAGGGAG TTGTCCAAAG 480
AAATGATGAA GGCTGGGATC ATAGAGGAGA TGTTAGAGGA CACTTTTGAA AGCATGGACG 540
ATCAGGAAGA AATGGAGGAA GAAGCAGAAA TGGAAATTGA CAGAAATCTC TTGAAATTA 600
CAGCAGGGGC CTTGGGCAAA GCACCCAGTA AAGTGACTGA TGCCCTTCCA GAGCCAGAAC 660
CTCCAGGAGC GATGGCTGCC TCAGAGGATG AGGGGGAGGA GGAAGAGGCT CTGGAGGCCA 720
TGCACTCCCG GCTGGCCACA CTCGCCAGCT AGGGGCTGCC TACCCCGCTG GGTGTGCACF 780
CACTCCTCTC AAGAGCTGCC ATTTATGTG TCCTTTCAC TACACCTCTG TTGTGAGSAC 840
TACCATTTTG GAGAAGGTTT TGTTTGCTC TTTTCATTCT CTGCCAGGT TTTGGGATCG 900
CAAAGGATT GTTCTATAA AAGTGGCATA AATAAATGCA TCATTTTATG GAGTATAGAC 960
AGATATATCT TATTGTGGG AGGGGAAGA AATCCATCTG CTCATGAAGC ACTCTGAAA1020
ATATAGGTGA TTGCTGAAT GTCGAAGACT CTACTTTTGT CTATAAAACA CTATATAAAT1080
GAATTTTAAAT AAATTTTTC TTTAGCACTT GGCCCCATTG TAGATTGCC TGTGCAGTAA1140
ACTTT
1145

```

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1836 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

GTGCGACAT  GCGATGCGCC  GGAGGAACGT  TGCTCTTTGA  GGCCGACGCT  AGGGGCCCCG  60
AAGGGAAACT  GCGAGGCGAA  GGTGACCGGG  GACCGAGCAT  TTCAGATCTG  CTCGGTAGAC  120
CTGGTGCACT  ACCACCATGT  TGGCTGCAAG  GCTGGTGTGT  CTCGGGACAC  TACCTTCTAG  180
GGTTTTCAC  CCAGCTTTCA  CCAAGGCCCT  CCCTGTTGTG  AAGAATTCCA  TCACGAAGAA  240
TCAATGGCTG  TTAACACCTA  GCAGGGGAATA  TGCCACCAAA  ACAAGAATTG  GGATCCGGCG  300
TGGGAGAACT  GGCCAAGAAC  TCAAGAGGCG  AGCATTGGAA  CCATCGATGG  AAAAAATATT  360
TAAATTGAT  CAGATGGGAA  GATGTTTGT  TGCTGGAGGG  GCTGCTGTTG  GTCTTGGAGC  420
ATTGTCCTAC  TATGGCTTGG  GACTTCTTAA  TGAGATTGGA  GCTATTGAAA  AGGCTGTAAT  480
TTGGCTCAG  TATGCAAGG  ATAGAATTCA  TTCCACCTAT  ATGTAATTAG  CAGGGAGTAT  540
TGTGTTAACA  GCTTTGCTG  CCATAGCAAT  CAGCAGAACG  CCTGTTCTCA  TGAATCTTCA  600
GATGAGAGGC  TCTTGGGTGA  CAATTGGTGT  GACCTTTGCA  GCCATGGTTG  GAGCTGGAAT  660
GCTGCTGCT  GTGATGCGT  CAGTGGTGGC  TCCTCTGACA  ATATTAGGGG  GTCTCTTCT  720
TGGCCGAGCT  GCATGGTACA  CAGCTGGCAT  TGTGGGAGSC  CTCTCCACTG  TGGCCATGTG  780
TCGGCCAGT  GAAAGATTTT  TGAACATGGG  TGCACCCCTG  GGAGTGGGCG  TGGGTCTCGT  840
CTTTGTGCT  TCAATGGGAT  CTATGTTTCT  TCCACCTACC  ACCGTGGCTG  GTGCCACTCT  900
TTACTCAGT  GCAATGTACG  GTGGATTAGT  TCCTTTTCAG  ATGTTCTCTC  TGTATGATAC  1020
CCAGAAAGTA  ATCAAGCGTG  CAGAAGTATC  ACCAATGTAT  GGAGTTCAAA  AATATGATCC  1080
CATTAAGTCG  ATGCTGAGTA  TCTACATGGA  TACATTAAAT  ATATTATGCG  GAGTTCGAC  1140
TATGCTGGCA  ACTGGAGGCA  ACAGAAAGAA  ATGGAAGTAC  TCAGCTTCTG  GCTTCTCTGC  1200
TACATCAAA  ATCTTGTTTA  ATGGGGCAGA  TATGCATTAA  ATAGTTTGTG  CAAAGAGCTT  1260
TCGTTGAAGT  TTAGAAGATA  AGAAACATGT  CATCATATTT  AAATGTTCGG  GATATGTGAT  1320
GCCTCAGGTC  TGCCTTTTTT  TCTGGAGAA  AAATGCAGTA  ATCCCTCCCG  AAATAGGCAC  1380
ACACATTTTC  AATTCTCATG  TTTGAGTGAT  TTTAAATGT  TTTGTTCTCC  GATATGTGAT  1440
AAGTTTTGTG  CATGAGAAATG  TAAGTCTTTT  TTTACTTTTA  AATTTTAGTA  GTTCTACTGA  1500
GTAACATAAA  TTTAGCAAA  CTGTGTTTGC  ATATTTTTTT  ATATTGTAAT  1560
TAATGTCATA  AGTGATTTTG  AGCTTTTGTA  AAGGGACAG  AGAGAAGGAG  TCACCTCGAG  1620
TCCTTTGTTT  TTTTAAATAC  TTAGAACTTA  GCACCTGTGT  TATTGATTAG  TGAGGAGCCA  1680
GTAAGAAACA  TCTGGGTATT  TGGAAACAAG  TGCTATTGG  TGCATTTCCT  CTGCGGTGG  1740
TAAACAAACT  GGTTCATCC  TGGAAACAGG  CACAGGTGAA  TGCATTTCCT  CTGCGGTGG  1800
CTCCCCAGTG  GCGCGCCTTC  CCAATAGGA  TGTGGG  1836

```

## (2) INFORMATION ON SEQ ID NO. 271:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1220 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

TGAAGTTCTA AGAGCTTTCC AAGTTTGGGA AGGTGTCCGG GTTTCTCGG ATTACTTCTC 60
TGAGCATGAA CGGAAGTCAC CCTTTGTGCC TTATGCGGTG ATTTTAATGA TAGGTGTCAT 120
ATATAGGAGG GAGTAATCTG TTTACATTCT GTTCTTCTCG ATGCACTCAC AAGCGGGTAA 180
CTAGGTGACA AGAAAAACAAA GATCTTATTC AAAAGAGGTC TTACAGCAAC CCAACGTCTC 240
ATCTTCCCAT AGTAAAGATG ACGGGGCCCT GAGGTAAGCT ACAGGCAACA CCACTTCCGC 300
GTTTCTCTTG CGCCCTGGTC CAAGATGGCG GATGAAGCCA CGCGACGTGT TGTGTCTGAG 360
ATCCCGGTGC TGAAGACTAA CGCCGGACCC CGAGATCGTG AGTTGTGGGT GCAGCGACTG 420
AAGGAGGAAT ATCAGTCCCT TATCCGGTAT GTGGAGAACA ACAAGAAATG TGACACAGAT 480
TGGTTCCGAC TGGAGTCCAA CAAGGAAGGA ACTCGGTGGT TTGAAAAATG CTGGTATATC 540
CATGACCTCC TGAATATGTA GTTTGACATC GAGTTTGACA TTCTATCAC ATATCCTACT 600
ACTGCCCCAG AATTTGACGT TCCTGAGCTG GATGGAAAGA CAGCAAAGAT GTACAGGGGT 660
GGCAAAATAT GCCTGACGGA TCATTTCAAA CCTTTGTGGG CCAGGAATGT GCCCAATTTT 720
GGACTAGCTC ATCTCATGGC TCTGGGGCTG GGTCCATGGC TGGCAGTGGA AATCCCTGAT 780
CTGATTGAGA AGGGCGTCAT CCAACACAAA GAGAAATGCA ACCAATGAAG AATCAAGCCA 840
CTGAGGGCAG GCAGAGGGAC CTTTGATAGG CTACGATACT ATTTCTCTGT GCATCACACT 900
TAACTCATCT AACTGCTTCC CCGGACACCC TCCACCTCTA GTTGTACTA AGTAGCTGCA 960
GTAGGCATTG CTGGGGAAGA AACAAACACA CACCAACAG TACTGCTACT TAGTTCTTAA1020
GGCTGCACAG GGAAGGGAAG GACTGGGCTT TGGACAATCT AGAGGTAAAT TATATCCGCC1080
CCCAGGTGGA GCAACATGCG ATTCGTGGAG CACGGGGGTA ACTGAAAGTG AGTACATATA1140
GTCTTTCTGG TTTCTGGAGA TAACCCATCA ATAAAGCTG CTTCCTCTGS TAAAAAAA1200
AAAAAAAAA AAAAAAAAAA

```

1220

## (2) INFORMATION ON SEQ ID NO. 272:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

CGCAGTGC GC AGGCGTGGGG CTCCTCTCCTT GTCAGTCGGC GCCGCGTGGC GGCTGGTGGC 60
TCTGTGGCAG CGGCGGCGGC AGGACTCCGG CACTATGAGC GGCTTCAGCA CCGAGGAGCG 120
CGCGCGCGCC TTCTCCCTGG AGTACCGAGT CTCCTCTCAA AATGAGAAAG GACATATAT 180
ATCTCCATTT CATGATATTC CAATTTATGC AGATAAGGAT GTGTTTCACA TGGTAGTTGA 240
AGTACCACGC TGGTCTAATG CAAAAATGGA GATTGCTACA AAGGACCCCTT TAAACCCCTAT 300
TAAACAAGAT GTGAAAAAAG GAAAACTTCG CTATGTTGCG AATTGTTTCC CGTATAAAGG 360
ACATATCTGG AACTATGGTG CCACTCCCTCA GACTTGGGAA GACCCAGGGC ACAATGATAA 420
ACATACTGGC TGTGTGGTG ACAATGACCC AATTGATGTG TGTGAATTTG GAAGCAAGGT 480
ATGTGCAAGC GGTGAATAAA TTGGCGTGAA AGTTCATAGC ATATTGGCTA TGATTGACGA 540
AGGGGAAACC GACTGGAAGG TCATTGCCAT TAATGTGGAT GATCCTGATG CAGCCAATTA 600
TAATGATATC AATGATGTCA AACGGCTGAA ACCTGGCTAC TTAGAAGCTA CTGTGGACTG 660
GTTTAGAAGG TATAAGGTTT CTGATGGAAA ACCAGAAAAT GAGTTTGGCT TTAATGCAGA 720
ATTTAAAGAT AAGGACTTTG CCATTGATAT TATTAAGAGC ACTCATGACC ATTGGAAGC 780
ATTAGTGACT AAGAAAACGA ATGGAAAAGG AATCAGTTGC ATGAATACAA CTTTGTCTGA 840
GAGCCCCCTT AAGTGTGATC CTGATGTGCG CAGAGCCATT GTGGATGCTT TACCACCACC 900
CTGTGAATCT GCCTGCACAG TACCACAGA CGTGGATAAG TGGTTCATC ACCAGAAAAA 960
CTAATGAGAT TCTCTGGAA TACAAGCTGA TATTGTCTCA TCGTGTTCAT CTGGATGTAT 1020
TAGATGAGAA AGTAGTAGCT TTTCAAAGCT TTAATTTTGT AGAAGCTCAT TAACTAAAGT 1080
AAATCTCTCT GTGACTAATC CAATATATCT AGAATTTTAT CCATCTAAGC CATTTTTCAT 1140
ATCTCAACTA GACTAACTTT TAGCACATGC TTAATATCA AAGCAGTTGT CATTTGGAAG 1200
TCACCTTGTA ATAGATGTGC AAGGGGAGCA CATATTGGAT GTATATGTTA CCATATGTTA 1260
GGAAATAAAA TTATTTTGGT GAAACTTGA AAAAAAAA AAA 1303

```

## (2) INFORMATION ON SEQ ID NO. 273:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1586 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

CGGCTCGAGC GGCTCGAGAT TCGAGGTCGT GGTGGTCTTG GAAGAGCGTC GAGGGGGCG 60
TGGACGTGGA ATGGGCGGAG GAGATGGATT TGATTCTCGT GGCAAACGTC AATTGTATAG 120
GCATAGTGA AGTAGATAGT CTGGCGTGAA GCACGAGGAC AAACGTTGAG GTAGCGGATC 180
TCACAACTGG GGAAGCTGCA AAGACGAATT AACAGAGTCC CCCAATACA TCCAGAAAC 240
AATATCTTAT AATTACAGTG ACTTGGATCA ATCAAAATG ACCTGAGAAA CACTGAAGG 300
TGAAGAACAT CATCCAGTG CAGACACTGA AATAAGGAG AATGAAGTTG AAGAGGTTAA 360

```

```

AGAGGAGGGT CCAAAAGAGA TGACTTTGGA TGAGTGGAA GCTATTCAAA ATAAGGACCG 420
GGCAAAAGTA GAATTTAATA TCCGAAAACC AAATGAAGGT GCTGATGGG AGTGGGAAGAA 480
GGGATTTTGT CTTTCAAAAT CAAAGAGTGA AGAGGCTCAT GCTGAAGATT CGGTTATGGA 540
CCATCATTTT CCGAAGCCAG CAAATGATAT AACGCTCAG CTGGAGATCA ATTTTGGAGA 600
CCTTGGCCGC CCAGGACGTG GCGGCAGGGG AGGACGAGGT GGACGTGGGC GTGGTGGCG 660
CCCAAACCGT GGCAGCAGGA CCGCAAGTC AAGTGCTTCT GCTCCTGATG TGGATGACCC 720
AGAGGCATT C CAGCTCTGG CTTAACTGGA TGCCATAAGA CAACCTGGT TCCTTTGTGA 780
AGCCTTCTGT TCAAGCTTT TGCATGCTTA AGGATTCCAA ACGACTAAGA AATTAATAA 840
AAAAGAGCTG TCATTCATAC CATTACACCC TAAAGACTGA ATTTTATCTG TTTTAAAAAT 900
GAACTTCTCC CGCTACACAG AAGTAACAAA TATGGTAGTC AGTTTGTAT TTAGAAATGT 960
ATTGGTAGCA GGGATGTTT CATAATTTT AGAGATTATG CATCTTCAT GAATCTTTT 1020
GTATTGCTGC TTGCAAAAT GCATTTCCAA ACTTGAATA TAGGTGTGAA CAGTGTGTAC 1080
CAGTTTAAAG CTTTCACTTC ATTTGTGTT TTTAATTAAG GATTTAGAAG TCCCCCAAT 1140
TACAAACTGG TTTTAAATAT TGGACATACT GGTTTTAAAT CCTGCTTTG ATATTACAC 1200
ATGGTCACT GGCACATGTT AAACCTTGT TGTCCAAT TTAGTGTGTG TGGAACTACT 1260
ACTATATGTA TTTTAACTTA GTTTTAAAT TTTCATTTT GGGGAAAAAT CTTTTTAC 1320
TTCTCATGAT AGCTGTTATA TATATATGCT AAATCTTTAT ATACAGAAAT ATCAGTACT 1380
GAACAAATTC AAAGCACATT TGGTTTATTA ACCCGTGGCT GGCCTGGCAT GGGGCCCATT 1440
TGGGGTCCAA ATTATACTG ATTTACATT TCAGCGATAT TACTTTTAAA TGCTGAGTT 1500
CCCATTTAAA ATCTAACTAG ACACCTAATG GGAAGTGGT TAACCACTAT GTGGTAGCCA 1560
CGGGCCAG

```

## (2) INFORMATION ON SEQ ID NO. 274:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 144 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

KQVKCAKVS LFLFQYCAI DSCIKFVNAG SSWLSSVTLW SMSSVLSLAS NVGRVRIKSE 60
GCSTGDKLSL GVPASKATEP ISFRRSSCS LCCWLSALAS DFFRRSYSGR YLSYSSAAL120
VTCTKSSNP VPTAETPTT LSEL

```

144

## (2) INFORMATION ON SEQ ID NO. 275:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 401 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

MPNFCAAPNC TRKSTQSDLA FFRFRDPPAR CQKWVENCRR ADLEKTPDQ LNKHYRLCAK 60  
 HFETSMICRT SPYRTVLRDN APTIFOLTS HLNPNHSRRH KRIKELSEDE IRTLKOKKID120  
 ETSEGEQKHK ETNNSNAQNP SEEEGEGQDE DILPLTLEEK ENKEYLKSLE EILILMGKQNI80  
 IPLDGHAEDE IPEGLFTPDN FQALLECRIN SGEEVLKRKF ETTAVNTLFC SKTQQRQMLE240  
 ICESCIREET LREVRDSHFF SIITDDVVDI AGEHLEPLV RFVDESHNL R EEFIGFLPYE300  
 ADAEILAVKF HTMTETKWGL NMEYCRGQAY IVSSGFSKKM KVVASRLLEK YPQAIYTLCS360  
 SCALNMWLAK SVPVMGVSA LGTIEEVCSF FHXITTTAFR T 401

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

MLISGTLSHG TTQIQYXXEE HHADMYRSDL PNPDTLSAEL HGWRIKWKHR GKDIPLPSTI 60  
 YEALHLPDIK FFPNVYALLK VLCILPVMKV ENERYENGTK ASLKHI 106

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 398 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
GRKCNKFWON AQTSGIEEPS ETKGSMQKSK FVKYKLVPEEE TTASENTEIT SERQKEGICKL 60
TIRISSRKKK PDSPPKVLEP ENKQEKTEKE DEKTNVGRITL RRSPRISRET AKVAEINDQK120
ADKKRGEDED EVEEESTALQ KTDKKEILKK SEKDTNSKVS KVKPKGKVRW TGSRTGRWK180
YSSNDESEGS GSEKSSAASE EEEKESEEA ILADDDDEPCK KCGLPNHPEL ILLCDSGSG240
YHTACLAPPL MIIPDCENFC PPCQHKLLCE KLEEQQLDLD VALKKKERAE RKERLVYVG300
ISINIIIPPQ EPDFSEDQEE KKKDSKKSKA NLEERSTRT RKCISYAFDE FDEAIDEAIE360
DDIKZADGGG VGRGKDISTI TGHRGKDIST ILDEKIIT 398
```

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 198 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RRQAVVWYPLS QESHRRISG WFGPHFLHG SSSSARMASS LSFSSSSSEA120
ADDFSLPDP SLSLEYFHL PRVREPVRT LPLGFTLLTL EFVSFSDFEK ISFLSVFCKA180
VDSSSTSSSP SPLFLSAF 198
```

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 202 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GRLPFSGRGR GKQVTSQDGV ASLPLKLRRL FGGVTRGFNM RIEKCYFCSG PIYPGHGMMF 60  
 VRNDCKVFEF CKSKCHKNEK KKRNPVKVRN TKAFKKAAGK ELTVDSFEF EKRRNEPIKY120  
 QRELWNKTID AMKRVEEIKQ KRQAKFIMNR LKKNKELQKV QDIKEVKQNI HLIRAPLAGK180  
 GKQLEEKVMQ QLQEDVDMD AP 202

## (2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

IINCKLFTSC FPECFGPPNF ARIALLPKVF MTFRFAKSEH LAIVADEHHA VSRIDGPRTE60  
 ITLFDTHVEP ACNPTKQTPK LERK 84

## (2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

RLEPRSVTRS RRAVSRLSAR PGKVSAMMAF LASGPYLTHQ QKVLRLYKRA LRHLESNCVQ 60  
 RDKYRYFACL MRARFEEHKN EKDMAKATQL LKEAREEEFWY RQHPQYIFP DSPGGTSYER120  
 YDCYKYPEWC LDDWHPESEK MYPDYFAKRE QWKKLRRESW EREVQLQDE TTPGGPLTEA160  
 LPPARKEGDL PPLNWWIVTR PREREM 206

## (2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 139 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCHAV 60  
DADGTRILPR PPSAAGWSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVA PAYKAA120  
TFFADGSGRV PTPRTPLRR 139

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SSWSGVIPFF FSCSCLPFLY60  
PPRWRQIHDL KDTQYLLNS 80

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LMMTIYALSN EFAPKINEEQ LSFFPLLSVQ LWHAQRFLD SWSGVIPFF FSCSCLPFLY60  
 PPKWRQIHDL KDTQILLNS 80

## (2) INFORMATION ON SEQ ID NO. 288:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 206 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSF LLLVALSYTL ARDTTVKPGA 60  
 KKDTKDSRPK LPQTLSRGWG DQLIWTQTYE EALYKSKTSN KPLMIHHLD ECPHSQALKK120  
 VFAENKEIQK LAEQFVLLNL VYETTDKHLN PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180  
 YAYEPADTAL LLDNMKKALK LLKTEL 206

## (2) INFORMATION ON SEQ ID NO. 289:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 77 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GNPELPWRKF QQHSCSLWP SPTLWFEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60  
 LRHMKKLYIN FRQATNP 77

## (2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

GGXGXQLLXP XAXQGXPAAS CXKQDVHLXR CXTVVVRWYQR ITGMPXXAPT RNFSKFQRXV 60
MDLHGFPKEX GQXEXQEXLQ WEGRSSSGKC RISXSILPKS TIXXFLKXXW XXIRXQSPXT120
WXRTRYLRGSS ISEFSPGSGCL PNWLEGGPRM TXAKWPKFEL                      160

```

## (2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

RHXPMLXGXH GHRAHSCLGW SQXALWDXAW GLXXXGSXQX RKKEAXWCXV VGXVGXCXXP 60
XEXMXXGFEQ NXXGFPNXXV SXLGXXXWNR XAERNMXGCC AKXVNXMXDH XXGFQXRQIR120
GLCSHAHTGX NCHVSXSGSD TQLCXGLSFM                      150

```

## (2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

RAAKILKGGI QEVAEQLELE RIGPOHQAGS DSLTGMFAFF KMREMFEDH IDDAKYCGHL60  
YGLSGSSSYV QNGTGNAYEE EANKQS 86

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

IKAKFNLNAF FFFFLRSEI GTVILSTERQ TIKWAMKGGG KVLIVRGIQ PEIKPIYKHV60  
CSSK 64

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 226 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ASTIMDLLFG RRTTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIAD IKKMAKQGQM 60  
DAVRIMAKDL VRTTTRYVRKF VLMRANIQAV SLKIQTLSN NSMAQAMKGV TKAMGTMRQ120  
LKLFPQIQIM MEFERQAEIM DMKEEMNDA IDDPMGDEED EEESDAVVSQ VLDELGLSLT180  
DELSNLPSTG GSLSVAAAGK KAEAAASALA DADADLEERL KNLRRD 226

## (2) INFORMATION ON SEQ ID NO. 295:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

KILGIHWLSR SGRGTQSLRR FLRSRRSRSAS ASARAEAAAAS AFFPPAATLS EPPVEGRFDS 60  
 SSVRLSPSSS RTWDTTASLS SSSSSSPMGS SMASFIISF ISMISACRSN SIMIFNIWGN120  
 FSCLFMVPM LVTPEMACAI ELLDLSWIL RDTAWMLARI NTNLR 166

## (2) INFORMATION ON SEQ ID NO. 296:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 233 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

KPEGARRQVF VMGLFGKTQE KPPKELVNEW SLKIRKEMRV VDRQIRDIQR EEEKVKRSVK 60  
 DAARKGQKDV CIVLAKEMIR SRKAVSKLYA SKAHMNSVLM GMKNQLAVLR VAGSLQKSTE120  
 VMKAMQSLVK IPEIQATMRE LSKEMMKAGI IEEMLEDTFE SMDDQEEMEE EAEMEIDRIL180  
 FEITAGALGK APSKVTDALP EPEPPGAMAA SEDEGESEEA LEAMQSRLAT LRS 233

## (2) INFORMATION ON SEQ ID NO. 297:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

LMFFQSQNLQ ERWLPQMRMG RRKRLWRPCS PGWPHSAARG CLFRWVCTHS SQELPFYVSL 60  
 ALHLOCEDYH FGEQSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRSIDRY ILLWGGERNP120  
 SAHEALLKI 129

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 351 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TWCTTTLAA RLVLRLTLPs RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60  
 RGRTOGELKE AALEPSMEKI FKIDOMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120  
 IWPQYVKDRI HSTYMYLAGS IGLTALSATA ISRTFVLMNF MMRGSWVTIG VTFAAMVGAG180  
 MLVRSIPYDQ SPGEKHLAWL LHSGVMCAVV APLTILGGPL LIRAAWYTAG IVGGGLSTVAM240  
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFMSMFLLYD300  
 TQKVIKRAEV SPMYGVQKYD FINSMLSITM DTNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN



## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RVAFATVVGG RNIDPNEDTK TRPRPTPRGA PMFRNFSLGA HMAVERPPT MPAVYHAALM 60  
 RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120  
 MKFMRGTGVLV IAMADKAVKP ILPAKYI 147

## (2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 188 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

RRLEVSyrQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEVQSL 60  
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLKYE FDIEFDIPIT YPTTAPEIAV120  
 FELDGKTKRM YRGGKICLTD HFKPLWARNV PKFGLAHMA LGLGFWLAVE IPDLIQKGV180  
 QHKEKCNQ 188

## (2) INFORMATION ON SEQ ID NO. 301:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

SKFGHIFGPG RFEMIRQAYF ATPVHLCCLS IQLRNCNFWG SSRICDRNVK LDVKLIFQEV 60  
 MOIFAFSKFP SSFLVGLQSE PIVVSILVVL HIPDKGLIFL LQSLHPQLTI SGSGVSLQHR120  
 DLRHNTSRGF IRLHGPGRKR NAEVVLPVAY LKAPSSLLWE DETLGCKCTS FE 172

## (2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AVRRRGALS L SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV.FLKNEKGQYI 60  
 SPFHDIPIYA DKDVFHMVVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFFYKGL20  
 YIWNYGAI PQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180  
 GETDWKVI AI NVDDPDAAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240  
 FKDKDFAI D IKSTHDHWKA LVTKKTNKGK ISCMNTTISE SPFKCDPDAA RAIVDALFPF300  
 CESACTVPTD VDKWFHHQKN 320

## (2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 85 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RVLCSNLHFC IRPAWYFNH VKHILICINW NIMKWRYILS FLIFEEDSVL QGEGRGALLG60  
 AEAHSAAGVL PPPLPQSHQ ARGAD 85

## (2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 247 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSLK HEDKRGSGS 60  
 HNNGTVKDEL TESPKEYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120  
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKE EAHAEVSVMD180  
 HHFRKPANDI TSQLEINFGD LGRPGRGRGR GRGGRGRGRGR PNRGSRDTS SASAPDVDDP240  
 EAFPALA 247

## (2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

SFGILKHAKA LNRVRHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60  
 VHLVLPCHRV LGGQGLQN 78

## (2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 293 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ATRGAEQDGG ASAARPRRR AGLLQRAAP CSLLPLRLTW TSSSNASRED SWLKSIFVRK 60  
 VDPKDAHSN LLAKKETSNL YKLQFHNVPK ECLAYNKIC QEVLPKIHED KHYPTLVGT120  
 WNTWYGEQDQ AVHLWRYEGG YPALTEVMNK LRENKEFLEF RKARSDMLLS RKNQLLLEFS180  
 FWNPEVPRSG PNIYELRSYQ LRPGTMIWNG NYWARAIRFR QDGNEAVGGF FSQIGQLYMW240  
 HHLWAYRDLQ TREDIRNAAW HKHGWEEELVY YTVPLIQEME SRIMIPLKTS PLQ 293

## (2) INFORMATION ON SEQ ID NO. 307:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 208 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AHRNSTALLE GRGLQWDHDS GFHFLNKWNC VIVQFLPAMF VPCCIPYVFP GLKIPVSPKM 60  
 VHHVQLPNLR EESSDGFVTI LSEADCTSPV IAPFNHGSWS ELVAPEFIYI RSGSWHRLIP120  
 ETELQQLLIL PGEKHVTSCL TKFQKFLIFS EPIHDFCEGW IASFIPPEVD SLVLLAIPRV180  
 PSPHQSTRVV FIFVNLWQRL LTNFVVCF 208

**Claims**

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57 and 258-273
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, 258-273, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID Nos. 1-123 and 258-273, characterized in that it is expressed elevated in ovarian tumor tissue.

4. Nucleic acid sequence Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108 and 112, wherein they are also expressed elevated in breast tumor tissue.

5. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 for use as vehicles for gene transfer.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

7. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

8. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 7.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

10. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

11. A nucleic acid sequence according to one of claims 1 to 10, which codes at least one partial sequence of a bioactive polypeptide.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 10, together with at least one control or regulatory sequence.

13. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

14. An expression cassette according to one of claims 12 and 13, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

15. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

16. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 15.

17. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

18. Host cell according to claim 17, wherein it is a prokaryotic or eukaryotic cell system.

19. Host cell according to one of claims 17 or 18, wherein the prokaryotic cell system is *E. coli* and the eukaryotic cell system is an animal, human or yeast cell system.

20. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 17 to 19 are cultivated.

21. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 124-257 and 274-307, which can be obtained according to claim 20.

22. An antibody according to claim 20, wherein it is monoclonal.

23. An antibody according to claim 20, wherein it is a phage display antibody.

24. Polypeptide partial sequences according to sequences Seq. ID Nos. 124-257 and 274-307.

25. Polypeptide partial sequences according to claim 24, with at least 80% homology to these sequences.

26. Polypeptide partial sequences according to claim 22, with at least 90% homology to these sequences.

27. A polypeptide that is developed from a phage display and that can bind to the polypeptide partial sequences according to claim 24.

28. Use of polypeptide partial sequences according to claim 24 in a phage display process.

29. Use of nucleic acid sequences according to claim 3 in a phage display process.

30. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 124-257 and 274-307 as tools for finding active ingredients against ovarian cancer.

31. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides that can be used as tools for finding active ingredients against ovarian cancer.

32. Use of nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 in sense or antisense form.

33. Use of polypeptide partial sequences Seq. ID Nos. 124-257 and 274-307 as pharmaceutical agents in gene therapy for treatment of ovarian cancer.

34. Use of polypeptide partial sequences Seq. ID Nos. 124-257 and 247-307 for the production of a pharmaceutical agent for treatment of ovarian cancer.

35. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-307.

36. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.



37. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

38. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273.

39. Use of the genomic genes according to claim 36, together with suitable regulatory elements.

40. Use according to claim 39, wherein the regulatory element is a suitable promoter and/or enhancer.

41. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

1/10

### Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
~50,000 individual ESTs

Tumor tissue  
~50,000 individual ESTs

Priority list

High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

Low

~8,000 contigs  
+  
~25,000 individual  
sequences

~8,000 contigs  
+  
~25,000 individual  
sequences

## Comparison of databases

normal tissue-specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

### Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)



2/10

Principle of EST Assembly

~50,000 ESTs per tissue

Assembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Individual sequences

Contigs increasing in  
number and length

Iterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000-6000 contigs

~25,000 other individual  
sequences

~30,000 consensus-  
sequences per tissue

Figure 2a

REPLACEMENT PAGE (RULE 26)

2/10

# Prinzip der EST-Assemblierung

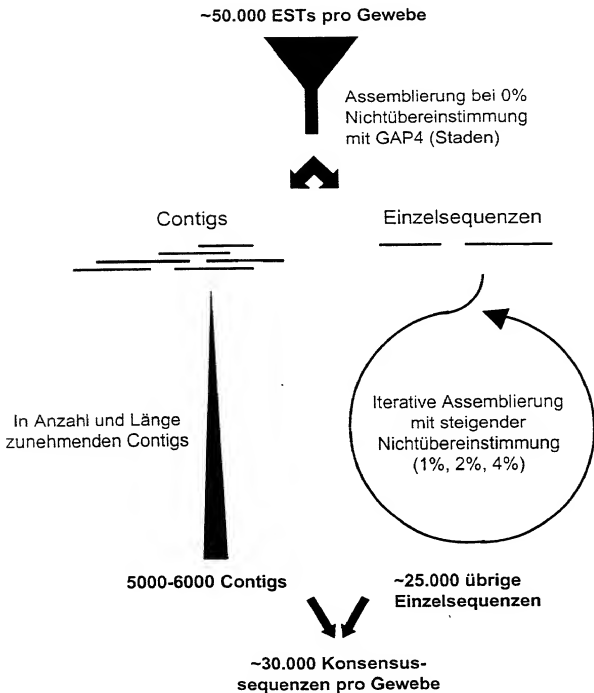


Fig. 2a

3/10

-50,000 ESTs of a tissue (e.g.: uterus tumor)

GAP4 Assembly 1st Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 0

GAP4 Database 1  
Contigs 1  
Individual sequences 1

unassembled  
ESTs

GAP4 Assembly 2nd Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 1

GAP4 Database 2  
Contigs 2  
Individual sequences 2

unassembled  
ESTs

GAP4 Assembly 3rd Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 2

GAP4 Database 3:  
Contigs 3  
Individual sequences 3

unassembled  
ESTs

Figure 2b1

REPLACEMENT PAGE (RULE 26)

3/10

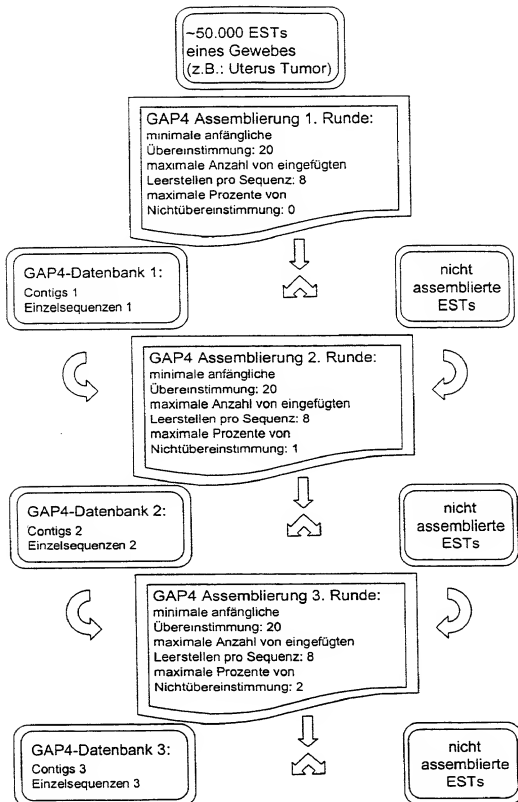


Fig. 2b1

4/10

GAP4 Database 3:  
Contigs 3  
Individual sequences 3

unassembled  
ESTs

Consensus 3

GAP4 Assembly 4th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 2

GAP4 Database 4:  
Contigs 4  
Individual sequences 4

unassembled  
ESTs

Consensus 4

GAP4 Assembly 5th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 4

GAP4 Database 5:  
Contigs 5  
Individual sequences 5

unassembled  
ESTs 5

Consensus 5

Individual sequences 5

Figure 2b2

REPLACEMENT PAGE (RULE 26)



4/10

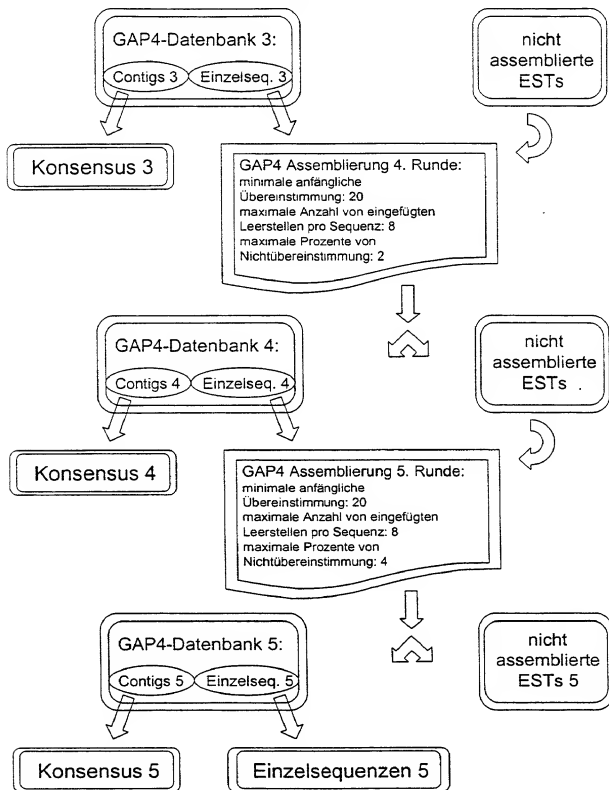


Fig. 2b2

5/10

Consensus 3

Individual sequences 5

Consensus 4

unassembled  
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 4

Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Figure 2b3

REPLACEMENT PAGE (RULE 26)

5/10

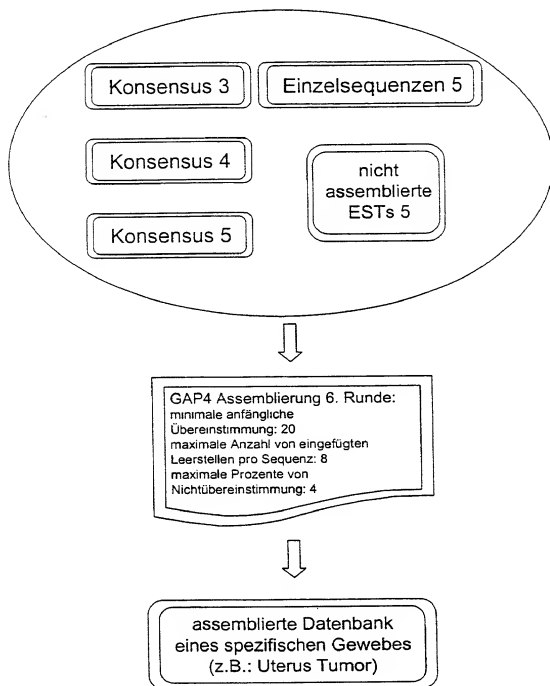


Fig. 2b3

6/10

Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Consensus 6

Read-in as individual sequences

Database  
of a specific tissue  
(e.g.: uterus tumor)

Database of a second  
specific tissue  
(e.g.: normal uterus)

GAP4 Assembly  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 4

Tumor tissue-  
specific ESTs

Non-tissue-  
specific ESTs

Normal tissue-  
specific ESTs

Fig. 2b4

REPLACEMENT PAGE (RULE 26)

6/10

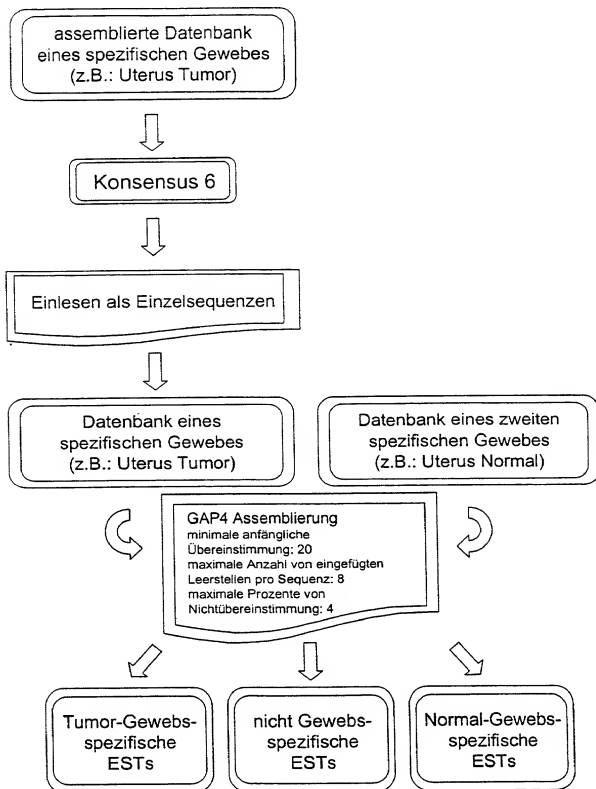


Fig. 2b4

7/10

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

Assembly at 4% mismatch

Normal tissue  
Specific genes

Cancer tissue  
Specific genes

Genes expressed in both tissues

Figure 3

REPLACEMENT PAGE (RULE 26)

7/10

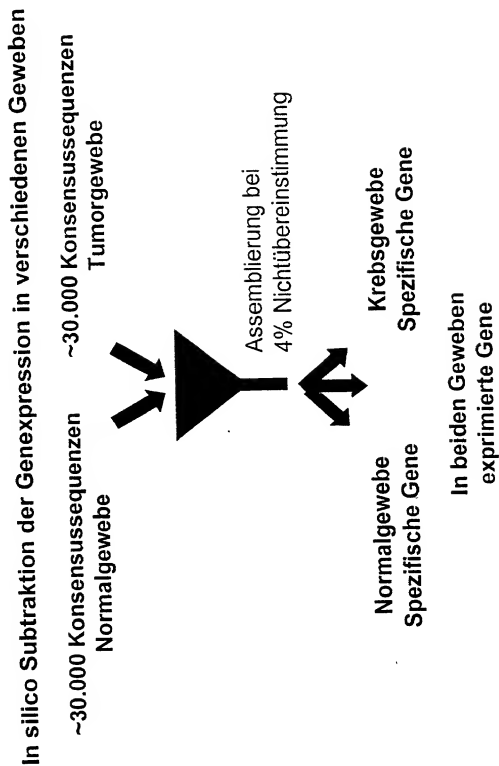


Fig. 3

8/10

Genes of interest

Determination of tissue-specific expression  
via electronic Northern (INCYTE LifeSeq and  
public EST databases)

Candidate genes for tumor suppressors or  
tumor activators

Figure 4a

REPLACEMENT PAGE (RULE 26)



8/10

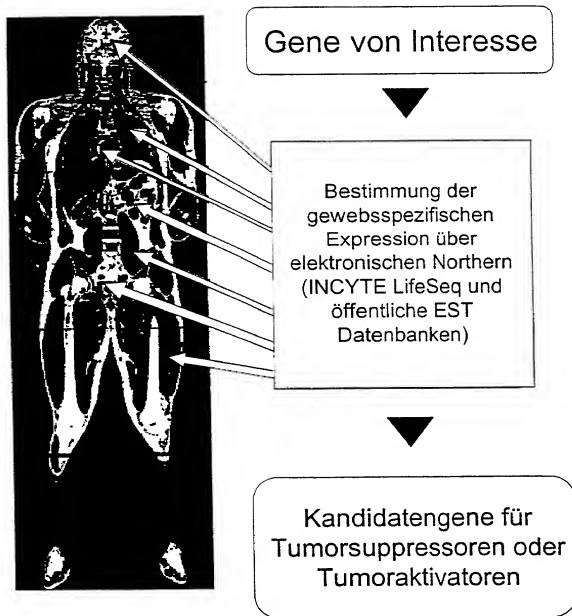


Fig. 4a

9/10

Partial cDNA sequence  
e.g., EST or contig  
s

...GCCTCAAGTTATC...

WHILE  $C_i > C_{i-1}$ 

Electronic Northern Blot

Fisher's Exact Test IF  $H_0$  EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

9/10

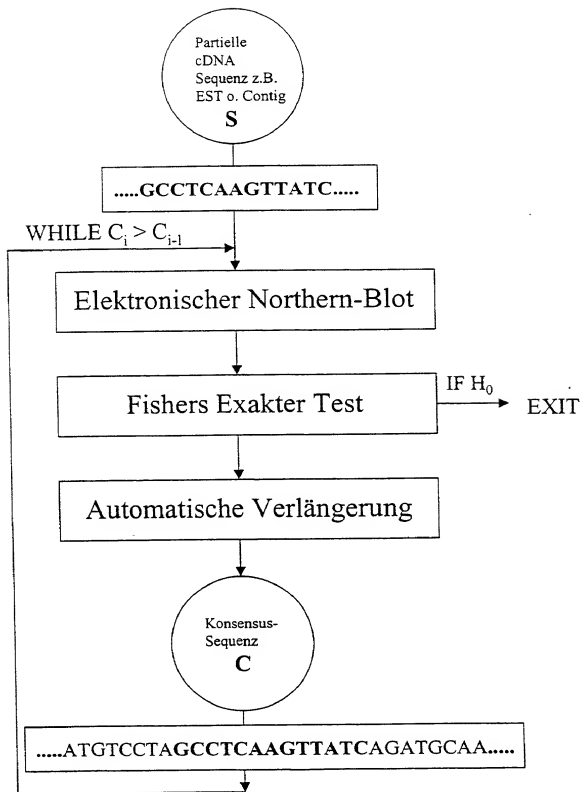


Fig. 4b

0001 152 2 2 07/10/1997 15:27

10/10

Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have  
chromosomal deletions in prostate and breast cancer leads to  
identification of candidate genes

Exon            Intron

Confirmation of candidate genes by screening of  
mutations and/or deletions in cancer tissues

Figure 5

REPLACEMENT PAGE (RULE 26)

10/10

Isolieren von genomischen BAC und PAC Klonen



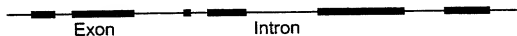
Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5

## DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

## HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 7 APRIL 1999 as United States Application Number or PCT International Application Number PCT/DE99/01087 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed

| PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119 |         |                      |                  |
|----------------------------------------------------------------------------|---------|----------------------|------------------|
| APPLICATION NO.                                                            | COUNTRY | DAY/MONTH/YEAR FILED | PRIORITY CLAIMED |
| 198 17 557.4                                                               | GERMANY | 09/04/98             | YES              |

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

| PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e) |             |
|----------------------------------------------------|-------------|
| APPLICATION NUMBER                                 | FILING DATE |
|                                                    |             |

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

| PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120 |             |                                       |
|-----------------------------------------------------------------------------------------|-------------|---------------------------------------|
| APPLICATION NO.                                                                         | FILING DATE | STATUS — PATENTED, PENDING, ABANDONED |
|                                                                                         |             |                                       |

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I, William Millen (19,544), John L. White (17,746), Anthony J. Zelano (27,963), Alan E. J. Branigan (20,565), John R. Moses (24,983), Harry B. Snubin (32,004), Bron P. Heaney (32,542), Richard J. Traverso (30,595), John A. Sopp (33,103), Richard M. Lebovitz (37,067), John H. Thomas (33,460), Catherine M. Joyce (40,668), Nancy J. Axelrod (44,014), James T. Moore (35,619), James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

## Correspondence Address:

MILLEN WHITE ZELANO & BRANIGAN, P.C.

Suite 1400

2200 Clarendon Boulevard

Arlington, VA 22201

TEL (703) 243-6333

FAX (703) 243-6410

Attorney Docket Number

SCM 1768

## DECLARATION FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled.

## HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 7 APRIL 1999 as United States Application Number or PCT International Application Number PCT/DE99/01087 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed

## PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119

| APPLICATION NO. | COUNTRY | DAY/MONTH/YEAR FILED | PRIORITY CLAIMED |
|-----------------|---------|----------------------|------------------|
| 198 17 557.4    | GERMANY | 09/04/98             | YES              |

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

## PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)

| APPLICATION NUMBER | FILING DATE |
|--------------------|-------------|
|                    |             |

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

## PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120

| APPLICATION NO. | FILING DATE | STATUS — PATENTED, PENDING, ABANDONED |
|-----------------|-------------|---------------------------------------|
|                 |             |                                       |

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I, William Millen (19,544), John L. White (17,746); Anthony J. Zelano (27,969), Alan E. J. Brangan (20,565), John R. Moses (24,983), Harry B. Shubin (32,004); Brian P. Heaney (32,542), Richard J. Traverso (30,595), John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460), Catherine M. Joyce (40,668), Nancy J. Axelrod (44,014), James T. Moore (35,619), James E. Ruland (40,921) and Jennifer J. Brangan (37,432)

## Correspondence Address:

MILLEN WHITE ZELANO & BRANIGAN, P.C.

Suite 1400

2200 Clarendon Boulevard

Arlington, VA 22201

TEL (703) 243-6333

FAX (703) 243-6410

## Declaration for Patent Application (Continued)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of sole or first inventor (given name, family name)

1- Thomas SPECHTSignature Thomas Specht

Date

29/08/00

Residence

Berlin Germany DEX

Citizenship

GermanPost Office Address Grabenstrasse 14, D-12209, Berlin, Germany

Full Name of additional joint inventor (given name, family name)

2- Bernd HINZMANNSignature Bernd Hinzmann

Date

29/08/00

Residence

Berlin Germany DEX

Citizenship

GermanPost Office Address Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

4- Armin SCHMITT

Signature

Date

Residence

Berlin Germany

Citizenship

GermanPost Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

4- Christian PILARSKYSignature Christian Pilarsky

Date

04/09/00

Residence

Schonfeld Germany DEX

Citizenship

GermanPost Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany

Full Name of additional joint inventor (given name, family name)

5- Edgar DAHLSignature Edgar Dahl

Date

29/08/00

Residence

Potsdam Germany DEX

Citizenship

GermanPost Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany

Full Name of additional joint inventor (given name, family name)

6- Andre ROSENTHALSignature Andre Rosenthal

Date

31/08/2000

Residence

Berlin Germany DEX

Citizenship

GermanPost Office Address Koppenplatz 10, D-10115 Berlin, Germany

☐ Additional joint inventors are named on separately numbered sheets attached hereto.

K:\PAT\Sch1762\Decl wpd



I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

Thomas SPECHT

Signature

*Thomas Specht*

Date

29/08/00

Residence

Berlin Germany

Citizenship

German

Post Office Address

Grabenstrasse 14, D-12209 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Berd HINZMANN

Signature

*Berd Hinzmann*

Date

25/08/00

Residence

Berlin Germany

Citizenship

German

Post Office Address

Parkstrasse 19, D-13127 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Armin SCHMITT

Signature

*Armin Schmitt*

Date

September 4, 2000

Residence

Berlin Germany, DEX

Citizenship

German

Post Office Address

Laubacher Strasse 6/II, D-14197 Berlin, Germany

Full Name of additional joint inventor (given name, family name)

Christian PILARSKY

Signature

*Christian Pilarsky*

Date

04/09/00

Residence

Schönfeld Germany

Citizenship

German

Post Office Address

Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany

Full Name of additional joint inventor (given name, family name)

Edgar DAHL

Signature

*Edgar Dahl*

Date

29/08/00

Residence

Potsdam Germany

Citizenship

German

Post Office Address

Eleonore-Prochaska-Strasse 6, D-14480 Potsdam, Germany

Full Name of additional joint inventor (given name, family name)

Andre ROSENTHAL

Signature

*Andre Rosenthal*

Date

31/08/2000

Residence

Berlin Germany

Citizenship

German

Post Office Address

Koppenplatz 10, D-10115 Berlin, Germany

□ Additional joint inventors are named on separately numbered sheets attached hereto.

X PATSCH 762 Dec 00

## Sequence Protocol

&lt;110&gt; metaGen Gesellschaft für Genomforschung mbH

422 Rec'd PCT/PTO 2 2 SEP 2000

&lt;120&gt; Human Nucleic Acid Sequences from Ovarian Tumor Tissue

&lt;130&gt; 51580AWOM1XX24-P

&lt;140&gt; PCT/DE99/01087

&lt;141&gt; 1999-04-07

&lt;160&gt; 307

&lt;210&gt; 1

&lt;211&gt; 2434

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

cggggattta cccgggttaa aaagcgaacc ttctcccgcc tacaccggaa ggtaccacaa 60  
 tatgggttagg tccgggttttc caacttggga aacgtatggg gaagcccggg gatggcttcc 120  
 ataaattttc cagcggatta tggcatttcc tccaggaat acctcttggt aaaggccctgc 180  
 ttgcacaaat gcatttccaa acttgaaata taggtgtgac cagtttaaaag 240  
 ctttcaactc atttgggttt ttttaataag gatttagaag ttcccccacac tacaaactgg 300  
 ttttaaatat tggacatact gggttttaata cctgctttgc atattcacac atggtcaact 360  
 gggacatggt aaactttgat ttgtcaaat ttatgctgtg tggaaatacta actatagtga 420  
 ttttaactta gttttaatat ttctattttt ggggaaaaat cttttttcac ttctcatgat 480  
 agctgttata tatatagtct aaacttttat atacagaat atcagtaact gaacaaattc 540  
 aaagcacatt tggtttatta acccttggct cttgcatggc tcattaggtt caaattataa 600  
 ctgatttaca ttttcagcta tatttacttt ttaaatgctt gagtttccca ttttaaaatc 660  
 taaactagac actttaattg gtgaaagtgt tttaacttac ttattgttgg taggcacatc 720  
 gtgtcaagtg aagtagtttt ataggtagtg gttttttctc ccccttcacc aggggtgggtg 780  
 gaataagttg atttggccaa tgtgtaatat ttaaacgtgt ctgtaaaata agtgtctggc 840  
 catttgggat gatttctgtg tgtgaaaggt cccaaaatca aaatggtaca tccataatca 900  
 gccaccattt aaacctttct tgttctaaaa caaaaaacca agggcgctgg ttgttaggg 960  
 gaggtggggg agtattttta tttttggaat ttgggaagca gacagcttta cttgtagggt 1020  
 ttggaaacgc agcactatac atgaatatata aaccaaaaac ctttactggt tctaaattct 1080  
 ctgatttgct attatttggt tgaagttaga gtatccaca gaagtggtta gatctctt 1140  
 ctctcttccc ccatttagaa attaggtaaa taatggatct ctataatggg agcatcacca 1200  
 cttattaaaa cacacataga atgatgaatt aaaaaagttt tctaggatgt tctttattcc 1260  
 tggcacattt attgataaac agtgaaggaa tttttaaaaa atttttaaga atgtttgtc 1320  
 acgtcacttt tagaaatggt ctacctgtat atggttaagt ccagttttaa aaatatgg 1380  
 catcttccat tttaaacatt tctatttagc tgattgtgtc tcacatacat ttctaaaga 1440  
 aactttttat ttataagagt taacttttgg ataaagtta ttaactcag ttactactaa 1500  
 ttgtgacatt taggaagga ggtaattggt ttaaatgatg gataaacttg tgctgtgt 1560  
 ttggatctga tggatctgag catgttctgc actggtgcta atgtctaata ctgtgagag 1620  
 ttaccacaca tacgtgtcac ccagagatta atttagtcca tatgaactat tgacccattg 1680  
 ttcatgtaga cagcaacata cgcactctca aatcagtggt tttagacttt taattttat 1740  
 aactcatttc caaacatgta ccatgtttta taaacctctt gatttccagc aacatactat 1800  
 agaaaaaccc tgcactctca aacacaactt ctcagtgtca cttcttgctg gtcagagct 1860  
 caacatagca atatatggta tgttgcaagc ttccaagata gccctgaactt aaaaagttgg 1920  
 tgcattagtt gtactctgat gatataaatt tgccctctag ttcaactttg gtcacagct 1980  
 aaaactgtga accctacttt ctcttattgg tgggttaataa ctgaaaaata agtttatt 2040  
 tctgctcac ttctaaaaag tctataaaac aatcaaatag gatcatgttt attgtcatgt 2100  
 gtttctctggt ttctgacctg tgtgcacacc cctgtgtgtt tataattttt aaatggaatt 2160  
 ttatatgggg tttttatttg ctaaaaacca ggctgttgaa tcacatttgg gaaggtact 2220  
 tactttatgt actaatgact taattgggaa agttgaaatc ttgtaaaaata caaaactc 2280  
 ggactcttgc ggaatttaac taattgtcac ttogttaggc agatgcactt ttgtgataa 2340  
 tggaaagtga agcataccga atgtcacttt tggttgacaa acggggcctaa tagtcgggg 2400  
 ggaatccctt aacgggttag ggtcccaagt atgg 2434

&lt;210&gt; 2

<211> 798  
 <212> DNA  
 <213> Homo sapiens

<400> 2

```
gcctatatgt gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaagg 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa tagagacttt tagcacactt cacttgtttc tagaagtcca gaatttgga180
cctccacgtg aaagaactgt tcttacctct gaactggggg ctcccataag ggataatttt240
cctccagagta gcaaaagtct tcttattaga gaaattctgt gactcagatg aagtcaggga300
tagaagacccc ttggacctgg caggttaatt ctgattattc ctgggctctt cctctgtatt360
tatgcgaagg aggtatatact gagctgatac tcttccaagg ctacaacttc aagttttatc420
atttgtaactc aagtactttt gctgctgagg aatggaatca aaagaacgta gtctcctgtg480
gaccacctca gatctctatt attaggctag atgtatagcc tctactcccc cagcttctgt540
ctcttgcccc tgcactgtaa gttgcccctt tattagcagc caaggaaaag ggaacatgat600
gctttaccag aacggtggca gagtctcctt ggcaatcaac caacgttgct atgaaatgat660
cctccacactg tatagctcat tataggacgt caggtttgtt gaaaaaagtg ggcaagacat720
gattaatgaa tcagaaatcct gtttcattgg tgacttggat aaagactttt taatttttaa780
aaaaaaaaaa aaaaaaaaaa
```

<210> 3  
 <211> 882  
 <212> DNA  
 <213> Homo sapiens

<400> 3

```
attccaaaaca tggcggctcc actagggggt atgttttctg ggcagccacc cgggtcccct 60
caggcccccgc cgggccttcc gggccaagct tgccttcttc aggcagctct aggcgctctc120
agactcttcca gcagtacttt ggtggcagag ttggagtcac ctcttcgaggc ttgctttgca180
tgctcgttgta gtcaggacta tgtcaatggc accgatcagg aagaatttcg aaccggtgtt240
gatcagtgta tcagagaagt tctggatatt gcaagacaga cagaatgttt ttcttcacaa300
aaaagattgca agttatctgt ccagaaacca gagcaagtta tcaaaaggag tggttcagaa360
ctaaggaatg aattacagcg gaaagatgca ctagtccaga agcacttgac aaagctgagg420
cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagcccg cagactccct480
cagggcctcct tggcctacct ggagcaggca tctgccaaca tccctgcacc tctgaagcca540
acgtgagcaa agggcagagg cagttggcct atgagtgggc tgatgcgtga ggttggccac600
acattccttc ctgtggactt gacatttttg aagaactctt tgccagataa tgagttcatt660
ttagtttata gctcccattg aaaaattttc cactattttt ataagctgtt aatttcttga720
gtactttata actgtctgtg agcttggata aaccaagtaa gtattttttt ttgtctttta780
gcaaaagttaa gactgtgaat atgatgcac agattctttt ttatggtggc ttgtctgttt840
ttaaattttt gcatgacttt taaaaaaaaa aaaaaaaaaa aa
```

<210> 4  
 <211> 2901  
 <212> DNA  
 <213> Homo sapiens

<400> 4

```
actgagtga gataaatca ggaactgaa acagaaaaaa attgatgaaa ctcttgagca 60
ggaacaaaaa cataaagaaa ccaacaatag caatgctcag aaccccagcg aagaagaggg 120
tgaaggcgaa gatgaggaca ttttacctct aaccottgaa gagaaggaaa acaagaataa 180
cctaataatc ctatttgaaa tcttgattct gatgggaaag caaaacatac ctctggatgg 240
taactcaggtt gataaatcc cagaaggctc ctctactcca gataactttc aggcactgtc 300
ggagtgtcgg ataaattctg gtgaagaggt tctgagaaaag cggtttgaga caacagcagt 360
taaccgtgtg ttttgttcaa aaacacagca gaggcagatg ctatagatct gtgagagctg 420
ttatcgagaa gaaactctca ggggaagtga agactcacac ttcttttcca ttatacctga 480
cgatgtagtg gacatagcag ggggaagaga cctactcgtg ttggttaggt ttgtgtgatg 540
atctcataag ctaagagagg aatttatagg ctctcctgct tatgaagccg atgcagaaat 600
tttggctgtg aaattttcca ctatgataac tgagaagctgg ggattaaata tggagattgt 660
tcgtggccag ctttaccattg tctctagtgg attttcttc aaaaatgaaa ttgttgctgt 720
```

```

tagactttta gagaaatata cccaagctat ctacacactc tgcctcttct gtgccttaaa 780
tatgtggttg gcaaaatcag tactgtttat gggagtagtc gttgcattag gaacaattga 840
ggaaagtgttg tcttttttcc atcgatcacc acaactgtct ttgaactctg acaacgtaat 900
tgctgtctct tttcagaaca gtaaaagaag gggtaaaaga ctgaaggaaa tctgcattcc 960
tcagtggaaca ggcaggcatg atgcttttga aatttttagt gaactcctgc aagcacttgt1020
tttatgttta gatgtataaa atagtacac aaatattaga tggaaataact atatagctgg1080
ccgagcattt gtactctgca gtgcagtgtc agattttgat ttcattgtta tctatttgt1140
tcttaaaaaa gtcttatctt ttacaagagc ctttgggaaa aacctccagc ggcaaacctc1200
tgatgtcttc tttcggccgc gtactgtgac tgcagtactg cattcactca cttcattgt1260
tggaaaaaat tgaagttttat catgaatttt ggtttgagga agccacaat tttggcaacca1320
aactttgat tcaaatgaaa ctccctggga aattcccgag agctcaccag ggtgaacttgg1380
taactctagc aaacctctgag agttactata aagaaccctc aagtgtccca acagtggagc1440
cacatttcca ggaacttaaa gatatattct cagaacagca cctcaaaagt cttaaatgct1500
tatctctggt gctccctagtc atgggacaac tcaaatcaa tacgtcggag gaacaccatg1560
ctgcactgta tagaagtgac ttaccacaac ctgacacgct gtccagctgag cttcattgtt1620
ggagaattca atggaaacac aggggggaaa atatagagct tccgtccacc atctatgaag1680
cccctccact gcctgacatc aagtttttct ctaattgtga tgcattgctg aaggtcctgt1740
gtattctctc tgtgatgaag gttgagaatg agcggtaga aaatggagca aagcgtctta1800
aagcattatg gaggaaacact ttgacagacc aaaggtcaga taacttggct ttgcttaacca1860
taaattttga tcaaaacac gacctggatt taatgggtga cacatatatt aaactctata1920
caagttaagt agagcttctc acagataatt ccgaaacctg gggaaaaacc taagagact1980
ttaaaaaata gctttcttat atttgatatt tggaaagaaa agccgtaagg tttgataga2040
ccacttaact acaaatatct tttgcctata ggaactccat gaatacatta gccattgata2100
atctacctgt ttaaatggcc cctgtttgaa ctctcaagct ttgaagacct cctgttctt2160
ccagaagaga acgttgaaga tgccatgttt ccttttgcgt gatctctgtt gatggacct2220
tggaaatggt tcaagttaagt cattttagac atagcattta ttatcactgt ggtactctac2280
ttgttgggtt ttatgaattc ttgaagaaa tatattttga agaggtgtgg gaggaaggaa2340
tacattttat aaaaatgtgt agtgaagccc acaattgacc tttgactaat agaggtttta2400
agtgatttaa aaatctatc ttgacaggtta caagaaatta ccggagaaaa gcttgtgagc2460
tcaccaaaac aggattttcag tgtagatttt gtctttcttg aacttaaaaa acaaatgac2520
aaagtgtgaa tggaaaaagcc tgctgttgtt ccacatctcg ttgctgttta cattctctt2580
tggagcctac atcttcttaa gctttttagc aggtatatgt tgaacacttc tggttcatgt2640
ttgagcaga atcagaggcc atggataactg acaactgatt tgtctgtttt tttctctgt2700
ctttttccat gactcttata tactgcctca tcttgattta taagcaaaac cttgaaaaacc2760
tcaaaaaaa gtgttgttgt ttatctagaa aaatatggaa aatattgctg ttatttttgg2820
tgaagaaaaa caattttgta tagtttattt caatctaat aaaatgtgaa tttgttttaa2880
aaaaaaaaa aaaaaaaaaa a

```

<210> 5  
 <211> 579  
 <212> DNA  
 <213> Homo sapiens

<400> 5

```

aaagaagaag aaagaagaag aagaagattg tagctagggg gagagtaggt gaaaagatga 60
acaacatgac cgggaagatt tcttaattct accacagcct ggctctacct taagtcttta120
ataaaagctt gactgaaggt accaaggtgt gctgaagtgg aagcagaagt ctccaaagtc180
cagcatggta gacatcagtg gtgtgaacca agcagacagc ccaaggccaag gtgaacctca240
aaaatggaac ctcaagctca tgcagtcagc ctgccctccc caccagaaa gtccttgtccc300
agcccaacat cagtcctctc gagtgtgttt actagaaaac aaggaagaa tctctgtaa360
aaatatagac agagtatgcc ctggctttct cctctgtcag gaaggatgga tctcccatct420
ccatacctat ttctcccac actggcccca gaaatactta attcaactat ttgaaaataa480
agattgtttt tggtttgagg gcatagggat ccatctatcc ttatttttta tgaaggacta540
aattagcttt gtatgttatt aaatgtgtct cgtcaatgc

```

<210> 6  
 <211> 2809  
 <212> DNA  
 <213> Homo sapiens

<400> 6

gcaggggcctc gtgcggtttg cataaatagg tttctctact cttctctttt tcctctcttt 60  
 atccctcact cctctcccta aacctcgctt cagcacaatg gactaattct agcatctctga 120  
 tcataaggcc cctcatcttt ctaatgtggt tcaaggaatc tttttaggaa aaatatccag 180  
 attattcatc cacttttttt agtatctact aacaactcct tttttctctc agagagttat 240  
 gaaggaaacag gtgtgctctg tctggagtca agctaaacac atgattttgt tttatcagcat 300  
 ctggagcaga agtgaaatgt gtctttctgt gagacagtta ttgtctactg aagctttatg 360  
 gcttgtttgc actgattact ccaggatcca aaaacttggt gaaagtcact gaacactca 420  
 aggcacaaat ttttaccagc ctgagtgctc gtcaccatag ttgtcataat gaatatgaat 480  
 cccattgtgtg ttgtgtgat gaaactcctgt agttgtattt tcttgaactg aaatatattga 540  
 ctcacaaat taaagactca ttgtcatttt tcatcttggt atattgtggt ccaagttgac 600  
 atattataat tttttgcttt ctggtaagct tagcttttaa aatgcatttt cctgtgctct 660  
 gctctttaat agtatataat gcttatattt atagtgggtt tcacagacta taaaattgaa 720  
 tgtatgaat tttttattat atcagtgctt ttaataatga agtatatttt ggagtaatgg 780  
 tgcgtgcttg tagcgagtta ttaatcatag taagattttt ttctctcatt ttgctttttt 840  
 tgtttcatat taacaatttt tttttacac ggacacaccc ccttgacagt ttctccaaat 900  
 attaaaaatc tttgaatagt tatgctgtga tctgaaacact gctcaagcca tcaagcagtc 960  
 ttcatacagt tgcattata aaatctcatt aaatctcca agaaaaaata tatgagaal020  
 tttttatttc tgaccatgca tccctggat ttctgagttt cagttcagat tgtagatgac180  
 aatataagct gcttccgaa atgtccaaca tctgaaatgt aagttccatt tcccttgag140  
 agaagccctg agttccatga agtatggatt accatttgta tttttcacta acagtaaatg1200  
 tttttttttt attaatgtgt tgccttagga atgatgaatt acattttttg ttctctctal260  
 ccataaaact cgtattcctt cagctcagcc ttctctgat gttgtttctt tataaagggt1320  
 tgagctgtgt atgcagggtat tgcacagcta acagtacaaa tcatttttaa gaggaagctg1380  
 gcgctgtatg cagccagga gacacactct caggacactg gacaagacag taatattca1440  
 acttttaatg ctgattaaag agtataggt aaagaatacg taggtataca taatgtgtg1500  
 gacaaaattt caactttatt atattttata tatttttttt ttaattttgt aaatactac1560  
 cagtttttga gtgtgctctg ttgattttgt tgatttttaa gttattagtaa taatgccag1620  
 gaaactatca tttagggagg tttagttggt ttgctgttgg actggggagg atgat ttaaal680  
 tttagtgcta gaaaccaatt tttagtgact cacagtttat catttgcag acagagaggt1740  
 gctataaaag cctactgtaa gtcatatcaa aaaagttcag aggaagatta gtaaatatt1800  
 atcaataaaa ataaacattt tgtttttcta atatcttaac atatctctcc ctttaggag1860  
 agaaactgtg aaaaactgtg gagctagagc gaataactga agagaataac cgaaaaattg1920  
 cagaagcaca agccaaactg gccgaagaac agttgagaa ttgttgaagaa caaagaaaga1980  
 ttcatgagga aaggatgaaa ctgaaaacag aacgacaacg tcaacaaaaa aaaaacca2040  
 aaatattcct gggcaagggg aagtcagagg caaaaactgtc cttctcatta aaaaacca2100  
 attaaattgt aaactctgaa ctttttcaaa agaaaaatgg aaaaactttg ttgtgtagct2160  
 tcatgttgaa gtggtttttt gttttgtttt ttgttttttt aatttgtaaa atctggaaag2220  
 tttagcttgt tcaatagggg ctatgctctg caatctcctt tttttttttt tttttctc2280  
 ccactaaagt aaactcctat cagatcattg ttgtattcta agggagtgcac tattttcac2340  
 ctgtttggat tctatatagg tggctgagg aagagcagat cacattgtaa aactatggat2400  
 ggctgtgata ggcttttact gaacccactg acttcagagt tatactctgt ttgtcatac2460  
 ataactgtg ttttctgac tttttgtttt ttatatatt tataaaaaaa gaaaagttg2520  
 gtgattgcat tgggaaattc coagggtatt actggaccta tgggtgtgat tgttaacca2580  
 gttcctctgt gatactgttg cctctgatgt tccgataca ggttaaggaaa cagttgtcga2640  
 actctgatac aaagtatata tacagttcag tattgtctct gttcattttg tttttattc2700  
 attgacaaaa tcaaacacag atctccatt gtgtaaataa atgattttgc tgaataaagt2760  
 aaagtcttaa attcaaaaaa aaaaaaaaaa gaaaaacaaa aaaaaaaaaa 2809

<210> 7  
 <211> 910  
 <212> DNA  
 <213> Homo sapiens

<400> 7

agttcggcac agagaaagta ttttaacctc cctgtagaga tctctgctcat ggaaaggtgc 60  
 caaactgttt tgaatggaag gacaagtaag agtgaggcca cagttcccca cacacagggg120  
 cttttgtatt tttctacttt ttccagccctt tactttctgg ctgaagcactc cctctggagt180  
 gccatgtata agtggggcta tttagagttca tggaaacatga aacaacactga aatgagttgg240  
 atgatccgtg cttaatgatc aagtgttact tatctaataa tctcttagaa agaacctgt300  
 tagatcttgg ttgtgtgata aatatataag acagaagaca tgaggaaaaa caaaaggtt360  
 gaggaataca ggcatatgac ttataactta acatcagatc tttttcataa tatcctacta420  
 ctttgttttt actagctcca taccacacac ctaaacctgt atattgaaat acatatga480

```

aagtcataaa tgtgccatat ggatatacag tacattctag ttggaatcgt ttactctgct540
agaatttagg tgtgagattt ttgttttccc aggtatagca ggcttatgtc tgggtggcatt600
aaatttggtt ctttaaaatg ctttgggtggc acttttgtaa acagattgct tctagattgt600
tacaaaacca gcctaaagaca catctgtgaa tacttagatt tgtagcttaa tccatttcta720
gactctggag ttgaattgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca780
tgtcttagct gtaaaaaatga gaaagtgttg gtttggttta aaatctggta actccatgat840
gaaaagaaat ttattttata cgtgttatgt ctctaataaa gtattcatct gataaaaaa900
aaaaaaaaa
910

```

```

<210> 8
<211> 1447
<212> DNA
<213> Homo sapiens

```

```
<400> 8
```

```

gcgacggcgg cttgaaaagt gcttctctgga gcgcagacga ggtcatgaat catgtgacgg 60
tggcttgagg aggaactcgt cttttaaagct gtccctggaag tgacagcggg gagaaccagg 120
cagcccgagaa accccagcttg tggagattga tctctgcgaga gaaggggggt tcatatggcg 180
gatgacctaa agcgattctt gtataaaaag ttaccaagtgt tgaaggggct ccatgccatt 240
gtttgtgtcag atagagatggt agtacctgtt attaaagtgg caaatgacaa tggctccagg 300
catgctttgc gacctgggtt cttatccact tttgcccttg caacagacca aggaagcaca 360
cttggactct ccaaaaaataa aagtatcact tgttactata acactacca ggtgggttcaa 420
tttaactcgt tacctttggt ggtgagtttc atagccagca gcagtgcaca tacaggacta 480
attgtcagcc tagaaaaagg acttgctcca ctgtttggaag aactgagaca agttgtggaa 540
gtttcttaat ctgacagtgg ttctcagtgt tactcttact tcattataac aacacaatat 600
caatccagca atcttttagac tacaataata cttttatcca tgtgctcaag aaagggcccc 660
tttttccaac ttatactaaa gagctagcat atagatgtaa ttatagata gatcagttgc 720
tatattttct ggtgtagggt ctttcttatt tagtgagatc tagggatacc acagaaatgg 780
ttcagctcat cacagctccc atggagttag tctggctacc agatatggat gagagattct 840
attcagtgga tcagaatcaa actggtacat tgatccactt gagccgttaa gtgctgcca 900
tgtacaata tgcocaggct tgcagaataa agccaacttt ttattgtgaa taataataag 960
gacatatttt tcttcagatt atgttttatt tctttgcatt gagtggaggaa cataaaatgg1020
cttggtaaaa gtaataaaat cagtacaatc actaactttc cttgtacat attattttg1080
agtatagatg aatattacta atcagtttga ttattctcag aggggtgctgc tctttaatga1140
aaatgaaaaa tatagctaat gttttttctc caaactctgc tttctgtaac caatcagtg1200
tttaattggt gtgtgttctt cataaaattt aaatacaatt cgttattctg tttccaatgt1260
tagtatgtat gtaaacatga tagtacagcc attttttcca tatgtgagta aaaaaaaa1320
agttattttt aaaaataaaa aaaaaaaa aaataaatat tttttgttct agactttttc1380
caaaaactta aacataaata atatactctt tcagccacat gaataataa tgagtgtttc1440
ttgtaaa
1447

```

```

<210> 9
<211> 671
<212> DNA
<213> Homo sapiens

```

```
<400> 9
```

```

agcgcgggtg agcgggggtg ggatctgaac atggcggcgg ttgtagctgc tacggcgctg 60
aagggcgggg gggcgagaaa tgcccgcgct ctcgggggga ttctgcagg agccacagct120
aacaaggctt ctcatatacag gaccocgggc ctgcaaaagcc acagctcccc agagggcag180
gaggaaacctg aacccctatc cccggagctg gaatacattc ccagaaaagag gggcagaagc240
cccatgaaag cgtgsggact ggcctggggc atcggtctcc cttgtggtat cctcctctt300
atctccacca agcggggaagt ggacaaggag cgtgtgaagc agatgaaggc tcggcagaa360
atcggtgtgt ccaacacagg cgagtatgag agccagaggt tcaggcgctc cctccagact420
gcccctctcc cttgtgttgg gtctgggggt cagacctgag gagcgctgcg acctcctag480
gctattgact gtaagtcctt cagggtttgg ccagattcca gtctgtgctt ctgaggtcca540
ccagagggcg catgaagccc aggcgtgttg caaacccccc cctcgccccc accaagggac600
ccaccaaaag caaataaagt tattgagtg tttagtagaa ggaaaaaaa aaaaaaaa660
aaaagtcgac c
671

```

```
<210> 10
```

<211> 803  
 <212> DNA  
 <213> Homo sapiens

<400> 10

```

gaagatgagg tggaagaaga gtcaacagct ttgcaaaaaa ctgacaaaaa ggaatttttg 60
aaaaaatcag agaaagatac aaattctaaa gtaaaaccca aaggcaaaagt tcgatggact120
ggttctcgga cagctggcag atggaaatat tccagcaatg atgaaagtga agggctctggc180
atgtaaaaat catctgcagc ttcaagaagag gaggaagaaa aggaagatga agaaagccatc240
ctagcagatg atgatgaacc atgcaaaaaa tgtggccttc caaaccatcc tgagctaatt300
ctctctgtgt actcttgcga tagtggatcac catactgcct gccttcgccc tcctctgatg360
atcatcccgag ttggagaatg gtcttgccca ccttgcccaac ataaactgct ctgtgaaaaa420
ttagaggaaac agttgcagga tttggatggt gccttaaaaga agaaagagcg tgcccgaacga480
agaaaagaac gcttgggtgta tgttggtatc agtattgaaa acatcattcc tccacaagag540
ccagactttt ctgaagatca agaagaaaag aaaaaagatt caaaaaaatc caaagcaaac600
ttgcttgaaa ggaggttcaac aagaacaagg aaatgtataa gctacagatt tgatgagttt660
gatgaagcaa ttgatgaagc tattgaagat gacatcaaag aagccgatgg aggaggagtt720
ggccgagggaa aagatatctc caccatcaca ggtcatctgt ggaagagcat ctctactatt780
ttggatgaaa aaataataac gcc

```

803

<210> 11  
 <400> 11  
 000  
 <210> 12  
 <211> 828  
 <212> DNA  
 <213> Homo sapiens

<400> 12

```

agcacttcca ggctgggggtg tttgtttgga ctggagaagg gagggcgcg ggaagggcac 60
gtcgagcggg ggagcgggcg tgccctgtgga gatccgcgga ggccgacagg attcgtttggc120
tgccgtcccc gctgctgtgc attgggttaa aaacgcacac caacatcagc catgaaaagt180
ccaagtcgca gcagtactag cccaagcatc atcaatgaag atgtgattat taacggtcat240
tctcatgaag atgacaatcc atttgcagag tacatgtgga tggaaaatga agaagatttc300
aacagacaaa tagaagagga gttatgggaa gaagaattta ttgaacgctg ttccaagaag360
atgtctggaag aggaagaaga gcatgaatgg tttattccag ctcgagatct cccaacaact420
atggaccaaa tccaagacca gtttaatgac cttgttatca gtgatggctc ttctctggaa480
gatcttgttg tcaagagcaa tctgaatcca aatgcaaaag agtttgttcc tgggggtgaag540
tacggaaata tttgagtaga cggggccctc ttttgggtgct gttagcacia ttcccact600
tgaaggcgag tattagaaga ctttaattgta aaagctctct tctcactgtg ttacacttat660
gcatctgcaa agcttttgtt agtcttgcat gcttaataaa agtgcgtgga cacttgttac720
ctaagtaaaa agcttggttc aaaccatttt actgggaaaa taggatggg gccccatggc780
cttggatggtt ggaagaccgc caagggggaag gaaccaccag gcccaagt

```

828

<210> 13  
 <211> 552  
 <212> DNA  
 <213> Homo sapiens

<400> 13

```

ttggttttcg gcgccaacca atgtgggagc tghtaatgta agagcttcc aaccaaagct 60
tggtattacc gtgtgggggtt tcgttttttt cgtgggtggtt tatttgattt tgattttttt120
ttctttttat tgatcttttg gaaaacacat tcagaattat atctcgtttc tacttaaatg180
tagtgcttag gggttaatttt ttgtactgaa gtcctttatg tgggggtgcat gctactggga240
acaagttttt ttcaaaaagc ttcaatcaga atcacgtgc attactgaga cctctgttat300
cactagacct ctgtccctcc cgcagaagac tgttggattg aacaaaaata tatgtatttt360
gattttacta aagtcctgtt aaatttttta gggacctgcc acttttgact tgggatacag420
tgatgtacac ttgtattatt aaagcactca ataaactact gtggctgata actgcaaaaa480
tgggaacccg acatttgcct tgtgtcctgg tgaccgctgt agccctacgt gcagtggagg540

```

cttgtctaatt tc

552

&lt;210&gt; 14

&lt;400&gt; 14

000

&lt;210&gt; 15

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

```

gcggtatttaa tatttaattt atttttttta cttataggtc atgttgatgt ctatgataaa 60
cagatgtttt gccctctgaca gcagaacttc ctttcatttt tctcattcgt ttctcttgggt120
gggttcattt ttttgaatca accacacttc attattttcta ttaagcaatt tgacaggact180
gttctagcct gcagtgtagt aaacctttctc atcgaaaact tttccattct cctctaaaaat240
gcttgctaatt gtcaaaagtgt gtctctgatt cttctgggca ctagaaaaac catcgaaaaga300
ccgtacaaac acagtcattt cggctctatc ttcaatgaag acatctgaat ctaaggccct360
gggtggatca aattgctgtt cagaggggat atacagggaa atggtaatgg tagactcaact420
aaaaaggact gaaccaggct ccaactgtat gtctcactgga gctgtcatct ttattttcact480
ctctttctcg tttttgcctt gaaatgtagct gtccagtttc gtaaaagccc ttctggatggg540
tgaatccagc tccatagact ccaaggacgt gctgaccacac ttggctggctc catagtgtc600
gtctcataaa cttccgggct gggggcgccg gtccctccgg gctctccagc ccggcgctc660
cacagcttgg gccgcgcgct cctcgccgca cccggggtct ggctggagcg gctcggccat720
ggggcgcgct agcgtctggg agcctggtca gccgcgcaga ggccccgcac ccggggccgc780
cccgctctgg tgtgcgcgcc ccgcccaggc ccgagctccc cctccgcaga ccgggtccct840
ctctccggcc gggctggaga ccgagcccca ccgcatgct gtccctctgg acccgaggg900
ggcgccgcca ccaaggcggg gccggctcac gaccccggag agctccgcgc ggagtgtcg960
gtctcgccc cgccccccc cgcgacacagg gag

```

993

&lt;210&gt; 16

&lt;211&gt; 2273

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

```

ctgcacctta gaaaaaaaaa gaaaaatcaa aaaaaacaaa aaacaaaaac aaaaaagaa 60
ggaaaaatctt ggagggtggg cgtgggaact caggacccca gagtggcgag tgggtgtggg 120
aggagagagc tctctccccc tttctgtgt gagaggaact cttagtgtct ggtgcagcta 180
ttaaattgtc aatgtgtgcaa gttagcttgt ttacacgcga caacatagct catttgtaaa 240
ccatgtgata agctgtgtat ttacaatat atacacaaac atcaactttt ccttgataa 300
aaaaaagtcg tgcctgggtc tgggaaactat atgctttttc atttttaagt caggacttga 360
atactgattc cagtttaatga gcagctaaag tccaatcgtt ctaatacagtg gacccccctag 420
ccatccggcg ctggcgaatat acaatttttt tccccctcca agtttgtaac actccctctc 480
cagaaaaggca ttgtgcacaa caggattatt tttaaatgat tctgaatttg aattaaactt 540
ttggagaatt ctgtatgccc cttagaagaa ttgggacacg tattgagtgt cacaaagctg 600
gggctgggaa ttgctgggtc aatgtttcat tagacttaag aacctaaaa ttttctcagt 660
tgggtgggata aaaccactaa cgtctagaaa ctgtttttctc atgcagctat gtttctctta 720
tttatgcctt gaggactaat ttctgggttt ctgactgtta atgcactgtt gacctcata 780
atggtgcctt acgcaagcga tccctctctg gggggtctca tacagggggtg tgggcgatgc 840
atgctttatt aaggctcttg ttcacctgg cagtgtactg tatcaacgta taatacagaa 900
aaaaaatctc ttttaaggtc tccttcacaa agacatagag tgaacctccc ttatcatgtc 960
agttatttgt caacacttga gccaacttga ctgtcagtg taaaatggaa aacaggaaaa1020
tggaaaaaatc tgaccaattc tgccaccttg agactttcat atagaccttg cacaacaatt1080
cttagatata cacaccggtc gtattttaaata tgaatacatt tcacacatat taaagatacal1140
gaagtatttaa aaaaaccccc atgttaattgt atttgcttaa aaggcacaaag ttccacatcat1200
ctgtctagct atctgttggg aatacagaaa gtatacact tttttaaaaa agtgggcagat1260
attcttgtgt atgtatatatt gtgtgtacag tatgtgtatg tgtgtatata tatatatatt1320
atcatatgat aatatataaaa tatttttttt aaggagaaac tagaattgtt agctagaaaa1380
ttccacagcc tgtgaagaaa tatttcaaaa tggccataaa ggaggtaaaa atgaaaacca1440
taacctaaat tttatagagg ctttatcttt aatttaacga tgtgcggagg actttcttgc1500

```



```

ttgaatctgt tccgggctgt ctgctctgtc catcaaatgg gcaggtctgg aatggggcac1560
cttcggccgt tcagaagtgg cctgaacaga atgctgggaa ccaggcttgg ctcggacacal620
ctaaggtttt gattttgaaat ttacagccta ttagaagatc taacctaaga gtaagctaac1680
cacagggatt cttttgtaga acacttttta tgcagatgaa gctatttttt ccagcagaat1740
gattcttcca gtttttccaa ggagtaattt ccccgaaatt gcataccacg gcgtggacag1800
ctgatatttt acccagctgc tggcttgggg gtgtggctct ttgctttata tatatatacal860
cacatctgag tctggctggg ctggatattt gtttgatctt cctggaaatt gcaggtgact1920
aacgctcaca taacttggtt tttttttatc tgggctgatg aatacattta cctaagaaac1980
tcattctgtt ttactttaaga ggggaagtgc agttttcttt tggcagttca gaatccaagc2040
acttgatttg ctgggttttg aaaactcctt ttttggcctt ctatgtgctt agccataaca2100
attccattaa gcaagaaggt aagcaaaaaga caaaaaaaa aaagggaaaa aaaaaaaact2160
tcgacgggct tgtctcactt acgaaacatg tcggagctgt ttgctctggg ggggctgggt2220
accgtacctg tcaatgcctg ggattttcca taaatttagc acggggacata aag 2273

```

&lt;210&gt; 17

&lt;400&gt; 17

000

&lt;210&gt; 18

&lt;211&gt; 986

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

```

gcgcgatata aacagttgga agagaaaatg gtacagcagt tacaagagga tgtggacatg 60
gaagatgctc cttaaaaatc tctgttaacca tttcttttat gtacatttga aaatggcctt120
tggatcactgt gaactgctaa attattttat tttttacata aggtcactta aatgaaaagc180
gattaaaaga catctttcct gcattgccat ctacataata tcagatatta cggatgttag240
attgcatctc agtggttaaat ctttactgat agatgtactt aagtaaatca tgaaaattct300
acttgtaact atagaagtga atttgaggag taaaatgggt gtgctatttg gataatggca360
ctaggcagca tttgtatagt aactaatggc aaaaaattcat ggctagtgtg gtataaaaata420
aaatattctt tgcagtaaaa tattcccttt gttaatgtta tagaaggggg gatacaaaaa480
ggaaactaca atttgtatgg cagtgtcaga tattttttat ttagtatttc ctgtttttgg540
ttatttgcac cttagaagag cataatgaca ttgtttgatg aagcctaatt atgctggact600
gttttgacct ggtttaaccc ttctgatagg tagttgtgga tgctggggat gagaactgaa660
taactcttgc ctggagtgac actacactct agaatttcca ctttggagaa tactcagttc720
gttttgacct gttctgatag aacagacttt actttcttag ccagcattg atctagaagc780
agaggaaatc cagcgccttt taaaagttgt tatgtggttt tcttttaaaa agctcctgt840
tttggaaagt agaatttatg ggtacaacgt atgttcatta ttgtacata aaataaaaacc900
atttaaaaag ttaaaaaga aaaaaaaaag gggggaaaaa aaaagagaaa aaggaaagg960
aaaaagaaaa aggaggggag aagaga

```

&lt;210&gt; 19

&lt;211&gt; 526

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

```

gcgtctatat tacatttatt gacactggat atttattatc tgttatatac caggcaaaat 60
ggacacacca tcaggagata agacctgtat cttacgtgta agatgaaact tatgcaaaag120
gcacagaaca aattatttgt tcacagttac ttttaactct tcagacaaat cctgagtcct180
ctttatagaa acttctattt gctaaagttag caaccattca ttttttgggt taactcttcat240
gtatagtttt tctcaagtgto tcttcaataa ctgcataatg gatatagcca tttaatattc300
caaacataat ctgaaagact agaggaaatcg ccattaattt catttgtgtt tgacaaagcg360
tcactcaatg gattaaaacc ctctcctttt gtggcagtggt aacggatgta tacctaaaaa420
gaaaaaagag ttaattcacct ctctggataa tgaatgctat tagaagattt ttgacttctc480
ctaatttgat aattgccttt ctatagctat aatgttagaga gcaaaa 526

```

&lt;210&gt; 20

&lt;211&gt; 1765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

```

tttttttttt tttttttttt gctgtttttt atttattttg gattgtgtgc aaataataat 60
ttatttttaa aaaatctcaa aacatgttca aacacattca gtatgcaaga tccaccattg 120
gcacacacat taagaaagca cacacactag gcttctagtt gggctaatta aaatctctat 180
ggctggaagc gtggtgtggt gtacttaatt aagctttttt gaagtgcmaa gctatgcata 240
acagatgagc ttgaaagctg cagagtttaa gatagactta atttttcatg attttcccaa 300
agccagtcac gatatttatt taatttgggt tcttcagggt gcaccaatcc catgaagctc 360
aattggatac ttcactgtct ttgtcaggta ttcactgtgag aacttgacaa tgggttttgc 420
ccgaagatcg tagagaccaa gaggtttaag aagttctgac acatctctcc agtctgcggt 480
tcttgctacc tcagctgaag gatacttctc cagaacttc caaagcacag gtattgccat 540
tttgctgagc gtccgattga gaaatatagt agcgatgaga agcttccatg gattcatgaa 600
aagtgcttct tgaacagatg taaaaggtag ccgaggagggt gtccatttct taaaggcttt 660
acgtctgtggg gggctaaagag ctctcttgtt atatttctgt gaaaaataca ggtctgtttt 720
ccttctttct atctgtgttc gtgggtatgt atcttcagtg aagctcttcc tggttgggtg 780
gcagttgttg tccatttcag agccacgttt taaaaatgca gtatgcaaat gttctttctc 840
ttccacaact tctacttttg ttccgatttc ttcagattct aaaaaggtag cctcctactt 900
ctcgttgtgt tctgagtctt tggctgaaca aaatttgttt atgatgccag aagttttttg 960
ttcagaacaa aaatttgatc ctgaactcaa tgattcttct tttttttt caaggctgtt 1020
ttcttcactg gtccacatga ggggtctcacc acatgctcca gcacagaaa tgcagacagt 1080
tctatcaagc tgactttttt gtgcaacagg ttcaacttca gcattctgct tattacacac 1140
agattctctt ttgctatcac ttgaaacaaa acctgaacag ctcttctcac atcctttttt 1200
agttttctta attgggatcc ctctcaaaat agtcaccttt cctttggggt ttctaacctt 1260
tctgaagtta acatcatcaa caccctcctc tcttttcaaa agcaaatgag tggagatgaa 1320
gttagagagt cctctgtctc cctgcaactc tgaactacta ctggcgcca taaacacatc 1380
ttttttgac ttgcttcggg tcttgagggt ccagtgtgaa ttgtactttt ggtttttagt 1440
attggatgct agggctgccca tgcctgagtc tttatatctt gacttgatag cccttttaga 1500
aagtcacgta aaatcaaaat ctcttggttt aagagaagtc tctccatttt tctgaagata 1560
attagcaagt gaacttttgg atctgaaact cagtcctgtg gggctagaaa atgatattaa 1620
aggaaactta ctgctagtaa atagaaggga cttttaaaag aactggacca catttcagat 1680
ttaataattt ttccaattg ttgccatagg tatctgtcat ttaaaatga aaaagagtga 1740
taaatgacac ttttaattgg ttccc

```

&lt;210&gt; 21

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

```

gttttttttt gttttcttta aatttggatg tctctacacc actcctgatt tgtaggacta 60
aatagatcta ttatttccaa tgcaaaattgt gtaacattta tttcttccctt gattttttaa 120
aatacttttag tattcttaac tatgtatgtg ccttctctta cactgagttc ttttttgctc 180
ctttcagctg ctacacacaa cctgtctggt ggagtcatag ctgttaattc catattattt 240
ctctacacac ctgcaacatt tagtgtatta ctggtaacct ctgtgttctt agtaaaccaa 300
tgaattgcaa actggacttg taacaggatc atacatagag caacaaatga gctactggct 360
ttgtaagata tgaagttagg aatttcacag tcatgtctcc aaatttcatg gcagagttaa 420
aaaaacaata taagactgtg gtaaggtaga aacgcaaatg caatttgcgt tgactaattt 480
cttaggagctt atttctctat gtaaaacccc tgttcttctc tctctgccac aagacagggt 540
acaaagcttt ctcaaaccatg ctctcaggtg tccacacctg agacattgtt tgtggatac 600
tctcaagggt tctcaacaag caaaaaaatc agaccaaatg ctaagagcaa gcaactcata 660
cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaattgttt 720
tgctaattaa ctaaaaataat agccgc

```

&lt;210&gt; 22

&lt;211&gt; 659

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

```

agcagactca caccagaact acattccctg gccccctgcc tgtgtgettc tggccaggcc 60
ttggttgcca agtctgaccc gagaaaagga tctgcagaaa atcagactat gggatcactt 120
tggtttgcca ttgggaatga cattctttcc cccccagga aaacctttgg gactttcaga 180
gacatttggt ctaggcaacc acatggtcag cctcaaatgt gagaggctca gtacccctcc 240
tatccctaga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc 300
tgtgatcttc tggaaagtat ctatgttgtg tatatcttgc atccaaagcc agagggaacc 360
acaatgacta ctaaaaacgtt ggtctcaatg ccactctagc cctgcctctc gaatttgacc 420
atagtggcgt tcagctgata gagcgggaag aagaaatatg cattttttat gaaaaataaa 480
atatccaaag gaagatgaaa ctaaatggag aaattgaaat acatctactg caagaaaaaga 540
tcacattctc gaaaatgaag attgctgaga agcaaaagca aatttgtgtg acccagaata 600
tactcgccgc caagaggtcc ctggatgccg acctagctgt gtcctcaaat cagtttttca 659

```

<210> 23  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 23

```

cgcagtgcgc agccgtgggg ctctctctct gtcagtcggc gccgcgtgcg ggcgtggtggc 60
tctgtggcag cggcgccggc aggaactcgg cactatgagc ggcttcagca ccgaggagcgl 120
cgccgcgcgc ttctccctgg agtaccgagt cttccctcaa aatgagaaga gacaatatat 180
atctccattt catgatattc caatttatgc agataaggta aggcattcct tgttttggac 240
acagctctct tactcagatc agctagtctc acatatgaat ttctttatat gtctctcaac 300
aagtgcctaa aatgcctcgt tgtgctgtga gtaaaagctt gttgattagg ctgggcgc 357

```

<210> 24  
 <211> 890  
 <212> DNA  
 <213> Homo sapiens

<400> 24

```

cggaggcagc ggaaagccga gccaggcgcc tgcgcgtggt gaagagtagg ttcagagtgc 60
attcccggaac ccggggcgcg gcgcactcgc caggcgcgcg gactccgctc agtttccggt 120
gcggcggaaca ccaaaagtccg ggaacttaag cattttcggt ttctagggtt gttaccgaagc 180
tgacggagcg agatgagggt ggaacgcacc ggtgttgatg gtccagatgg tctccgggagc 240
cggcgagggt ttacgagggg agggaggcag aacttcgatg tgaggctca tctcggggca 300
aatgggcttc ccaaacactc ctactcgttg gaacctcggc ttttctcctc ttctcgatg 360
gtggtgtctt tctttgtgta ttttttgcca tgacttgctc gctgatatc aaattaaaga 420
gttggttctt gagtgaattc tgaaaaatgc tacaaaactc tctgaataag aagacaggac 480
tctcaataga agaatttcac atctccaagg gacctctcct tctcttttac actttgttac 540
taatttgcag aactctatta attgggtagg atttaccaca ttccatgcta agttcttcaa 600
attaaacccct ttggttcgtg tttaaaaaact ttcaaacatc tgatggctt acaggggctg 660
aatataaaaag catttgtact taaagggtct gtgtattatc taagaaatat agtaattgct 720
tttaattgtt taagagttga tcagggttta ctatggatgg caagttaatg ggaatgataa 780
taaggggaag gttttttatg aatttcaaaa gtcaatttat ttcaaaagcg gggggaaggc 840
ttttgagagg agggggggcc aaggtgttcc tggggtttgc cgaggggagg 890

```

<210> 25  
 <211> 651  
 <212> DNA  
 <213> Homo sapiens

<400> 25

```

gccgtatatt gcatactaca tcagcaaaa gtgttcggcg ttataaagcg ggcgctacgc 60
cacctcgagt cgtgtgtcgt ccagagagac aaataccgat actttgctt ttgatgagag 120
gcccggtttg aagaacataa gaatgaaaag gataatggcg agggccaccca gctcgtgaag 180
gaggccgagg aagaattctg gtacgcctcag catccacagc catatctct cctgactct 240
cctggggggc cctcctatga gagatacagc tgctacaagg tcccagatat gtgcttagat 300
gactggcatc cttctgagaa ggcaatgtat cctgattact ttgccaagag agaacagtgg 360
aagaaactgc ggaggggaaa ctgggaacga gaggttaagc agtcgcagga ggaacgcaca 420

```

```

cctgggtgggc ctttaactga agctttgccc cctgcccgaaggagggtga tttgccccca480
ctgtgtgggtg atattgtgac cagaccccgg gagcggcgcca tgtagaaaaa gagagacctc540
atctttcatg ctttgaagtg aaatatgtta cagaacatgc acttgcacctc ataaaaaatc600
agtgaatagg taaaaaaaaa agtgccattg tagtatgcaa taataagcgg c 651

```

```

<210> 26
<211> 1256
<212> DNA
<213> Homo sapiens

```

```
<400> 26
```

```

ctcagagcga attcggctcg agctttcattc tgaccattcca tatccaatgt tctcatttaa 60
acattaccoca gcattcattgt ttataatcag aaactctgggt ccttctgtct ggtggcactt 120
agagctctttt gtgccataat gcagcagtat ggaaggaggga ttttatggag aaatggggat 180
agtccttcattg accacaaata aataaaggaa aactaagctg catttgggtg tttgaaaagg 240
ttattataact tcttaacaat tcttttttca ggaacttttc tagctgtatg actgttactt 300
aaactatcta aaatagagca ttttgggtatc ttctatctga ccatccatc caatgtttct 360
catttaaaaa taccocagca tcatgtttta taatcagaaa ctctggctct tctgtctgtg 420
ggcacttaga gtccttttctg ccaataatgca gcagtagtga gggaggattt tatggagaaa 480
gggggatagtt cttcatgacc acaataaata aaaggaaaaac taagctgcat tgtgggtttt 540
gaaaagggtta ttatacttct taacaattct ttttttcagg gacttttcta gctgtatgac 600
tgttacttga ccttctttga aaagcatctc caaaatgtctc tatttttagat agattaacat 660
taaccaacat aatttttttt agatcgagtc agcataaatt tctaagtcag cctctagctg 720
tggttcatct ctttcacctg cattttattt ggtgtttgtc tgaagaaaag aaagaggaaa 780
gcaaatcacga attgtactat ttgtaccaaa tctttgggat tcattggcaa ataatttcag 840
tgtgtgtgat tattaaatag aaaaaaaaaa ttttgtttcc taggttgaag gtctaattga 900
tacgtttgac ttatgatgac cattttatgca ctttcaaatg aatttgcttt caaaaataat 960
gaagagcagc tgtccttctt tctcttttta agtggtcagc tgtggcatgc tcagagggttc1020
ctgctggattg ccagctggag cgggtgtgata cctctctttt tcagctgttc gtgccttctc1080
ttctgtgatc caccaaagtg gagacaaata catgatctca aagatacaca ctacctactt1140
aattccagct gatggagac caaagaattt gcaagggtat ggtttggtat cactgtaaat1200
aaaaagagggt cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 1256

```

```

<210> 27
<211> 694
<212> DNA
<213> Homo sapiens

```

```
<400> 27
```

```

gtttctaaag gatgtgtaag aaaccagagg taaagggtctc gcgatattctt aagacatccg 60
cggtagtacg cttcagtgag ccacagcgct agagaagtag gagaagctcg cgagatctgt120
cgcgcttgcg aggagactag gagggggagg agagggggatc tgcgaaaagg aaagagggtcg180
ggagcgctcg cgagatctcg gaccacccaa cctgaaagggt ctgtaggagg ttgaaaggcc240
cagagaggagc ctccggggcaa atggccggag ctgggacgac catgctgcta cgagaagaga300
atggctgttg cagtcggcgt cagagcagct ccagtgctgg ggattcggag ggagagcgcg360
aggactcggc ggctgagcgc gcccgacagc agctagaggc gctctctaac aagactatgc420
gcattcgcat gacagatgga cgggacactg tggctgctt cctctgcact gaccgtgact480
gcaatgtcat cctgggctcg gcgcaggagt tcttcaagcc tgcggattcc ttctctgccc540
gggagccccc tgtgtcgggc ctggccatgg taccgggaca ccacatcgct tccattgagg600
gagagaggga gagctcgacc gggcctccgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaa aaaa 694

```

```

<210> 28
<211> 1927
<212> DNA
<213> Homo sapiens

```

```
<400> 28
```

```

gcgagtattt attttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
agcctgttta acttttgata caaagtaaca ttttagtaca gaaaatccca gctctgcagc 120

```

```

tcagtacctg  tctgtgcaca  ctgtaccatc  tcagtccttc  tctgctgcta  acttagaaaa  180
cagccctcat  ccccgagagg  tctgtcaggt  aatcccttga  gaatagtcta  cagtttttca  240
tagtttgtct  gagctagaaa  actgttacct  gtaaaacaaa  ggacagcatt  gaggactgaa  300
acttgtctct  tttttgaaca  actgtgcaag  aaaatatatc  ccttttttaa  aaacatcagt  360
tatggctaaa  ctacaatcta  gtgtctagaa  ttacaagaaa  taaaatgaaa  tcaaagattt  420
ctgcgtatga  aaatgaaatg  ttaggaacag  tattaaaata  taggtcctac  cccaacgaca  480
cttacacaga  gcccgataga  gtacctatta  ttaacaggac  gcatagctta  aggaggaacc  540
aacatcaaat  ttbagccaga  catatctagc  ctacagaagt  caaaaaaaa  aaaagccccc  600
aaacgaagac  accccactgc  agtaggggtg  atgccgtgag  tgctgtaatc  ctgtccttca  660
agacccctagt  ttttcttttt  agactggtta  tagtgacaat  aaccattatg  ctccccctaa  720
aagctctcaa  ttcaatgtct  gaaacatgaa  tgttttcata  tcaaaaaaaa  ctgattgacc  780
tgccaccctc  taaaagtttt  aagaattacc  ctgcaaacat  tgcaactgat  aagggctgtc  840
cgacttacag  agcctaaagg  ggaccccaat  gcaggcatca  gcacagctgc  acaccactgc  900
gacccctcag  gaccctctgc  cagcgagctc  tcacggagca  gacacagctc  tcaagttaata  960
agcacagatg  gaggagaaac  gagaggctgt  ggaaggcagg  agagaaaggc  cgagagacgag  1020
gtttgtgaag  atgccaaagt  caccctcccc  attgtgggag  gaaaaatgca  aaggcactgg  1080
ttctgtctgc  acaggcagtc  tgagcaccct  gagttgtgac  gtccctccag  gagaggtgcc  1140
accaaggagc  agtaggtttg  tcaaagctct  ggtccccaca  acaagaacct  cccaagacaa  1200
agcagcccc  attgaggttc  caaggctcgt  ttgctgaaga  cgggaacgaa  accaacacaa  1260
aagcgcagg  gggttgacag  aggggacagg  ggctgggcac  cggaacatg  gagccgttca  1320
agtaaacata  aaccacaaaa  tacttagaaa  aggtctgtaa  acgagtgtac  cgaaaggttc  1380
tctttcgagc  atctctgatc  agctggctaa  agaaagggtg  gtgctgaacc  cgtctttagt  1440
gttatctgtt  ttgtgttaaa  gcacacgtgt  gacacgggca  gagtgtgtgg  gctctgggct  1500
ggatcgacgc  cagccgtggc  cctctgtcta  caaaggaggt  gcttctgggt  cctggttccg  1560
gatctctccc  ccgcatgttc  atagacggac  agacttctac  tttcagtcgc  tagaaaagag  1620
ctgagtcgtg  gtccccctca  ggcggccagg  tgcagtcatc  cacagcacag  cattctccta  1680
gagcgggcag  gctggaatcc  acaggacttt  attttgtctt  tgattgacca  ttgccaagat  1740
ctgagtgcaa  atcgttgaca  ctggctctcc  ctggatgacc  cctgcacaa  agccccccag  1800
acacgtcatt  cagctcagag  taagacccca  ggtttgaggc  aaggcagtag  agcttgactt  1860
ctttctactg  tgtggctgtc  tgctttgtgc  tccttggcac  tctgtccat  ccccactgag  1920
ctctcctt  1927

```

&lt;210&gt; 29

&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

```

gcctttttat  tttttttttt  tggctgttat  gctgcattta  ttatgagaat  caacagtc  60
cagtttaata  ttgactaaat  ctgtgtgttc  actctggaca  ttaacgaaaa  agactggaa  120
agggctacag  cgctgctttt  atgtctacac  ggttatgctt  ggactctgac  tcccgacg  180
aggttagatt  aggaatttat  ggcagtgaca  ttaccatcaa  tgggaaacac  ctctcctt  240
cttcaggatt  ctctgttagt  gaagagagca  cccagtggtt  ggctgaaaac  atctgaaag  300
agggagaaag  acctaaaaata  atcagtatct  cagagggtct  taaggtgcca  aagagttc  360
ctggacattt  aagtgcacac  aaaggcatac  ttccggaatc  gccaaagtca  aactttct  420
ctttctcttc  tctcagagac  aagtgcagac  caagagtcta  ctgctttagt  ggcaactaca  480
gaaaactcgt  gttaccacaga  aaaacaggag  caattagaaa  tggttccaat  atttcaag  540
tcgcacaaac  ggaatgtgct  tcctttgccc  atttaggggt  tcttctcttc  ctttctct  600
tgtttatgct  tcgttctctt  tttcagtttc  catcagatct  cccctcctg  ccaactgga  660
cagcagggtt  gc  672

```

&lt;210&gt; 30

&lt;211&gt; 269

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

```

cgcataccta  gccgcgagct  cacacaaggc  aggtgggtga  ggaaatccag  agttgccatg  60
gagaaaaatt  cagtgctcag  attcttgcgc  ctgtgggcgc  tctctacaaa  tctccacagg  120
gatagcacag  tcaaacctcg  agccaaaaag  gacagggaag  agtctcgagc  caaactgc  180
cagaccctct  ccagaagttg  ggggtgaaca  ctcatctgga  ctacagagta  tgaagaagct  240

```

```

ctatataaat cgagactagc aactaaccc                                269

<210> 31
<211> 604
<212> DNA
<213> Homo sapiens

<400> 31
tgcgagggcg ggatagctgt ccaaggtctc cccagcact gaggagctcg cctgctgcc 60
tcttgcgcgc ggaagcagc accaagtcca cggccaacgc cttggcacta ggggtccagaal20
tggtctacaac agtccctgat ggttgcgcga atggcctgaa atccaagtac tacagacttt180
gtgataaggc tgaagcttgg gcatcgtcc tagaaacggg ggccacagcg ggggtgtga240
ctctcggtggc cttcatgtct actctccgca tcctcgtctg caaggtgcag gactccaaca300
ggcgaaaaat gctgcctact cagttctctc tcctcctggg tgtgttgggc atcttggcc360
tcaccttcgc cttcatcatc ggaatggacg ggagcacagg gccacacgc tctctctct420
ttgggatcct cttttccatc tgcttctcct gcctgctggc tcatgctgtc agtctgacca480
agctcgctccg ggggaggaag cccctttccc ggttggatgat tctgggtctg gccgtgggct540
tcagcctagt ccaggatggt atcgctattg aatatattg cctgacgatg aataggacca600
aggt  604

<210> 32
<211> 781
<212> DNA
<213> Homo sapiens

<400> 32
ctttaatgtg cctagagcaa tggaatgggg caacttgggg gcggtggaat tcaagacgct 60
ctggctgaag attcagaagt atctggtaac tctcttttcc tcttgggcat cctctcctct120
gttctaatcc tcccttacac tcattccttg tccattgtat tctgaccaca tctctaatca180
tggtcaaaac tattgagtc tgggcacatt ggtcatgaag gaacaagaag gcaatgagag240
acctctatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaaag gggccagcac300
tggccaagct cttatgcttg ctctgaaacc ttcttgggag gagtcaatag ggtctccttt360
tgaagtgctc cctggccttt tgagaaagca gtgtgttgga gggagatggt tctggcagg420
gcctggaatg gttgttttct acttgggatt tcttctctgc tttaggagat ctattgggaa480
acctgattata accactcggg caccatcgat gccacagaga tgaggacagc cctcaggaa540
gcaggtttca cctccaacag ccaggtgcag cagaccattg cctgcggta tgcgtgcagc600
aagcttggca tcaactttga cagcttctgt gcttgtatga tccgctgga gaacctctc660
aaactattca gcctcttgga cgaagacaag gatggcatgg ttcagctctc tctggccgag720
tggctgtgct gcctgttggg ctgaccgcgc aaacttgacc tagaagatgg ggggggcctc780
c  781

<210> 33
<211> 304
<212> DNA
<213> Homo sapiens

<400> 33
ggccactgcg gcgagacgcg aggaactgtc gctcgtaact gtgcgcctcg ctttgccttt 60
ctctcgcaac catgtctgac aaaccgcata tggctgagat cgagaaattc gataagtcga120
aactgaagaa acagagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac180
aggagaagca agcaggcgaa tcgtaaggag gcgtgcgcgc ccaagtatgc actgagatgc240
gagaagtgtt gcgtcgaatt tacctgcttg agggggtaaa gttgggaagg tggaaaaagg300
gtgg  304

<210> 34
<211> 1528
<212> DNA
<213> Homo sapiens

<400> 34

```

```

aattcggatc catggggccac agtggatggc ttgaaatgtg gctgagcgct tcggacactt 60
cggatccatg gtggccaccc caagacgcgc cccagccgcg catggcccggt atctccggg 120
atcctgcctt ctgtccctgc tccctggccgg gttttgtccg ccgggcccggg gacaagagaa 180
gtctaaagaca gactgccaag cgggtatgag tggtaacctc tacgagtatg gagccctcac 240
catcgatggg gaggaataca ttcccttttaa gcagtatgca ggcaaatata tccctcttgt 300
caacgtagcc agctactgag gtctgcacaga ccaatacctt gaactgaattg cactacaaga 360
agaactctgg ccatttggct tggctcaattc gggcttccct tccaaacctt ttgggaaaaa 420
gagggccagg gagaaactcg agatactccc cagtctcaag tatgttcgac cagggtggggg 480
ctttgtgcct aaatttccagc tctttgagaa aggagatgtg aacgggggaga aagagcgagaa 540
attctacact ttccctgaaga actcctgccc tcccactgca gaactcctgg gctccactcg 600
ccgctctctt tgggaaacca tgaagatcca tgacatccgc tggaaacttg agaagtctct 660
ggtggggcca gatgctcacc cggttatgcy ctggtaccac cggaccacag tcaggaacct 720
caagatggac atctctgctt acatgaggcg gcaggcgacc ctgagcgcca ggggggaagta 780
atcgatggcc ccacctctacc cccatccatg gccatccatg caaggggcca ggaggggctc 840
ttcaggaaagg aaagccacatt cccagtcatt cacccccacc cccagattct cttctctatt 900
acataaaaaa caagcctggc acaactgtgt tatctgaacca ctgtggacac gtgacaattg 960
tcccagtggt tgcattggct caccagccag tatctgctg ctgtaaacc cttgaaacc 1020
catctgtgtt tacggcttgg cacaacaccc tcatattttt ttcagcttcc tgttcccaat 1080
gagcccaaaag gaacacaaag ttctaggtcc aatggttctg ctcaaacctg aaactcttcc 1140
ttggggccag catctccacc atgcccacac ccaagctctg cagctctctt cttcttctct 1200
gaaggacctc cctgagcccc caagcccatc cccagctctg cctgagacca gccaaagcaal 1260
ctgtgagcgc gatggccgtg taccctcagg cagggggtgt gtctctatga agggggggcc 1320
cgaagccctt gtggggccgg ctcccctgag cccgtctgtg gtgcccagccc ttagtgcatt 1380
caggcttagg ctcccaggca gggacactac ccccgcgct ctggaggaga tgctatctct 1440
tcactctgtc cactgtgatc tcaacacccc catctgccca gtaaggtct tcttcgagca 1500
aaaaaaaaa agaaaaaaaaa aaaaaaaaaa

```

```

<210> 35
<211> 499
<212> DNA
<213> Homo sapiens

```

```
<400> 35
```

```

ggcagggtctc agcgtctctc cccctgctcc gctctctcgc agggccagg cgcccttggc 60
cttagggacc aacttctctt accgccatgg agtctgacct gggagcagcc ctggagccca 120
cctcccagaa gcccggtgtg ggggcccggc acgggggaga tcccaagctc agtcccaca 180
aagttcaggg ccggtcggag gcaggggag gtcgggtccc aaagcaagga caccacagct 240
cttcgcactc cagcagcagc tccagcgatt cggacacgga tgtgaagtc cagcgtctg 300
gctccaagca gcacgagagc atcccgggca aggccaaagaa gccccaaagt aagaagaagg 360
aagaagggcaa gaaggagaag ggcaagaaga aggaggctcc cactgaagg gccctggaca 420
gggtcattaa aacctctctc tctgctacg agtaccaccc acctggagct aagatgctta 480
ggtggggggg ggcgcgccg

```

```

<210> 36
<211> 1396
<212> DNA
<213> Homo sapiens

```

```
<400> 36
```

```

gggcaccctg tagttgggaa cagcgggaag ctggtccggg ggaactgagta aggtgtctgg 60
atcggaggga ggttcggggt gccatcgggc ggctggaaga gctcgactcg tcccgctggg 120
aaagccggag tctgagtgga accctggacg acttgacagag cggctggcgc agtcatggcg 180
gactactcga agtcacagcc aaagaaattc tgtgattact gcaagtgtct gatagcagc 240
aataggcccta gtttgaatt tcatgaaaga ggaagaatc ataggaaaaa tgtgaaaaa 300
aggatcagtg agattaaaca gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtttg ctgcaatgga gccagctgctg ctgaagacat accaagagga ttgaaaaaga 420
cttgcttgat agtcagaat tttggagcca agcataacac cagtaaacag cactatccca 480
cctacctcga catcaaatca acagaagaaa agagaagaga aagaagaaa agaatctccc 540
aaagggcaga ttggtagaag gcataacctc tgaagggtac cattactatt atgactttat 600
ctcaggagca tctcagtggt agaaacctga aggatttcaa ggagacttaa aaaagacagc 660

```

```

agtgaagacc gtttgggtag aagggtttaag tgaagatggt ttacacctatt actataatc 720
agaaacagga gaatccagat gggagaaaac tgaatgatct attccacaca ctatgatct 780
gcctcttagt aagggtcaatg aaaattcact tggcacccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg ggggaacagga agcagagaag ggagggggtct ctacagagac 900
agaaaagcca aaaataaagt ttaagggaata agtgatggag gaagtgaacc 960
agaaaacacag aaagaaaaaa gtattcagaa acagaattca ttagggttcaa atgaagaaaa1020
atcgaaaaact cttaaagaaat caaaccata tggagaatgg caagaaatta aacaagaggt1080
tgagttctcat gaggaggttag atttggaact tccaagcact gaaaaatgat atgtatcaac1140
ttcagaagctt gatgtggcg gagaaaccaa agtggtattt aaagaaaaaa cagtcaattc1200
tcttgagatt atggcagatg gagggtggccc agtcttcaaa aagagaagaa cttgaaattc1260
ggaaaatctt aggaataatt aagggtcaacg aggtgatgat ccaatagttt ccaggggagag1320
ctttttgtt acatgctttt tagggaccag aatggggaga ctttttcca ccccccaggt1380
ttgtcccgctg ttttgt

```

1396

&lt;210&gt; 37

&lt;400&gt; 37

000

&lt;210&gt; 38

&lt;211&gt; 808

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

```

cctctgtcca ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc 60
ttggagttct tctagctcct gccctagcta actataatat caacgtcaat gatgacaaca120
acaatgctgg aagtgggcag cagtcagtgat gtgtcaacaa tgaacacaat gtggccaatg180
ttgacaataa caacggatgg gactcctgga attccattct ggattatgga aatggctttg240
ctgcaacacag actctttcaa aagaagacat gcattgtgca caaaatgaac aaggaaagtc300
tcggctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag ggtaaggagac360
caggagagacc aactcccaag ggctctgatg actcagtcac cccaaacaaa tctgatgacc420
tgagcaagtt cggaaaaaac attgcaaaaca tgtgtcgtgg gattccaaca tacatggctg480
aggagatgca agaggcaagc ctgttttttt actcaggaaac gtgtacacag ccaggtgtac540
tatggattgt ggacatttcc ttctgtggag acacggtgga gaaactaaaca attttttaaa600
ggcactatgg atttagtcat tgaatatgc tgtgcagaaa aaatatgggc tccagttgtt660
tttaccatgt tctctgaaa tttttctcta ctagttaatg ttgatttctt taagtttcaa720
taaaatcatt tagcatgtaa acggagaact ctgggggcta gtaaccacaa ggtacggagc780
aaagatcacc aggtgggaa gaggtgga

```

808

&lt;210&gt; 39

&lt;211&gt; 1139

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

```

tttttttttt tttttttttt ttttttgcag caatacctcc tttatttgat cctgttttat 60
gtccacatat gtactgtatt atcacagatg caactgattt atcatagagc actcagaaaa 120
catggaagaa tattttttaa aatcgaaata tctatttcaa gtcaaccagt gttaaccccc 180
gtgtgctctc tgccagttct ttctccccc tgggagtcac acaaaatgat aatctcctag 240
aaagagaaat tctctgtctc tctgactctt tcaacttaga cgctgcgacc ttccattgtt 300
gttcaacatc tccactcgg agcgtcacgt gctgagaggt gtctataaat ggaattggct 360
taactatctc ttactcgtgaa ggtggacatt tagggagttg ccagttttca gtgtcctaaa 420
acaactgcct tagacgcgaa agaattcaca ggtcactcgt tcccttcgct gaaattctct 480
tcgcagagcc ttcaactgac cgaagctgga atttgtctcc gtaaattgag gaaataaagc 540
catcggtttc ccaggtgaac acgcagttta gcttggggat aactttcagg gctctctctt 600
tgggtgataa ttgtaaaatt tgctttgttt cctgtagaag gattcctgta atccccact 660
aagaggggca ttggattttt gtcaactgaa taatagcccc gtgaagatct gcttttaaga 720
gcttggcctg aatcactctg ggtcgtgctg ctggccttag cccactgca acgtccctga 780
tgtactgttt ccagagttca tggagagggg ggaaaaaggg gaagcctttg gctttctctt 840
taatttcaaa gagcgcgagc tccctccttt gcttggcaga gtagcctttg gctttctctt 900
tcttctcctt ggcgtgtggt cgggtgaagt actccaggac caccgcttg cctgtcagct 960

```



```

ggctctcgcg  ggctctcgagg  ctcacgagg  gcgtctcgcg  ttcaggaagg  ccctcacgaal020
ggctctcgagg  gcgtctcgctc  ctgaaggctg  gacatcgagg  tcattcgctc  cttctcgaga1080
caatgcagtg  tagatcacac  tcttcattct  cggacgcgtt  ccggcgctct  ctgatgagc 1139

```

```

<210> 40
<211> 2177
<212> DNA
<213> Homo sapiens

```

```
<400> 40
```

```

ggccacgcgt  ccggtcgcg  ccggcagcga  acagcagcag  cagtcagcct  tcattcagga  60
aagcacgcca  gttgctctca  tgcgtttatt  gtctttcaat  gtgctcata  ttaaaaaaac  120
cacaggagaa  ccaatatgga  aggtactcat  ttatgacaga  ttgggccaag  atataatctc  180
tcctctgcta  tctgtgaagg  agctaagaga  catgggaatc  actctgcata  tgcttttaca  240
ctctgatcga  gatcctattc  cagatgttcc  tgcagtatac  ttgttaatgc  caactgaaga  300
aaatatcgac  agaattgtcc  aggatcttcg  aaatcaacta  tatgaatcat  attattttaa  360
ttttattctt  gctatttcaa  gaagtaaaat  ggaagatat  gcaaatgcag  cggttagcagc  420
tagtgtagta  acacaagtag  ccaagggttt  tgaccaatat  ctcaatttta  ttactttgga  480
agatgattag  tttgtattat  gtaatcaaaa  taaggagctt  gtttcatact  gtgccattaa  540
caggccagat  atcacagaca  cggaaatgga  aactgtttat  gacactatag  ttgacagcct  600
cttctgcttt  tttgttactc  tgggtgctgt  tectataatc  agatgttcaa  gaggaacgag  660
agcagaaatg  gtacagtgga  aactagacaa  gaaacttcga  gaaaatctaa  gagatgcaag  720
aaacagctct  ttacaggttg  atacacttgg  agctggccaa  ttcagcttcc  agaggccctt  780
attagtcctt  gttgacagaa  acatagattt  ggcaactcct  ttacatcata  cttggacata  840
tcaagcattg  gtgcacgatg  tactggattt  ccattttaa  aggggttaatt  tggaagaatc  900
ttcaggagtg  gaaaactctc  cagctgtgtg  tagaccaaag  agaaaaaaca  agaatcttta  960
tgatttaact  ccggtttgata  aattttggca  aaaaacataa  ggaagtccat  tcccagctta  1020
tgcagaatac  gttcagcag  aactagaatc  ttacagagca  caggaaagat  aggtcaaacg  1080
acctaaaaag  attatgggag  tagaagggga  agatgaagg  gccataagta  tgccttctga  1140
caataccgct  aagctaactc  cagctgtttg  ttctttggca  gaactcctgt  agaaaaaag  1200
acttattgat  ctccatacaa  atgttgccac  tgcgttttta  gaacataata  agcgaagaaa  1260
atttgatgta  tattttgaat  atgaagaaaa  aataatgagc  aaaactactc  tggataaatc  1320
tctctagat  ataatactag  accctgatgc  aggaactcca  gaagataaaa  gaggttgttt  1380
tcttatctat  tataataagca  cacagcaagc  accctctgag  gctgatttgg  agcaataata  1440
aaaaagcttta  tccagagtc  gatgcacact  taactcttta  caatatatac  gagtggaal  1500
ggcttttacc  aagatggcct  cagctccggc  cagctatggc  agcactacca  ctaaaacca  1560
gggtctttta  tcacagagtc  tgaatacagg  atcacagttt  gtgattgga  gagtgaagaa  1620
cctgggtttt  aaacagcaaa  atctaccctg  tactcgtatt  ttggacaatc  ttagtgagat  1680
gaagtcaaac  cccgaaactg  atgactatag  atattttgat  gccattgttt  tgcggggcaa  1740
tgacagctca  gttcccagaa  ataaaaatcc  attccaagg  gccattgttt  tctgtgtggg  1800
aggagggca  tacatttgat  atcagaatct  tctgtgactac  ataaagggga  aacagtgcaa  1860
acacatttta  ttatggctgca  gtgagctttt  taatgctaca  cagttcataa  aacagttgtc  1920
acaaactgga  caaaagttaac  acagaagaac  cttaactatg  taattactct  ggaatgtgga  1980
taaatgttaa  aagaagaaaa  gttagaagag  caatatgttt  cttctctgtg  aacagtgctc  2040
taacagtgaa  aatcagagtt  atttgttaat  ttttaaggaa  attatatata  taatatgtat  2100
tgattaaaag  aaacatttca  gaaataaaat  ttcaacattg  taiaaaaaaa  gtcggctacc  2160
tcacggata  atatcgc  2177

```

```

<210> 41
<211> 402
<212> DNA
<213> Homo sapiens

```

```
<400> 41
```

```

ggcgaggcc  ccagccagct  caggctacac  tatccaggga  tcagcatggc  cgtccggcag  60
tggttaactg  cctctgacct  ggctgccctc  ctgttgtgtg  acagggaagt  gccagtgcca  120
gcaggaaaag  tccctttctc  aagaatgcca  atctgtgaac  acatggtaga  gtctccaaac  180
tgttccagca  tgtccaaact  ggtctcgagg  actgatgggc  tcacataata  gaatgaatgc  240
cagctctgct  tggccggagt  aaaaaccaaa  caggacatcc  agatcatgaa  agatgccaac  300
tgctgatccc  acaggagcac  ctcaagccat  gaagtgtcag  ctggagaaca  tgggtgggca  360
tggagaggat  atgacatgaa  ataaaagatc  cagcccaact  ga  402

```

<210> 42  
 <211> 1349  
 <212> DNA  
 <213> Homo sapiens

<400> 42

```

cttctttttgc catcccatatt ccttggtgacct gcaccatttc cccaattatt ggccaatccc 60
taggcttttct ggggttttaca atgggttgcga ccacaatcag gctcatagat ggctccaatt 120
taaaaaaataa ggaataagggtg atggataaaa taagcagatc aaggggaagtg tgctatcata 180
aaataaactgt agcttcaaca tcttgagtagc cagtttctctg gcagatagta aaactccaat 240
cacacagggat ttttctcgaa ggggtgtaaa ctgggttgaa aattcttcag tccacagagca 300
gcttcacacat gcccaattaga aactgacaga cactagatgt gcttggaaga ttaaacacta 360
cgtacagaaa cagcaggttac taagctcctc agtagttct tgtctttttt aagtttcgt 420
gaatcgacag ttgtgcacac gtgctatatt ctggtgggtca aaaccaagta aatactgtgt 480
aaagttggca gattttttcca gctaaagatc agaaaaaaca aattttctga taaaacagg 540
ttagagtcag aaacactctc taaagtgcac aactgatggt ccacgatctc aaatagctaa 600
aaactctcgca gaatgggaagg gagagacgtg aaacagggaa ataaattaca gctagtgcta 660
gttaatttag gaaaaaggaa aaataaacca aactcaagtc ggtaaaagttt atcaaaat 720
tcaatgatgt agctttcccc actctctgtc acacacgctt gctaaacaag atattaaatt 780
aaggccaaat ttaacctgaa tgcgtttttt tttttctttt tattaagatc tgagatagga 840
acggctacat tttagactga aaggcagaca ataaaaatggg ccatagaagg ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac gatatataca gcatgtgtgt 960
agctcgaaat aaaaaataaa ggactatttc atgtcatgac tgcttgttgg cttctctctc1020
atatgcatc ctctgtccat tctgtacata ggatgaacca gaaccaaggc atacacaaatg1080
accacaatat ttggcatcat caatatgac ttcaagaac atttctctca ttttggaaaa1140
ggccattctc ttgagcaatg aatcagatcc tgcctgatgt tgggttccta ctgttccag1200
ctctaatctg tctgccacct cctgtaatcc accttgaga ttttctctgt cattttgat1260
gtgaagtacc tcatgaagag ctgcaaaaat ctctaactgt tctgccacct cctgtaattg1320
cgagtcagtg attgacgaaa taatagtgc

```

<210> 43  
 <211> 3552  
 <212> DNA  
 <213> Homo sapiens

<400> 43

```

atttaactctt cattcttcta ctatcccaaa tcttaatttc aatatcaaac ctaattaaac 60
acaatcaactt cccactgtac accaccacat caatcaaaat ctcttcatt attagcctct 120
taccocctatt aatattttcc cacaataata tagaataat aattacaacc tggcactgtg 180
tcacataaaa ttcaatagaa cttaaaaata tgcctaaaaa tgacttttct tctactctgt 240
ttacatctgt agcccttttt gtccacatgat caattataca attctcttca tgatatatac 300
actcagacc aaacatcaat cgattcatta aatatcttac actattctgt attaccatgc 360
ttatctctac ctacgccaac aacatatttc aacttttcat tggctgagaa ggggtgggaa 420
ttatatcttt ctactaat ttgagtggt acggacgaac agacgcaaat actgcagccc 480
tacaagcaat ctctataac cgcatcggag acatcggatt cattttagct atagtgtgat 540
tttctctaaa cataaactca tgagaacttc aacagattat attctccaac aacaacgaca 600
atcataattcc acttataggc ctattaatcg cagctacagg aaaatcagca caatttggcc 660
tcacccatct accactatca gcaatagaag gccctacacc agtttcagca ctactacact 720
caagtacaat agtagttgca ggaattttcc tactggtccg attccacccc ctacgacta 780
ataataactct tattttaaca actatacttt gcctcggagc cctaaccaca ttatttacag 840
ctatttggct tctcacccaa aacgacatca aaaaaatcat tgctttctct acatcaaggc 900
aactaggcct gataaagtgt acgctaggaa taaaccaacc acactagca ctactacat 960
tctgtaccca cgcattcttc aaagctatac tctttatagt cctcgggtca atcattcata1020
gctcgggaca cgaacaaagac atccgaaaaa taggaacacat ccaaaaaact ataccattca1080
ctatcatcag ctctagtaac ggaagcctcg cctccacagg aataccattc ctaacagggt1140
tctactcaaa agactctaat attgaagcaa ttaataactg caacaccaa cctcggagcc1200
taactaattac actaatcgcc acttctataa cagctatgta cagcatagca atcatttact1260
tcgtaacaaat acaaaaacgg cgctttcccc ccttaacttc cattaacgag1320
acgtcataaa cccaatcaaa cgcttagcat tcggaagcat ctttgcagga tttgtcatct1380
catataatat tccaccaaac agcattccag tctccacaat accatgattt ttaaaaacca1440

```

```

cagccctaata tatttcagta ttaggattcc taatcgcaat agaactaaac aaacctaaccal500
taaaactatc aataaataaaa gcaaatccat attcatcttt ctgggggttt1560
tcccatctat tattcacgcg attcacacca ttaaaatctct caacctaaagc ctaaaaaacat1620
ccctaactct cctagacttg atctgggttag aaaaaaacat cccaaaatcc acctcaactc1680
ttcacacaaa cataaaccat ttaacaacca accaaaaagg cttaattaaa ttgtactctta1740
tatcatctct aattaacatc atcttaatta ttatcttata ctcaattaat ctcgagtaac1800
ctcgataata ataaaaatc cgcgaacaaa agatcaccca gctactacca tcattcaagt1860
agccacaact tatattgccc ctaccccaat cctctcttcc aacataactc caacatcatc1920
aacctcatat atcaaccaat ctcccaaac atcaagatta attactccaa ctctatcata1980
ataatataag acacaaatta aaaaaacctc tataatcacc cccaatacta aaaaacccaa2040
aattaatcag ttagatcccc aagtctctgg atattctcca gtacgtatag cagtctgata2100
tccaaacaca accaaatccc cccctaataa aattaaaaaa actatataac cactctgata2160
tccacccaaa cctaaaccca ttaaacaccc aacaaaccca ctaacatta aacctaaacc2220
tccataaata ggtgaaggct ttaattgctaa cccaagacaa ccaacccaaa ataatgaact2280
taaaacaaaa atataattat tcattatttc tacacagcat tcaactgcga ccaatgacat2340
gaaaaatcat cgttgaattt caactacaga aacaccattc ggatccatga aaaaacaccc2400
cattatttaa aattattaac cactcattca ttgacctacc tgccccatcc aacattctac2460
catgatgaaa ttgtgggttc ctctcaggag tctgcctaat agtccaaatc attacaggtc2520
ttttcttagc ctatcacata acatcacaga caataacagc cttttcatca gtaaacacac2580
ttttgctaga cgtaaaattac ggggtgactaa tccgatatat acacgcaaac ggagcctcaa2640
tattttttat ttgcttattc ttctcatgtc gacgaggctt atattatgga acacatttat2700
ttatagaaac ctgaacattt ggagtaactt cactgtctgc agtcatagcc acagcattta2760
taggctacgt ccttccatga ggacaaatatt cattctgagg tgccaagatt atataacac2820
tccatcacgc catcccatat attggaacaa ccttagtcga atgaatttga gggggcttct2880
cagtagacaa agccacactt acccgattct tcgcttccca ctctcatcta ccatttatta2940
tcgcggccct agcaatcggt cactcctctc tccctccaga aacaggatca aacaacccaa3000
caggattaaa ctcagatgca gataaaaatt catttcaccc ctactatata atcaagata3060
tccataggtt tctctatata ttcttaattc tcaataacct agtattatbt ttcccagaca3120
tactaggaga cccagacaac tacataccag ccaattctacg ctcaatcccc ccccatatta3180
aaccgcgaat atatttccca ttgcatagc ctcaatcccc aataaaactag3240
gagggtgtct agccttaatc ttatctatcc taatttttagc cctaataacct ttcttcata3300
cctcaagaca acgaagccca atattccgcc caatcacaca aattttgtac tgaattcctag3360
tagcccaact acttatctta acctgaattg gggggccaac agtagaacac ccatttatta3420
tcattggcca actagctccc atctcatact tctcaatcat cttaattctt ataccaactg3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaac acgatcggtt3540
gacatatagg gc

```

3552

```

<210> 44
<211> 601
<212> DNA
<213> Homo sapiens

```

```

<400> 44

```

```

tttttttttt tttttttttt tgcaattcaa atgaacgttt atttcttaaa cccacacaga 60
gtaaggggag agcttagaga tgctcggcac agcatcttct atccaggatc acctctcgt120
tctttctctt ttgctgggag catcttagat ttatattcatt ttctacaaag ctaatatcct180
gaatggcagt cgcaggttta ttcaaaagtt ggagttctct cagggaagtag gggagactgg240
attccagcgt aatggaaatt tctactgtgat gtctgtgttc tcatgtaatt ctccagaaa300
gcgcgaggag actgtctcaa catcagtaga gaactcagaa ttctgtttgt ttgcggtcgg360
cgtgaaagtc atgatctgct cagagtcagt gcttaaatca ctactctgat aatcctctag420
aggagctttt gtccctctgt atgatccag ttggtcaaa agtgaattta gtaggtcaat480
gattgaaatt tgtagttctt tattgattga aactaatctt gacaggggga aaacacagtt540
cagaccacag aagacagtga tcaccaggac ctgtaaaagc atcatgcttt agtaggggtta600
a

```

601

```

<210> 45
<211> 2147
<212> DNA
<213> Homo sapiens

```

```

<400> 45

```

```

agaaggggaa caaaaaaaaa aatatctgaa ttttgaaaaa ccacaaagct acaacactga 60
ccctctcttt tttttgagac ggagttttgc tcttgttacc caggctggag tgcagtgccg 120
tgatcttggc tcactgcacac ttccgtctcc cgggttcaag tgattctcct gccctcagcct 180
cccaagtagc tgggtttata ggtgcccgcc accagaccgg gctaattttt tagtttttagt 240
agagacgggg ttccaccagc ttggccaggc ttggtctaaa tgacctcttt atttttaact 300
tggtactctt ctattctgcc aaaagacaat ttctagagta gttttgaatg ggttgatttc 360
ccccactccc acaaaactctg aagccagtgt ctagtctact aaaaaaagag ttgtatataa 420
tatttaagat gctgagttatt tcataggaaa gctgaatgct gctgtaaagt gctctttaag 480
cttttttttt ttttaatccc ctctcaatga atgaactag ggaatttcca ggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt ctcttctgtt tgagaagcag 600
tggttggggc atttttaaga ttggtggcta ctcttgtttt ccctcatgat aataaatttg 660
tcataactca gtaaacatgaa ctgccccta gaggtagttg ttaataattt tgaaattatta 720
aggtcttgcc aagctcttga tgattcacac ctgtactact gattattaag caggacagac 780
tgagctttct gttgcaataa ctttggagga gaaagtaatt tctaaatata cagagaggt 840
acttgactat atatgttgca tctctgctct ccctcatat taattttga taaagatttt 900
aatttatgta aaactcttaa agcagaatca aagctctctt tggggaaagt gcaagctttt 960
aggtatggca agacctgtga tgaatgtac caaagcatta ccgcatggta gagaacacac 1020
tcgattaaaa atgttaagct ctgtgaaaaa taaaatgtgc aagctcttcc gatggcaca 1080
aacaagggtt aatgctcttt ggggcacatt ctttagaggg ctgtctgagt ttgtaaatat 1140
aatcgacttt tgtttgtgtt acatgacttc ctgtcactca ttgaaaaact gcacaattca 1200
gtttcagctc tggattactt cagttgacct ttgtgaaggt ttttatctgt gtagaatggg 1260
tgtttgactt gttttagcct attaaatttt tattttcttt caactctgat taaaagttaa 1320
acttactaaa agaaaagagg ttgtgtgtca cattaaatgg ttttgggttg gctctcttta 1380
gtcaggtctt ctgaaccatt agatatcctg aacttagagc tcttcaatcc taagattttc 1440
atgaaaagcc tctcacttga acccaaacca gagtactctt actgcctctt tctcaaatgt 1500
tcaggaaaaa catgtccagt tcagttcttt caaaatgagg gagaacattt tgcctgcctt 1560
gtaatacaaa gactcagtcg ttatttttta aactgcattt taaaaatttg atagtataat 1620
aacaataaag agtaagccac cttttatagg caccctgtag ttttatagtt cttaactcaa 1680
acattttata ttctcttctt ttgaaaaaaa cctacatgct acaagccacc atatgcacag 1740
actatcacgt gagttgagtt ggctctccca cagctctttga ggtgaattac aaaaagtcag 1800
ccattatcat ctctcctgag ttattgaaat gatttttttt gtacattttg gctgcagtat 1860
tggtggtaga atatactata atatggatca tctctacttc tgtattttatt tatttattac 1920
tagacctcaa ccacagttctt ctttttcccc ttccacctct ctttgccctgt aggtgtactt 1980
gtatgtagtc atgcactttg tattaatata ttagaaatct acagatctgt ttgtgacttt 2040
ttatactggt ggatctttat aatcaaaact ttactagggt tattgaataa atctagcttt 2100
actagaaatt aaaaaaaaaa aaaaaaaaaa ctcaagacta gttctct 2147

```

```

<210> 46
<211> 623
<212> DNA
<213> Homo sapiens

```

```

<400> 46

```

```

cccacgcgtc cccggaaaag cggcgggcgg cgacaggacc gaggggcctt agttgggtggg 60
caagtcgggg atcccagaaa gagaagcgtg acccggaagc ggaacacgggt gtccgtcccal 120
gctccggcct gccagtgaag ttctaccatc ttgtcggggc ccggaagacg 180
ccagaggagc tactgcggca gaaccaggag gccctgaacc gtgccatgag ggaagctggac 240
cggagcgcag agaaactaga gaccaggag aagaaaatca ttgcagacat taagaagatg 300
gccaagcaag gccagatgga tctgtctcgc atcatggcaa aagacttggt gcgcaccggg 360
cgctatgtgc gcaagtttgt attgatcgcg gccacatccc aggtctgtgc cctcaagatc 420
cagacactca agtccaacaa ctcgatggca gaaccgatga aggggtgcac caagggcatg 480
ggcaccatga acagacagct gaagttgccc cagatccaga agatcatgat ggagttgag 540
cggcaggcag agatcatgga tatgaaggag gagaggattg aattgttgca tttgatgatc 600
cgtgggtgtt tgggggaagt tta

```

623

```

<210> 47
<211> 781
<212> DNA
<213> Homo sapiens

```

```

<400> 47

```

```

gcggggtatat tgcaagcttg aaaaactaaa agatctgtga aagatgctgc caagaaggcc 60
cagaaggatg tctgcagatg tctggccaag gagatgatca ggtcaaggaa ggtctgagc120
aagctgtatg catccaaagc acacatgaac tcaagtgtca tggggatgaa gaaccagctc180
gcgggtcttgc gagtggctgg ttccctgcag aagagcacag aagtgatgaa gggccatgcaa240
agtcttctgt agatccaga gattcaggcc accatgaggg agttgtccaa agaaaatgatg300
aaggctggga tcatagagga gatgttagag gacacttttg aaagcatgga cgatcaggaa360
gaaatcgagg aagaagcaga aatggaaatt gacagaattc tctttgaaat tacagcaggg420
gccttgggca aagcaccocg taaagtgaat gatgcccttc cagagccaga acctccaggaa480
gcgattggag cctcagagga tgaggggagg gaggaagagg ctctggaggc catgcagttc540
cggttgccca cactccgcag ctaggggctg cctaccoccg tgggtgtgca cacactctcc600
tcaagagctg catcttttatg tgtctcttgc actacacctc tgtgtgagg actaccattt660
tgagagaagg tctgtttgtc tcttttcatt ctctgccacg gttttgggat cgcaaggga720
ttgtctttat aaaaatggca taaataaagt catcattttt aggaaaaaaa aaaaaaaaa780
a

```

<210> 48  
 <211> 1714  
 <212> DNA  
 <213> Homo sapiens

<400> 48

```

gttgcgacat gcagtcgccg ggaggaactg tgtctcttga gggcgacget agggggcccg 60
aagggaactc gcgaggcgaa ggtgaccggg gaccgagcat ttcagatctg ctccggtagac 120
ctgggtgcaac accacatgat tgggtgcaag gctgggtgtg ctccggacac taccttctag 180
gggtttccac ccagctttca ccaaggccct cctgtgtgtg aagaattcca tcacgagaa 240
tcaatggctg ttaacacctc gcagggaata tgccaccaaa acaagaattg ggatccggcg 300
tgggagaact ggccaagaac tcaaagaggc agcattggaa ccacgcatgg aaaaaatatt 360
taaaatgatg catagtggaa gatggtttgt tgcgtggagg gctgtgtgtg gctctggagc 420
attgtgtcat tatggcttgg gactgtctaa tgagattgga gctattgaaa aggcctgtaa 480
ttggcctcag tatgtcaagg atagaattca ttccacctat atgtacttat gaggagat 540
tggtttaaca gctttgtctg ccatagcaat cagcagaacg cctgttcca ccaattctac 600
gatgagaggg tcttgggtga caattggtgt gacctttgca gccatggttg gagctggaat 660
gtctgtacga tcaataccat atgaccagag ccaggcccca aagcatcttg ctgtgtgtct 720
acattctggt gtgatgggtg cagtgtgtgc tctctgaca atattagggg gtccctctct 780
catcagagct gcagtgtaca cagctggcat tgtggggagg ctctccactg tggccatgtg 840
tggcccgagt gaaaagtctc tgaacatggg tgacccctcg ggagtgggcc tgggtctcgt 900
ctttgtgtcc tcatgtggat ctatgtttct tccacctacc acgtgtgctg gtgccactct 960
ttactcagtg gcaatgtacg gtgattagt tcttttcaag atgttctctc tgtatgatac1020
ccagaagctg atcaagcgtg cagaagtatc accaatgtat ggaagtccaa aatatgatcc1080
cattaaactcg atgctgagta tctacatgga tacattaaat atatttatgc gagttgcaac1140
tatgtcggca actggaggca acagaaaagaa atgaagttag atagtttgta caagcagct1260
tcttgaagtg ttagaagata agaaacatgt catcatattt aaatgcagta atcctctccc gtaatgtgac1320
gcctcaggtc tgcctttttt tctggagaaat tctgagtgat tctcaattta ttctgtgaa 1400
acacattttc aattctcatg tttgagtgat tcttaaatgt tttgttgaa 1500
aagtttgtgt agtgagaatg taagtctttc atattttttt ggaagtgcaga atattgtaat1560
gtactactaaa tttagcaaac ctgtgtttgc atagaaaggc agagaaggag ttaacctcag1620
taattctcat agtgatttgg agctttggta agcactctgg gttatttgga ttaggtgagg1680
tcttttgttt ttttaataac ttaggaaact ggtattgggg aaca
gagcccggtg ggaacacggg

```

<210> 49  
 <211> 831  
 <212> DNA  
 <213> Homo sapiens

<400> 49

```

cacccccagg ccctgctctg aggcaccgag aaacgaggag gcccggtggc agtctccacg 60
tgggtaccgc gcctctccgc gcccgtagcc accccgcgcg cggaagccga catctcgagt120
tctggcagaa gcaattttgc cgccgaggag cggacgggca ggaacccaat aagctgctc180
gcctcggagc tgaagcccggt actcaagatg gcggctcccg gcggcgctgg ccagtacta240

```

```

gaaggcgagg cgccgcggga ccatggcggc ggccggcgag gagcgagtc cagaggacgg300
agaagacgag gaagaggagg agcagttggt tctggtggaa ttatcaggaa ttattgattc360
agacttcttc tcaaaatgtg aaaataaatg caaggttttg ggcattgaca ctgagaggcc420
cattctgcaa gtggacagct gtgtcttttg tggggagtat gaagacactc tagggacctg480
tggtatattt gaagaaaaatg ttgaacatgc tgatacagaa ggcaataata aaacagtgtc540
aaaaatataa tgccatataa tgaagaagct cagcatgaca agaactctcc tgacagagaa600
gaagggaagg gaagaaaaa tagtggggtt ggaatggctg caaataaagg ataagtatt660
ctctcatcga cccaacatga tttgtaactt tctacatgaa aatgaagcag aagaagtgt720
agccttcagg ccagataaat ctttggaaat ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaacgg gggttgtgtt aaccggggga acccattgcy ccttgggaat t 831

```

```

<210> 50
<211> 744
<212> DNA
<213> Homo sapiens

```

```

<400> 50
tgaagttcta agagctttcc aagtttggga aggtgtccgg gttttctgcy attacttttc 60
tgagactgaa cgggaagtcac cctttgtgct ttatgcggtg attttaatga taggtgtcat120
atataggagc gagtaatctg tttacattct gttcttctcg atgcactcac aagcgggttaa180
ctaggtgaca agaaaacaaa gatcttattc aaaagaggctc ttacagcaac ccacgtctc240
atcttcccat agtaaaagatg accggccctt gaggttaagct acaggcaaca ccaactccg300
gtttctcttg cgccctggct caagatggcg gatgaagcca cgcgactgtg tgtgtctgag360
atcccggtgc tgagactcaa cgccggaccg cgagatcggt agttgtgggt gcagcgactg420
aaggaggaaat tcagctccct tatccggtat ttgggaacac acaagaatgc tgacaaagt480
tggtttccgag tggagtccaa caagggaagg aactcggtgt ttggaataat ctggtatata540
catgacctcc tgaatatgac gtgttgacatc gagtttgaca ttctctatca atatcctact600
actgccccag aaattgcagt tctctgagct gatggaagaa cagcaaaagt gtacaggtag660
gactgaatag gagatggcaa agagtcaaaag aaagccttaa ggaagaactc cgtggcgagg720
gggagagcat caggaaagagt agct 744

```

```

<210> 51
<211> 2017
<212> DNA
<213> Homo sapiens

```

```

<400> 51
tgccaccgga ggcgcgagc aagatggcgg cgcgagtgct gcgcgcccgc ggaggcgctg 60
ggccgcggcg cctctgcagc gggcgccccc ctgcagcttc ctgccaggcc tccggacatg 120
gacatctctc agcaacagat ctcgagaaga cagctggcta aaatccttat ttgtccggaa 180
agttgatcca agaaaagatg cccactccaa tctcctagcc aaaaaggaaa caagactct 240
atacaataa cagttttcaca atgttaaacc ggaatgccta gaagcataca acaaaattg 300
tcaagagggt ttgccaaaga ttacagaaag aactcaactac ccttgtactt tgtgtgggag 360
ttggaacacg ttgtatggcg agcaggacca agctgtccac ctctggaggt atgaaggagg 420
ctatccagcg ctacagaga tcatgaataa actcagagaa aataaaggaa ttgtggaatt 480
tcgtaaggca agaatgagca tgcttctctc caggaaagaa cagctcctgt ttgagttcag 540
tttctggaat gagcctgtgc caagatccgg acctaatata tatgaactca ggtcttacc 600
actccgacca ggaaccatga ttgaatgggg caattactgg gctcgtgcaa tccgcttacc 660
acaggatggt aacgaagcgg tcggaggatt cttctctcag attggcgagc tgtacatggg 720
gcaccatctt tgggcttaca gggatcttca gaccagggaa gacatcacgga atgcagcatg 780
gcacaaacat ggctggaggg aattggtata ttacaagatt ccacttattc aggaaatgga 840
atccagaatc atgattccac tgaagacctc gccctccagc taaagctgta gagtttctat 900
gtgcctacat acattctgtg gacaagattt tgtcgtaaat taattttaat ttgtgtacaa 960
tgaaaaaaga acaactgagg ttttaagctg ctgtatatag cttgtgagaa acctctttct1020
tttaaaattt acataattcac aagaaaaggaa agaattacag ttggactgat tgtgacagt1080
ccttctcgct cctcttgaaa caccctgtgt tgtccagtat accttataac acttagccaa1140
ttctcccacc cctccagaag gggctccagt tgaattctga atcatcttga aactaagatt1200
ccaacccaca aaaaaattta gccattttct tactaaaaaa accaaaaaaa caaatctgt1260
ttataatcac agatttttag acaaaatttc tgatcagga agaaatacaa attttgtcat1320
gtttctcaag cagtttttct gagtagtttc cgaggaggaa caaattacaa gtgtaccaa1380
taactgaaaa tgttttaact cactctcatt tgaagcagc ccacatagta gacaatgggt1440

```

```

tttccaagct  gggcaaggta  catttaaatca  gtaaatcagt  ttcacatcat  gtattgtgat1500
gtttcaatgt  gagacacaaa  aacaatggct  tgaacctgt  gtatcatatg  tgattttgaal560
tgaaacacct  tgaatagcac  taatttttat  ttgtgggtatt  ttctataaac  aaaaacaagta1620
cgctcaggaa  aagagggtttt  attttgtaaa  cgatcatttg  tgacctcaga  cactctctgg1680
ctaataatttt  aataagctca  cagcagataa  ttctgagatc  atgggtgagg  ggtggtgcat1740
gttgagattt  aaattggcat  aaagctgcat  actttttgtc  tagctgtttg  atttcatttt1800
ttaatatagtt  atgccaattt  tgtgactgtt  accatgtgaa  agtccctgtt  aaatgaacaa1860
ttgtctgccc  cacaatcaag  aatgtatgtg  taaagtgtga  ataatctcta  tatcaaatgt1920
caaacctttta  catgtgaatg  attttctcaa  agaactataga  aaagtcaata  aaatcctctt1980
aatttccaca  aaaaaaaaaa  aaaaaaaaaa  aaaaaaa
2017

```

```

<210> 52
<211> 856
<212> DNA
<213> Homo sapiens

```

```

<400> 52
cgcagtgcgc  aggcgtgggg  ctctctcctt  gtcagtcggc  gccgctgcgc  ggctgggtggc  60
ctctgtggcag  cggcggcggc  aggaactcgg  cactatgagc  ggcttcagca  ccgaggagcgc120
cgccgcgccc  ttctccctgg  agtaccgagt  ctctcccaaa  aatgagaaaag  gacaatcatat180
atctccattt  catgatattc  caatttatgc  agataaggat  gtgtttcaca  tggtagttga240
agtcaccagc  tgggtctaatg  caaaaatgga  gattgtgtaca  aaggaccctt  taacacctat300
taacaagaat  gtgaaaaaag  gaaaacttcg  ctatgtgtcg  aatttgttcc  cgtataaagg360
atatactcgg  aactatgtgtg  ccatccctca  gacttgggaa  gacccagggc  acaatgataa420
acatactggc  tgttctgtgtg  acaatgacct  aattgatgtg  tgtgaaattg  gaagcaaggta480
atgtgcaga  ggtgaaataa  ttggcgtgaa  agttctatggc  atatttgctt  tgattgacga540
aggggaaaac  gactggaaaag  tcattgccat  taatgtggat  gatcctgatg  cagccaattaa600
taatgatact  aatcatgttca  aacggctgaa  acctggctac  ttagaagcta  ctgtggactga660
gtttagaagg  tataagggttc  ctgatggaaa  accagaaaat  gagtttgcgt  ttaatgcaga720
atttaagaat  aaggactttg  ccatgtatat  tattaanaagc  actcatgacc  attggaagc780
atttagtgact  aagaaaaacga  atgggaaaaag  gatcatgttg  attgttcaac  tttctgttg840
gcccctcaaa  gtgtgc
856

```

```

<210> 53
<211> 540
<212> DNA
<213> Homo sapiens

```

```

<400> 53
gcatagacaa  agggcctcag  aatcgccgag  gcgcaattgt  gccctgggtc  gccaaagtgt  60
cgttcccaaa  gtataagcgc  tcgagcctgc  gcactctgcc  tgagaccctc  gaccagccgc120
aatacaacat  atctccggaa  acccgccggg  cgcaagcgag  cggttgccca  taagagccca180
gctgaaacga  gagtacctgc  ttcatgacaa  cgatcccaac  cgccgagggg  tcatcgaaaa240
tctctccttt  cttcgttggg  cctatgcaag  aacaataaat  gtctatccca  atttcagacc300
cactcctaaa  aactcactca  tggggagctct  gtgtggattt  gggccccctc  ttctcattta360
ttatattatc  aaaactgaga  gggataggaa  agaaaaaact  atccaggaaag  gaaaattgga420
tcgaacatctt  cactctctcat  attaatgtctg  gcaatgatga  ctatatgtat  tctcgtctaa480
ataaatcatc  tattaatcat  taaaaaaaaa  aaaaaaaaaa  aaaaaaaaaa  aaaaagtgc540

```

```

<210> 54
<211> 1912
<212> DNA
<213> Homo sapiens

```

```

<400> 54
tgtgtgaggc  ccaacagcgg  aatcatcgat  gcaggggcct  gaattaatgt  atctgtgatg  60
ttacagcctt  tcgattatga  tcccaatgag  aaaagtaaac  acagggtatg  gtctcagtcta 120
gtttgtctcc  aactgacact  tcagatatgg  aagcagtatg  aaggagagca  aaaccgggaag 180
accttatgga  ttcaaaaact  agatgtgtgt  ttgaattgcc  agcagagaat  gataaacacc 240
atgatgtaga  aataaataaa  attatatcca  caactgcctc  aaagacagaa  acaccaatag 300

```

```

tgtctaagtc tctgagttct tctttgggat acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaaggtgaa gtccagaggc tacggggagga gaaccaagcg ttcgaaggag 420
aagatggagt gcggatgagg aagacagtgc agagcaacag ccccatTTca gcattagccc 480
caactgggaa ggaagaaagc cttagcaccg ggctcttggc tctgggtggt ttgtctctta 540
tcgttgggtg aattattggg aagattgcct tgttagagga gcatgcacag gatggtaaat 600
tggattgggt gatccaccat atcatgggat ttaaatTTat cataaccatg tgcataaaga 660
aattaatgta tgaatgacat aaatataatg taacgatctt ttaccctttaa ttaccctctc ctgcacacac 720
atacacagat acacacacac aaatataatg taacgatctt ttagaagaat aaaaattgat 780
agtaactgat tgagggggaa aagaatgata tttattaaat acaaggggaa ccatgagtaa 840
tgccacaatg gcatattgta aatgtcattt taacacattg taggccttgg tacatgatgc 900
tggattacct ctcttaaaat gacacccttc ctgcctctgt ggtgctggcc ctggtggagc 960
tggagcccaa catgtctggg agtgcgggtc gctccacaca gtatgcccc cgtggccca1020
tcccggccga ggcgtcttcc cgtctcttca gttctgtcca agccatcaga cctctgggac1080
tgaatgaacg agtcagaagc ccaaggaatg tgcactgtgg cagcatcaga cgtactcgt1140
ataagtga gaaggtgtgtt gactgattga cccagcgctt tggaataaaa tggcagtgtc1200
tgtttacctt aaagggacca agctaaattt gtattgggtc atgtagttaa gcaaacctgt1260
tattcagaga ggcgtgtgtt atatttaact tatttaattg atttcatctc atgttttctt1320
attgtcacia gagtacagtt aatgctcgtt gctgctgaac tctgttgggt gaactggtat1380
tgctgctgga gggctgtggg ctctctctgc tctggaagt ctggtcatgt ggaagtggg1440
ttctattgga ggagtgaaat tctcagtagt gaagtgtttt ttctgggtca gtaataaaca1500
gaagagtagt cagctctcta tctcagtagt gacagtcaac tctaggttaa cttttttaa1560
cagcgcccaa gtccaagtct gagcctgacc tcccccttgg gacctagctt ggaatcagg1680
caaatggatc gggctgcaga gggttagaag cgggggcaac agcagtgtgt ggtggggagc1740
aaggggaagc agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga1800
atataattta tgccataaaa gaccaaccca gttctgtgtg actatgtagc actttgaa1860
gaaaaattat aataaagccc caaaattaa gaaaaaataa aaaaaatact gct 1912

```

&lt;210&gt; 55

&lt;211&gt; 1962

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

```

tttttttttt ttttatcgag caagaatctg ttaacagttt tttttttttt tatgttaaat 60
accatgggac aggatgttaa ggaatgaaaa ctacgtcaac aactgcctca caagggataa 120
gaaaaatttt gccatgatat tagcaaaagt aaaggaggaa aaatttacac tgtaagaggc 180
accatttccc caaggaatac ctctggcat ttccctgaat agtgggatta gcaatctaaa 240
taaatcatat ttcaaggagg aacagcaaca gataaaaatt aaagggatta taaaataaac 300
atttacaaga ctctgaacaa ttcttgaact cttattaaaa ccacaagaaa agacaatttc 360
ttattttatg aattctataa aggaactcaat gtgcaactga catctgctag tgatgactgt 420
gtaatatata caactgtccag tagccgaaca gtttgttttt atttgttttt ctaaccgtta 480
gagatcatta aaggcaaaagc ctatatgagc ctgtcacacac aaaaaaatgg tcaccgtggg 540
ccatactacc aatgaaattg taggttaaca gaaagtgaat aatcttttct ttggtcaagg aaaaaaaa 600
aaaaaagaaa gcactctgca tgcctcaact tacaagatga atttccctag aaagaatcca 660
atgaaaaatg gtcgaattac aacaagaagt gaaggaaag gactgggtgac atgactctaa 720
agggatcgag ttgaggttga tccaggttta tccgaatgtg ctacctttct cgaagctctt 780
ccttcatctc tcaagtgccg attttcttct gatagcttca catattctcc ctgaagctct 840
ttacactctt ccatagttt ccttgttttg gtatcattaa gtgaaacact gtgtgtgttt 900
ggcataggct gcatctgctt agatgcattc agtgggaacag ctttgttagt atccatatac 960
ttcaatttat cattttcatt gggcatttca aatagccttc tcaatttggg atccatataa1020
tcatcaggtt ttgcctcttt ccacacagct tccatattctg aagtgttttg ttgagcaaaa1080
atttgtctga ccataaaact gtgtttactt ttttctatcg gatctatagc aaagggctgt1140
agcattactg aaacagctcac agtgaccctt gggctcaatt ttccactggt ttccactca1200
cagtcacggc gagggtctgt agtcttcaat ttgaaacaca cttttctatc cgatggattt1260
cgcaattttaa gatttgtagt gactacatct gtgaaggggc ctttgaattt atggtctgtg1320
gcggcatcga ggacaggat ctgctcgtct tgcgcattgg ccttgaggcg gacgccatcg1380
gagagacagc gcagcagagg gggcggtctg ctgcgtgggg gcgggggagc atggcgagag1440
gggagggggg gcgagttcgc atctctcctt ttctgtgta gactctgttc aaccacattc1500
ttatgttggc agactctgct ccagattgat ttttagagca ccatcaactt ccatctctg1560
attctgattt tgttttgttt tgtttggggt ttctgaaact taaaatgctg ccccgaaaat1620
actatatttt tgagtttgtt ttctgaaagc ctccgtgctg ctggaatctt ggggggaaat1680

```



```

acaggatcct tcagcactga ggtgtttaag atttgcaact agcaatgcaa tttttctaa1740
atatggggag atttaccttt attaagaaat tatactaaca attgatgtcc ttgatcattt1800
tatgtttcca tattaccttt gattctacta ttgattgtgtg gtggtgaaac aagatcattt1860
caaacaaaaa ctgttaatttt gttatatattg attcaatgga attttaccaa aaaaaaaga1920
ctaaaaatgt gaaaaaaa aa aaaaaaaaaa aa 1962

```

```

<210> 56
<211> 1458
<212> DNA
<213> Homo sapiens

```

```
<400> 56
```

```

cggctcgagc ggcctcgagat tcgaggtcgt ggtggtcttg gaagagcgtc gaggggggcgg 60
tggacgtgga atggggccgag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtacgaggatc 180
tcacaactgg ggaactcgta aagacgaatt aacagagtc cccaataca ttcagaaaaa 240
aatatcttat aattacagtg acttggatca atcaaatgtg actgaggaaa cacttgaagg 300
tgaaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgagtggaa gctattcaaa ataaggaccg 420
gggcaaatgta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtgaagaa 480
gggatttgtt ctctataaat caaagagtga agaggctcat gctgaagatt cgggtatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttggaga 600
ccttggcgcg ccaggacgtg gcggcagggg aggacgaggt ggaactgggc gtggggggcg 660
cccaaacctg ggcagcagga ccgacaagtc aagtgtctct gctcttgatg ttgatgacc 720
agaggcattc ccagctctgg cttaactgga tggcataaga caacctgggt tctttgtga 780
acccttctgt tcaaaagctt tgcattgcta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattctatc cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat tttagaatgt 960
attggtgaca gggattgttt cataatttct agagattatg cattcttcac gaactctttt1020
gtatttgcgt ttgcaaatat gcaattccaa acttgaataa taggtgtgaa caggtgtgac1080
cagttttaag ctttactctt atttgttatt ttttaattaag gatttagaag ttcccccaat1140
tacaacactg ttttaaatat tggacatact ggttttaata cctgttttgc atattcacac1200
atggtcaact gggacatggt aaactttgat ttgtcaaat ttagctgtgt tgaataacta1260
actatatgta ttttaacctt gttttaatat ttctattttt ggggaaaaat cttttttcac1320
ttctcatgat agctgttata tatatatgct aaactcttat atacagaaat atcagtaact1380
gaacaaatcc aaaaacacat ttggtttatt aaccctggc tgccctggca tggggcccat1440
ttggggctca aattataa 1458

```

```

<210> 57
<211> 2188
<212> DNA
<213> Homo sapiens

```

```
<400> 57
```

```

ggggcccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 120
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 180
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 240
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 300
ccaacctccc cccacccccccc cccctacaa gcaacctggt aagccaacct gaattctact 360
cactctggcg tggaaagtat tatgacagaa tgcgacgagg aggtgatgta tatgatggt 420
gttatggagg tttttagtac tatggtggct ataataatta cggctatggg aatgatggct 480
ttgatgcag aatgagagat ggaagaggta tgggagagaa tggctatggg agagctgggt 540
atgcaagttc aggttttcat ggtggtcatt tcgtacatat gagaggggtt ccttttcgtg 600
caactgaaaa tgactatgct aatttcttct caccactaaa tccaatacga gttcataattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagttttgt acacatgaag 720
atgcagtagc tgccatgtct aaagataaaa ataacatgca acatcgatat attgaactct 780
tcttgaattc tacttccgga ggcggtctct gcatgggagg ttctggaatg ggaagctaac 840
gaagagatgg aatggataat caggggaggt atgggtttgg ttggttatggc cgtgggtggg 900
acaattacag tggaggatat ggtactcctg atgggtttgg ttggttatggc cgtgggtggg 960
gaggcagttg aggttactat gggcaaggcg gcatgagttg aggtggatgg cgtgggtggt1020

```

```

actgaaagca aaaaacaccaa catacaagtc ttgacaacag catctggctc actgactctt1080
ctacacagatt taattctctt tgtatttttaa gaactttata atgactgaaag gaattgtgtt1140
tccaaaattatt atttgggtaaa gcaacagatt gtgactgggaa aatgttttct gttaggtttat1200
ttgttgcata ctttgactta aaaaataaatt tttattatcca aaccactgat gttgatactt1260
tttatatact agttactctc aaagatgtgc tgccttcata agatttgggt ttacacctctg1320
tactatttagt tctacaagaa gtatgtgtgt gtaatttttag aggataatgg ttacacctctg1380
cgtaaaactgc aagtccttaag cagacatctg gaataagact tgacaaaataa tagtgttaac1440
ttttttcttt agttctctct ggacaacact gtaataataa agcctaaaga tgaagtggt1500
tcaggagtat aaattcagct aattatttct atattattat ttttcaaatg tcatttca1560
ggcatagctc tgaacatttg atgatctaag aggtattgat ttctgaaat tcaataattgt1620
gttactctggg tatgagagtg ttggaagctg aattctagcc ctgatttttg gagttaaacc1680
ccttcagcac ttgacggaat taccaaaataa gtctccaaaa aattgatagt tcagggttat1740
cgcaagatgt cttagagtag ggttaaggtt ctgagtga caagaattcca gattaagta1800
cataggttatt tactatggag tataattctc acaattgtat tttcagtttt ctgcccataa1860
gagttttaat aactgtataa atgatgactt taaaaaaatg taagcaacaa gtccatgtca1920
tagtcaataa aaacaatcct gcagttgggt tttgtatctg atccctgctt ggagttttag1980
ttttaaagact ctatatttag caaggaaaag gtgcttttta attttaacct ctttgataca2040
tatggctttt ttccaaattg gctaattggat caaaatgaaa cctgttgatg tgaattcagt2100
tattgaactt gttacttgtt ttgcccagaa atgttattaa taaatgtcaa tgtgggagt2160
aaaaaataaa aaaaaataaa aaaaaaaa 2188

```

<210> 58  
 <211> 1548  
 <212> DNA  
 <213> Homo sapiens

<400> 58

```

ctcgctagtt cgcgcggtag cgggagcgga gagcggacc cagagagccc tgagcagccc 60
caccgcgcgc gccgcgctag ttaccatcac accccgggag gggcgcgagc tgcgcgagcc 120
ggcccacagt accatcacgc caaccatgag cagcggagcc gagaccagcc agccgcgcgc 180
ggcccccccc ggcgcgcgcg cctcagcgcc cgccgagacc aagccccgga ctacggcgag 240
cgcgcgatgc agcgggtggcc cggcgcgcc cccatcgccg gcgcctgccc gcggggacaa 300
gaaagtcctg gcaagcgaag ttttgggaac agtaaaatgg ttcaatgtaa ggaaacggata 360
tggtttctac aacaggaatg acaccaagga agatgtattt gtacaccaga ctgccataaa 420
gaagaataac ccaggaagt accttcgcag tgtaggagat ggagagactg tggagtttga 480
tgttgttgaa ggagaaaagg gtgcggaggg agcaaatgtt acaggtcctg gtgggtttcc 540
agttccaagg agtaaatatg cagcagaccg taaccattat agacgtatc cagctcgtag 600
gggtcctcca cgcgaattacc agcaaaaata ccaagaatag gagagtgagg aaaaagacga 660
gggtccggag agtgtctccc aaggccaggg ccaacaacgc cggccctacc gcaggcggaag 720
gttccacact tactacatgc ggagacccta tgggcgtcga ccacagtatt ccaacccttc 780
tgtgcaggga gaagtgatgg aggtgtgctg caaccagggg cgaggagaaac aaggtagacc 840
agtgaggcag aatatgtatc ggggatatag accacgattc atcagaaggaa aatcaaaggag 900
aagacagcct agagaggacg gcaatgaaga agataaagaa aatcaaaggag atgagacca 960
aggtcagcag ccacctcaac gtccgtaccg ccgcacactc aattaccgac gcagcagccc1020
aagaaacccct aaaccacaag atggcaaaaga gacaaaagca gccgatccac cagctgagaa1080
ttcgtccgct ccgcaggctg agcagggcgg gctgcagtga atcccgctt accatctct1140
ccatcatcgc gttttagtcat ccaacaagaa gaaatattat attccagcaa taagaaatga1200
acaaagatt ggagctggaag acctaaagt cttgtctttt gccggttagc cagataaata1260
gaactatctg cattatctat gcagcatggg gtttttatta tttttaccta aagacgtctc1320
tttttcttaa taacaaacgt gtgttttaaa aaagcctggg tttttcact acgctcttaa1380
aggtttttaa atgtgttcat atcgtgtcaa gtgtgagatt ttaagaactt catttttaat1440
ttgtaataaa agttttcaac ttgatttttt caaaaaaagc aacaactgc aagcacctgt1500
taataaaggt cttaataat tgcctttgtg taaaaaaa ggaatat 1548

```

<210> 59  
 <211> 1254  
 <212> DNA  
 <213> Homo sapiens

<400> 59

ggaccgcttc ccccgagcca gcagcagct ttgacgtcat cgtgcgtgtg gtgccccctgc 60

```

tgccgggggct ggtgattgga ggaacccccc tgtctgacgg agggctgtag cctgtgagca 120
gcgagatcca gggacagagt ctccagctcg ccgcgcgcgc gccagagac 180
tgctgagccc gtccgtccgc cgccaccacc cactccggag acagaacatc cagtcatgga 240
taaaaaatgag ctggttcaga agggcacaact ggccgagcag gctgagcgat atgatgacat 300
ggcagcctgc atgaagctctg taactgagca aggagctgaa ttatccaatg aggagaggaa 360
ctctctctca gtgtgttata aaaaatgtgt aggagccgt aggtcatctt ggagggtcgt 420
ctcaagtatt gaacaaaaga cggaagggtg agagagccaa agtcttctat ttgaaaatga 540
cagagagaaa attgagacgg agctaagaga tatctgcaat gatgtactgt ctcttttggg 600
aaagtctctg atcccacaatg cttcacaaag agagagccaa agtcttctat ttgaaaatga 660
aaggagatta ctaccgtttac ttggctgagg ttgcccgtgg tgatgacaaag aaagggtattg 720
tcgactcagtc acaacaagca taccaagaag cttttgaaat cagcaaaaag gaaatgcaac 780
caacacatcc tatcagactg gggctggccc ttaactcttc tgggttctat tatgagattc 840
tgaactcccg cagagaaaag ctgctctctt gcaaagacag cttttgatga agccatttgt 900
gaacttgata cattaaatga agagtcatatc aaagacagca cgtaataatg gcaattactg 960
agagacaact tgacattgtg gacatcggat acccaaggag acgaagctga agcaggagaa 1020
ggaggggaaa ataacccggc cttcccaact ttgtctgcct cattctaaaa ttacacagtt1080
agaccatttt tcatccatgc tgtcccacaa atagtctttt gtttacgatt tagttttgggt1140
ttatgttaact tctatttgaa ttcttatatt ttccctgtgg gttttatgtt tagttttgggt1200
ggagtaggag ccagtttaac gtgtggggag ttgtctgttt ttctgtcttt ttgcgtcttt cagggtgggt1254
ccagtatggg ggggtgttgg gattttttgt taccagtttt tgagggttt ttgg

```

```

<210> 60
<400> 60
000

```

```

<210> 61
<400> 61
000

```

```

<210> 62
<400> 62
000

```

```

<210> 63
<211> 954
<212> DNA
<213> Homo sapiens

```

```

<400> 63

```

```

cctctctctt ttctttttct tctttttttt ttcctttttt ttttttgtga gaggcgggtc 60
acttttatgg tatagagact gcagagggac caggggcttt agctgttggc agctatgggt120
tccttaatcc agtccacata gttgttagacc ttgggttaga ctccaggcct gttcttctgg180
gcacagccat agccccagga gacaattctt tggagctctc cattggaagc cacaggggcca240
ccagatcatc cctggcagga atccttgcct ccctcgagga agcccacaca gaacatgttg300
ttggttaact ttcccagggt ggaggctctca cactcagcct ggctcagcac aggagcatcc360
aggcactgca gctcgtctgg gtatcgggca ccagaactca gagtgttgcc ccagccggag420
atgagggact cgggtccagc agctggaggg gcagtgggca gagagatggc ggacacgcgg480
gaattgatga gcgcagggtg ggagagcttg atcagagga gtgcattgtc cagagtgctg540
ctgttgtatt tgggggtggc gatgatcttg gccgcattga tgaactgttc atccccctcc600
aggactctga tgttgtgtgc tcccagtcct acctggatgc gggacttgtga ccagtgacct660
gctgcaccca cccactgttc gctgatgagg gacgaccgcg agaagtggtg gccagaattc720
aaggacacct ggtaggggac agaattctcc tcacagatgt agcccccaac gatcttgta780
tcatcatcaa agggggcagc aacagcagct gccaaaagg taaggatcag aagtagattc840
atgggtggtag agtgtgcctg attgctgggt gagaacccgt ctttatacct ccaggaggtg900
gggagaggag gtgtctgtga ggtgagggct actgctctcc ccagcacaaa caca 954

```

```

<210> 64
<400> 64
000

```

```

<210> 65
<211> 2213

```

<212> DNA  
<213> Homo sapiens

<400> 65

```

ggcgggaccgc cggggggctg aggcctgacct ctcgagagac tccctggcgcg gccgtcccg 60
cccggggggccc cagggtgcgct tcccctagag agggatatttc cgggtctcgtg gccagaggaa 120
caaccaggaa cctgggggctc agtctccacc cccagagtggg gcggatccgt cccggataag 180
acccgctgtc tggccctctgag taggggtgtga cctccgcagc cgcagaggag gagcgcagcc 240
ggcctcgaag aactctctgct tgggtggctg aactctgact ttgacctaga gtcatggcca 300
tggcaaccaa agcagggtact gtcaaaagctg cttcaggagt caatgccatg gaagatgcc 360
atgccctcga gaagggccatg aaagggctcgc gcaccgatga agcgcgaat attagcgtcc 420
tgacctaccg caacaccgcc cagcgcagagc agatcaggac agcctacaa agcaccatgc 480
cgagggacct gatagacgac ctgaagtcag aactgagtgg caactcga cagggtgattg 540
tggggatgat gacgcccacg gtgctgtatg acgtgcaa gaactggagg gccatgaagg 600
gagccggcac tgatgagggc tgcccaattg agatcctggc ctcgggacc cctgaggaga 660
tccggcgcat aagccaaacc taccagcagc aatatggac gagcctgaa gatgacattc 720
ctgctgacac atcgtttcatg ttccagcgag tgctggtgtc tctgtcagct ggtgggagg 780
atgaaagaaa ttaatctggac gatgctctcg tgagacagga tgcccagac ctgtatgagg 840
ctggagagaa gaaatggggg acagatgagg tgaattttct aactgtttct tgtccccga 900
accgaaatca cttggttgcac gtgtttgatg aatacaaaag gatatacac aagatatgtg 960
aaccagatga acatctgaa acatctggtg gctttgaaga tgcctctgct gctatagtaal020
agtgcattga gaacaaatct gcataatttg ctgaaaagct ctataaatcg atgaagggtc1080
tgggcaccga tgataacacc ccatcagagc tgatgggttc tcgagcaga attcacatgt1140
tggatattcc ggacacactc aagagactct atggaaagtc ctgtactcg ttcataagg1200
gtgacacatc tggagactac aggaagatc tgcgtgtctg tctgggaga gatgattaaal260
ataaaaaatc cagaaggaca ggaggattct caacactttg aattttttta acttcatttt1320
ctcacactgc tattatcatt attcagaat gcttatttcc aattaaaag cctcacgtg1380
cctcctcaga tatagactgt ctgtattatt attcactat aattagtcac tatgatgctt1440
taaaagctga ctctgacttc aaagcttata agatataaat ggagatttta aagtagaat1500
aaatatgtat tccatgtttt taaaagatta ctttctactt tgtgtttcac agacattgaa1560
tatattaaat tatttccatc ttctttttca gtgaaaaaatt ttttaaatgg aagactgttc1620
aaaaatcact tttttcccta atccaaattt tagagtggct agtagtttct tcaattgaaal1680
ttgtaagcat cgggtcagta agaattgcca ccagtttttc tatatttcat agtcaaggc1740
ttgaaagcat ctacaaatct ctttttttag gttttgtcca tagcatcagt tgatccctac1800
taagtttttc atgggagact tcttccatca catcttatgt tgaatcact tctgtagtc1860
aaagtatacc aaaaaccaat tatctgaact aaattctaaa gtatggttat acaaaccata1920
tacatctggc taccaaacat aaatgctgaa cattccatat tattatagtt aatgctttaa1980
tccagctctg aagtgaattg aaaaaaaat aagcttcaaa ctaggatctc tgggaatgat2040
gtaattgcct gaatttagta tgatataaag aaaaactttt tgtgctaaaa atacttttta2100
aaatcaattt tgttgattgt agtaatttct atttgacgtg tgcctttcaa ctcagaaac2160
attctgaaga tgtacttga ttaattaaa aagttcactt tgtaaaaaaa aaa 2213

```

<210> 66

<400> 66

000

<210> 67

<211> 2878

<212> DNA

<213> Homo sapiens

<400> 67

```

cctcgtgcag gtgcaccgct tggctcctaaa agctctggag gatggccggg catatgggtc 60
tccatgtgtg acaaaacaga tcacaagggt cctaattgaa tbtctgagat aatataaata 120
taatgtggag gctgtggagc tgcataattc gtttaatatg cgtacagatga 180
tcttcaccta gcgcagtc aa tggagaatgg cttaaactac atggctgttg catttgctat 240
gcagttagta aaaaactctgc tgggtggatga aaggagtgtt gctcatgta ctagctcaga 300
tctgttccac accattgaaa cctcatgagc gattaatgct cattccagag gcaatgctcc 360
agaagaatgt ccccgactga tgggaagtgt gcgatccaac tatgaagcaa tggatgatgc 420
tgctcatgga ggccccaaact ttatgatgca ttctgggact tctcaagcct cagagtatga 480
tgacctcca ggctcagagg agaaggcaga gtatctctcg agggaatggg tgaatctcta 540

```

ccattcagca gcagctggcc ggcagcagatc caaagctttc tctgcatttg ttggacagat 600  
gaccacagca ggaattactga agaccgatga tctcataaca aggttcttct gtctgtgtac 660  
tgaaattgtgt gttgaaatca gttaccgtgc tcaggctcctc agcagcagca atctcgtgc 720  
caatcccccc atgatccgag ccaagtgtcta tcacaacctg gatgcctttg ttcgactcat 780  
tgcaactctg gtgaaacact cagggggaggc acccaacctg gtcacaaggc ttaactctgt 840  
gaacaaggct ctctgttatag tagtggggagt tctccttcag gatcatgatg tctcgtcagag 900  
tgaatttcag caactctcct accatcgaaat ttttatcatg ctctccttgg aactcaatgc 960  
acctgagcat gtgttggaaa ccattaattt ccagacactt acagctttct gcaatacatt1020  
ccacatcttg aggcctacca aagctcctgg ctttgttatg gctggctgtg aactgattt1080  
ccatcggtga tttattgcaa gaatgtctgg acataccgca cagcagaagg ggtggcctat1140  
gtatgcacag ctactgatgt atttattcaa atatttagcg cctttcctta gaaatgtgga1200  
actacacaaa cctatgcaaa tctctacaaa gggcacttta agagtgtctg tggttctttt1260  
cgatgatttc ccagagtctc tttgtgatta ccattatggg ttctgtgatg tgatcccacc1320  
taattgtatc cagttaagaa atttgatcct gagtgccttt ccaagaaaca tgaggctccc1380  
cgaccctatc cactctaact taaagggtga catgttgagt gaaattaaca ttgctcccg1440  
gattctcacc aatttcaact gagtaaatgc acctcagttc aaaaaggatt tggattccta1500  
tcttaaaact cgaatccagc tcactttcct gtcgtgatct gcgagaacct acaggtatcc1560  
aatgaaacct ggaattcgcta caacctccag ctcatcaatg cactggtgtg ctatgctggg1620  
actcagggca ttgcgcacat ccacaacaag ggcagcacac ctccaatgag cctcactact1680  
cactcagcac acatgggat acatgggat ctccgaagct ccaatagcca cactcactac1800  
tatctctttt tgaatgcaat tgcaaaatcag ctccggtacc gaggccaata cgaagagcat1860  
ttcagtttga ccatgtctgta ccttttttga gaggccaata gtaaataggc cacactcttg1920  
attcacaagg ttctcttggga acggttgatt taataaaccca cgttttaagt cctggaacca tgaatttga1980  
attaccttca ttgagctgat taataaaccca cgttttaagt cctggaacca tgaatttga1980  
cactgtgccc cagaataatga aagattatct cagtgggtgc ccagctgctg catgggacag2040  
aagcagggccc agcaagtaat ggaagggaac ggtgcagtt agacgaacct catctcctgt2100  
tgtactgtgc agtctagagg ttctactgca cagagtctat aaactgactg aagaactcct2160  
tcaactcttc ctgactttcc cagcctcttg gtttgggggt atctgcccga actactgttg2220  
ggatcagcct cctgtcttat gtggggcagct tccaaagtgt aaatgcattt ttttgactct2280  
tggccaaaat ttgaagatg ctgtgaaat cattttgaac ttgtgtaaat acatgaaaga2340  
ggaaaacctt ttgtcgggac ttcttggctt ttgtcgaagt gtgtccaagg caagtacata2400  
aactgtgtacc ctgttaatga gaggcagctg atgccatgca ctgtctgag ggcatagtct2460  
catgtcttct gacattctct gtgtcccaaa gaatagcaaa aagccagttt gaattattatg2520  
taactttatt ttttaattgt gacaggggac ctggaatac actaagttat taaaaatgtg2580  
gatgtgtcag aattggatat tccaggaac atgggaaggc ctactattg gaatcccatg2640  
agtttccatt ttgtctctac ccaaacgtat tccaaagctg actgcatttg taccatctta2700  
ttcttttttg gggattatca cctcagccgc ctgagatggg ggtcagctct tatcataaag2760  
ggaaaaccga ccaggcctaa agcccacccc ctacctcac ccccccaac atctctcct2820  
gaaactttaa aaacagtggt ggattttagg gaaagggaac ccaaaaccgc attaatgt 2878

<210> 68  
<211> 701  
<212> DNA  
<213> Homo sapiens

<400> 68

atgatatttt ggaatgtatg ttttgattgt ttaaatctta aaaagtaatg ggaatctttg 60  
acctgtgggt atgtttttatt tttatgtgtg caaatctttaa ccatattctt tcttagttaa120  
agaggaataaa gcaagttgtct ccagaaaaac ctgtaaaaga acaaaagaca ggtgagact180  
cgagagccct gtcatcttct aaacagagca gcatgataac atgtttcaga240  
ttgggaaaaat gaggtagctt atgttttcgg atttttaaagg caaagtgtcta attgatatta300  
gagaacattg gatggatcct gaagggtgaa tgaaccaggg aagaaaagggt atttctttaa360  
atccagaaca atggagccag ctgaaggaaac agatttctga cattgatgat gcagtaagaa420  
aactgtcaaaa tctcagccat ataaataaaa cctgtactgt tctagtgtat ttaactctgtc480  
ttttttacatt ggcctttgtt tcttaaatgt tctccaagct attgtatgtt tggatgtcag540  
aagaatttgt aagatgaata ctttttttfa atgtgtcata ttaaaaatat tgagtgaagc600  
taattgtcaa ctttattaag gattactttg tctgcccacc acctagtgtg aaataaaatc660  
aagtaataca atcttaaaaa aaaaaaaaaa aaaagtcgag c 701

<210> 69  
<211> 817  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

gttttttttt tttttttttt ttttttttaa gcacagaaaagg cttttattac cacagaggaa 60
atcaggaagt gctggaggca gcttcgttag ctgtgtgtag agggaggagg cagcaggcgg120
gaaccggtca tcaatcatgt ctgggcagtc tcccaaccaa caggtttgtt tgggtcaggal80
gagggtcttt ctgggcgtgtg tgtgtgtatg atcaggaaagg tcagcctcaa caaatggggt240
tcttcttggg catagagcag ccagaatcgg ggacacagca tgacacagaca ccacttaaa300
atggaataca aattagggttc attacatcag gaagtacatt tcaccctgat catataaagg360
ggacaaggga gcaactgggt ctactggata gcctttcttt tagataaagt gcttttaaaa420
gtttaaactat ggacagggtc ttccctcagc taacagcaag cagcacacaa tcccaagtca480
ccttgaataa gctttgttat ctttgttatc tgtttattat tggatttga acgaaatgca540
tggagtagca gccggttaga gaatcctgtt tgatctggaa attttccgtg gagagcccaa600
aaggctggag aaccaagttc ccaagatctt ttaattacc taacatctct tcttttagtc660
ttgataacg tttctcaatt tgcttaggta atctcataca agcttctctt gcttgatgta720
ttgtagtagg ttccgcgctg ctgtcccttc cctgatacaca cagctaacga ggctcctcca780
gcatttctgt atttctctgt tggtaataaa agcttttc

```

&lt;210&gt; 70

&lt;211&gt; 2686

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

```

gcaaggccta ctgtcgctgt ggagggaggg tgtagccggt ctttgggggt agggcgtagt 60
ggcggaagag gttcggcgcc tgatggcgga tcaggatcgg aagcctgcgt aacttctctc 120
cttgatccgg gactctttcc actgatttca caatgacatc ctttcaagaa gtcccatatg 180
agacttccaa ctttgcccat gtcatctttc aaaaatgtgg caaagagttac cttcttaagt 240
cacactgtga atgtcattac accttaactc catatatcca tccacatcca aaagattggg 300
ttggtatatt caagggttga tggagtactg ctggtgatta ttacacgttt ttatggtccc 360
ctatgcctga accattatgt gaaggatcaa cagtcaattg tgtactagca ttccaaggat 420
cttactctcc aatatgtgat ggagaatttt atcagttctg ttacgtttacc cataaggggt 480
aaattctgtg agcaagtaca cctttccagt ttctccagtt gaccacaaaa gaagagctgc 540
ttacttga gaatgaaggaa aattctgaca tgttagtggt gaccacaaaa cgaggccttc 600
ttgagtgtaa aattgagaaa acctgaaaag aaaaagaaga actgttaaa ttaattgccg 660
ttgtggaaaa agaaaacagca caacttcgag aacaagtgg gagaatggaa agagaaacta 720
acctagatga aaaaagtgtg gaccaactgc aagcagaaca aaagggtctt actgaagtaa 780
cacaaaaggt aaaaaatggaa aatgaagagt ttaagaagag gttcagtgag gctacatcca 840
aagcccatca gcttgaggaa gatatttgtt cagtaacaca taaagcaatt gaataagaaa 900
ccgaattaga cagtttaaaag gacaaaacta agaaggccaca acatgaagaa gaacaacttg 960
aatgtcagtt gagacacagag aaggatgaaa aggaacttta taaggatcat ttgaagaata1020
cagaaataga aatatccaag cttatgtcag aggtccagac tttaaaaaat tttagagga1080
acaaagaaaag cgtgattact catttcaagg aagagatttg caggctgcag ttatggtgg1140
ctgaaaaagg aaactctgcaa agaaactttc tgcttacaac ctcaagttaa gaagatgat1200
gtttttttaa ggagcaactt cgtaaagcag aggaacaggt tcaggcaact cgggaagaag1260
ttgtctttct ggctcaagaa ctgagtgatg ctgtcaactg acagacacaga acgattggcag1320
acctgcatac tgcacagctt gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg1380
cagaacttaa actaaatgtc atgaaaaaag atcaggacaa gactgatata cttgaaacag1440
aactaagaag aagaattgaa gatctgaaac tccgtcttca tccgtcttca aaacaaactt gacattat1500
aagaaaaatt taaggaaatg caaaggctcc aaaaacaaat aaacaaactt tcagatcaat1560
cagctaataa taataatgtc ttcaaaaaga aaacggggaa agatcagaaa gttgaatgat1620
cttcagtaaa cacagaccca gccactctgt cctctactgt agatgtaaa ccatcaactt1680
ctgcagcaga gcagagattt gacatagtaa agtctgtgaa agtctgtgaa atgaccaag1740
aaattctgtg caaaaacagaa aagtataata aatgtaaaca actctgtcag gatgagaag1800
caaaatgcaa taaattatgt gatgaacttg caaaaatgga gctgaaatgg taagaacag1860
tgaaaattgc tgaatatgta aaacttgaaat tagctgaaat acaggacaa tataaagaac1920
ttaaaaggag tgcataaagt ccagacagaaa ggaaaaatgga agatggagca gatggtgct1980
tttaccagga tgaataacaa agggccacctg tcagagctcc ctctggggg ctggaagaca2040
atgttctctg cagcagcct gctcgaaact tttagtcggc tgatggctta gaggaactct2100
aggatagcaa agaaagttag aatgtgccta ctgctcctga tcttccaagt caacatttac2160
gtgggcatgg gacaggcttt tgctttgatt ccagctttga tgttcacaag aagtgtccc2220

```

```

tctgtgagtt aatgttttct cctaactatg atcagagcaa atttgaagaa catgttgaaa2280
gtcactggaa ggtgtgcccg atgtgcagcg agcagttccc tctgactat gaccagcagg2340
tggttgaag gcatgtgcag acccattttg atcagaatgt tctaaatttt gactagttaac2400
ttttttattt gagttaatat agtttagcag taaaaaaa aaataaaacc acactaaaaa2460
tagaccactg aggagaccat agagcggatg ctcttcagca cccctttatc cactttctga2520
ccaggagcta cttgtgagtt ggtgttacta ggtacagggg cagtctttgg cttatcaata2580
aattttaac tctgttaac ttacaaaaa ttaaaaaaa cgtactttat2640
ttatccctag ttgcagactg ctgaataaag gtcaggatt atccat 2686

```

&lt;210&gt; 71

&lt;400&gt; 71

000

&lt;210&gt; 72

&lt;211&gt; 922

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

```

ctgctctgaa aagccatctt tgcattgttc ctcatccgcg tcttctgtcg cggcagccgc 60
ctccgcccgc cgcctctctc gccgcccggg actccggcag ctttatccgc agagtccctg120
aaactctcgt tcttttttaa tccccgtcat cggatcacgc cgtgtcccca ccagtgcag180
cgcagccgta gacaccagct ccgaatcac caccaggagc ttaaggaga agaaggaa240
tgtggaagag gcagaaaatg gaagagacgc ccttgcatac gggaatgcta atgagaaa300
tgggggagcg gaggtctgca atgaggtaga cgaagaagag gaagaagggg ggtgatggt360
aggaaagagg tggagatgaa gatgaggag ctgagtcagc tacgggcaag cgggcagct420
aagatgataa ggaatgacat gtcgatacca agaagcagaa gaccgacgag gatgactaga480
cagcaaaaaa ggaaaagtta aactaaaaaa aaaaaggcgc cgtgaccta ttacacctcc540
acttccgctc tcaaatctta aacgttgtca ccttcgagta gagaggcccg cccgccacc600
gtggggcagt ccacccgcag atgacacgcg ctctccacca cccaacccaa accatgagaa660
ttgtcaacag gggaggga aaaggaccaa acttccaagg ccttgccttt ttctctaaaa720
gtactttaaa aaggaaattt gtttgtatgt tctatttaca ttgtatagtg ttgtacatat780
tgttaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcgttct840
tctggcctac ttctggactt ttacgttggt ggggtgttga ccatgttcaa ttataatccc900
aaaaagggga aaaaaaacct tt 922

```

&lt;210&gt; 73

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

ggaagtggcg gtgcgagggc tgcgtcacag cgagcggagc cgcggtccgc acggcagcgc 60
gtgcccgcag ctctccgcct ccccccgcgc gccagccgag gcagctccgc cccagtcgc120
ggcccacgca gcagcgcgca gacgagcccc agtagcagc ccaatggccg gtggaaacgc180
tacatcgaca acctcatggc ggacgggacc tgtcaggagc cgcgcctcgt gggctacaag240
gactcgcact cgtctgggc cgcgctcccc gggaaaaacgt tctcaacat cactgcact300
gaggtgggtg tcttgggttg caaagaccgg tcaactgtcg aggtatggga atttagcatg420
gggggcccaga aatgttcggt gatccgggac tcaactgtcg atgtcactgt caccagaact480
gacaagagcg tagctcgtct gatgggcaaa gaaggtgtcc atgtgggttt gatcaaacag540
aaatgttatg aaatggcctc ccacctctcg cgttcccagt actgacacct tctgtccctt600
ccccttcacc gcctcccaca gctttccctc ccttccctcc ccatacacac acaaacattt660
ttattttttg ggccattacc coataccccc tattgtgcgc aaaaaccacat gggctggggg720
ccagggctgg atggacagac acctccccct acccataccc ctccggtgtg ttggtggaaa780
acttttgttt ttgggggttt tttttttctg aataaaaaaa attctactta acaaaaaaaa840
aaaaaaaaa aaaaaaaaaa aaaggggggg 870

```

&lt;210&gt; 74

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

```

ataaaagagg aagagagtgc caggtcttca ctcactgcg actgcagaac tcagagctgc 60
tcttctctctg tggccaggttg gggaccagca tcatgaagtg gatgggtggtg gtcttgggtct 120
gcctccagct cttggaggca gcagtggtca aagtgccctt gaagaaatct aagtcctatcc 180
gtgagagccat gaaggagaag ggtctgcttg gggagttcct gaggaccacac aagtatgatgc 240
ctgcttggaa gtaccgcttt ggtgacctca gcgtgaccta cgagcccatg gcctacatggt 300
atgctgcctca ctttgggtgag atcagcatcg ggactccacc ccagaacttc ctgggtccctt 360
ttgacaccgg ctctcccaac ttgtgggtgc cctctgtcta ctgccagagc caggcctgca 420
ccagctcacc ccgctccaac ccacagcgagt cgtccaccta ctccaccaat gggcagacct 480
tctcctcgca gtatggcagt ggcagcctca ccggtctctt ttggtatgag cctggtatgca 540
tcacagagcat ccaggtcccc aaccaggagt tcggcttgag tgagaatgag cctggtatgca 600
actctgtcta tggcgagttt gatggcatca tgggctgggc ctaccctgct ctgtccgtgg 660
atgaggccac cacagctatg cagggtcatgg tgcaggaggg cgccctcacc agccccgtct 720
tcagcgtcta cctcagcaac cagcagggtct ccagcggggg agcggttgct tttgggggtg 780
tggatagcag cctgtacacg gggcagatct actggcgccc gtccaccag gaactctact 840
ggcagattgg cctcaagaag ttctctatcg ccggccaggc ctccggctggt tgttctgagg 900
gttgccaggc catcgtggac acaggcacct ctctgtctac tgtgccccag cagtacatga 960
tgtctcttct gcaggccaca ggggcccagg aggatgagta ttgacagttt ctcgtaactt 1020
gtataacgcat tcagaatctg cccagcttga ccttcatcat caatgggtgtg gagtctccctt 1080
ttgccacttc ctctctatct ctcagtaaca acggctactg caccctggga gtccgaccca 1140
ctctacgttc ctccagaac ggcacgccc tgtggatctc cggggatgct tctctcaggat 1200
cctactatct cgtctacgac ttgggcaaca acagagtagg ctttgccact gccgctatga 1260
cttgcgtcct gcacagctgg gctccccctc tctctctgac cctgcaccct cttagggcat 1320
tgtatctgtc ttctcactct ggaattcagc tcttcttttt ggactctgga cttctctaa 1380
taataaatag ttctctcttt aaaaaaaaaa aaaaaaaa

```

&lt;210&gt; 75

&lt;400&gt; 75

000

&lt;210&gt; 76

&lt;211&gt; 1712

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

```

gtggcagaaa acctcatgac acaatctctc cgctcccttg tgttgggtgga ggatgtctgc 60
agcagctaaa aaattctggg agggcttgggt tgtcagcagc agcaggaggg gcagagcaca 120
gcactcgtcgg gaccagactc gtctcaggcc agttgacgct ttctcagcca aacgcgcgacc 180
aagggaaaaat cactaccatg agaattgcag tgatttggct ttgctctacct ggcatacact 240
gtgacctaac agttaaacag gctgattctg gaagtcttga ggaaaagcag ctttacaaca 300
aataccocaga ttgctgtggc acatggctaa accctgacct atctcagaag cagaattctcc 360
tagtccccaca gaattgctgt tctcttgaag aaaccaatga ctttaaaccga gagacccttc 420
caagttaagtc caacgaaagc catgaccaca tggatgatat ggaatgatgaa gatgatgacg 480
accatgtgga cagccgggac tccattgact cgaacgactc tggatgatga tgatgacagt 540
atgattctca ccagctctgat gagtctcacc attctgatga atctgatgaa ctggtcactg 600
attttccacac ggaacctgcca gcaaccgaag ttttcactcc agttgtcccc acagtagaca 660
catatgatgg ccgaggtgat agtgtggttt atggactgag gtcaaaatctt aagaagtctt 720
gcagacatga catccagtac cctgatgcta cagacgagga catcacctca cacatggaaa 780
gcgaggagtt gaatggtgca tacaaggcca tccccctgtc ccaggacctg aacgcgcctt 840
ctgatttggga cagccgtggg aaggacagtt atgaacgag ctgactggat gaccagagt 900
ctgaaaccca cagccacaag cagtcagat tatataagcg gaaagccaat gatgagaga 960
atgacattca cgtgtgtatt gatagtcaag aactttccaa agtcagccgt gaattccaca 1020
ctgactgaatt tcacagccat gaagatatgc tggttgtaga ccccaaaagt aaggaaagag 1080
ataaacacct gaaatttctg atttctcatg aattagatag tgcattctct gaggtcaatt 1140
aaaaggagaaa aaataacaat ttctcacttt gcaatttagtc aaaagaaaaa atgctttata 1200
gcaaaatgaa agagaacatg aaatgcttct ttctcagttt atttggttga ttgtatcta 1260
tttgagttctg gaaataacta atgtgtttga taattagttt agtttgggtg ttcatggaa 1320
ctccctgtaa actaaaagct tcagggttat gtctatgttc attctataga agaaatgcaa 1380

```



```

actatcactg  tattttaata  ttgtttatc  tctcatgaat  agaaatztat  gtagaagcaal1440
acaaaaact  ttaccact  taaaaagaga  atataacatt  ttatgtcact  ataatctttt1500
gttttttaag  ttatgttata  tttgtgtgtg  attatctttt  tgtggtgtga  ataatctttt1560
tatcttgaat  gtaataagaa  tttggtgtgtg  tcaattgctt  attgttttc  ccacggtgtg1620
ccagcaatta  ataaaacata  acctttttta  ctgcctaaaa  aaaaaaaga  gaaaagaaaa1680
aaaaaagaa  aaaaaaggg  gaggggagggg  ag

```

&lt;210&gt; 77

&lt;400&gt; 77

000

&lt;210&gt; 78

&lt;211&gt; 1273

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

```

accgcccccg  ctgtgggtct  cagcagctcg  ggcggcgagg  ggggtggcag  cggcaaggca  60
gcccgctttc  gcgaaggctg  tcggcgcgcc  gcggcccgca  ggcaccggcg  acgcgccttc  120
cccgcgagga  cccggcaacg  gccttccccg  ccggccacgt  gcccaagagc  accggtcagct  180
ccgcggaagg  gcgcgcaagg  aagagcccaa  gaggagatcg  gcgcggttgt  cagctaaacc  240
tcctgcacaa  gtggaagcga  accgaaaaag  gcagcagcga  aggtcaaatc  ttcagacaaa  300
aaagtgcacaa  caaaaggaaa  aaggggagca  aagggaacga  aggcggaagt  ggctacacaa  360
gaaactaaag  aagacttacc  tcgggaaaaa  ggggaaacga  agactgagga  gactccagcc  420
tctgtagaag  caggagagaa  agaagccaa  tctgattaat  aacctatac  catgtcttat  480
cagtgtgtcc  tgtctccctt  ctgtacaat  ccagaggaat  atttttatca  actattttgt  540
aaatgcaagt  tttttagtag  ctctagaaac  atttttaaga  aggagggaa  cccacctcat  600
cccatttttt  aagtgtaaat  gctttttttt  aagaggtgaa  atcatttgct  ggtgtgttat  660
tttttgtttac  aaccgaaaaa  ctctagtgga  tatgtaat  tgggaggtct  tgactgtctc  720
gggtgtcagc  ttaacattcc  acagatgggg  ggttagtttt  tatatcctat  aatcaaaagc  780
atattaaatg  gcaatatgga  gtcagtcctg  cattaaatgt  ctggaacatt  ttaattact  840
tctattacca  tgtgtttttt  tagtagaatt  gtttccctaa  gaaaaccact  cttgtatcat  900
ggctctctct  gccagaattg  tgtgcactct  gtaacattct  tgtggtagtc  ctgttttctc  960
aataactttg  ttaactgtgt  gtgaaagatt  acagatttga  acatgtagtg  tacgtgttgt1020
tgagttgtga  actggtgggc  cgtatgtaac  agctgaccaa  cgtgaagata  ctggtacttg1080
atagctctct  aaggaaaaat  tgcttcccaa  ttttaagctg  gaaagtcaat  ggaataactt1140
taaaaaagaa  ttacataaca  tggcttttta  gaatttcgtt  acgtatgta  agatttgtgt1200
acaaattgaa  atgtctgtac  tgatctctaa  ccaataaaat  ctcatgtatg  aaaaataaaa1260
aaaaaaaaaa  aaa

```

1273

&lt;210&gt; 79

&lt;211&gt; 2342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

```

cctcggacca  ccggactggc  ctggggcggg  acgtggggcg  gggggcgagg  cgtgcggcac  60
cgtcgcaggc  tgaagcggcg  gcggcggtgt  ggactgtcac  tagcccgagg  ctgcggcatg  120
ctctctgggt  gctcgggtct  gtgagctgta  ccttcttctc  ggcagtgaat  ggctctgatt  180
cctctagtga  tgatgtgac  gaattaaact  catcaaat  caaccgagaa  gttattcaga  240
gtgatagtgt  gttgcttgta  gaattctatg  ctccatgtgt  tggctacgtg  caaagattaa  300
caccagaatg  gaagaaagca  gcaactgcat  taaaagatgt  tgtcaaaagt  ggtgacagt  360
atgcagataa  gcatcatccc  ctaggaggct  agtatgggtg  tcagggaatt  ctaccactta  420
agatttttgg  atccaacaaa  aacagaccag  aagattacca  aggtggcaga  actggtgga  480
cattgtaga  tgtctgcgtg  agtgcctctg  gccagctcgt  gaaggatcgc  ctccggggac  540
gaagcggagc  atacagttct  gggaaaaaag  gcagaagtga  tagttcaagt  aagaaggatg  600
tgattgagct  gacagacgac  agctttgata  agaattgtct  ggacagtga  gatgttgga  660
tggttgagtt  ctatgctcct  tggtgtggac  actgcaaaaa  cctagagcca  gagtgggctg  720
ccgacgcttc  agaagtaaaa  gagcagacga  aaggaaaaag  gaaactggca  cgtgtggatg  780
ctacagtcaa  tcaggttctg  gcctcccgat  acgggattag  aggttttct  acaatcaaga  840
tatttcagaa  aggcgagctc  cctgtggatt  atgacggtgg  gcggacaaga  tccgacatcg  900

```

```

tgtcccgggc ccttgatttg ttttctgata acgccccacc tcttgagctg cttgagatta 960
tcaacaggga catttgccaag aggaacgtgtg agggagacca gctctgtgtt gtgctgtgcl020
tgccccatatt ccttgataact ggagctgcag gcagaaatct tttctctggaa gttctctctgcl080
agtgccgaga caaatacaaa aagaaaatgt ggggggtgctt gtggacagaa gctggagcccl140
agtgctgaact tgagaccgcg ttggggattg gaggggttgg taccocggcc atggcgcccl200
tcaatgcacg caagatgaaa tttgctctgc taaaaggctc ctccagtgag caaggcatccl260
acgagtcttct caggagagctc tcttttgggc gtggctccac ggcacctgta gggcgccggcl320
ctttccctac catcgcttag agagagcctt gggacggcag ggatggcgag ctctccgtgg1380
aggatgacat tgacctcagt gatgtggagc ttgatgactt agggaaagat gaggttgtgcl440
agccacaaca gaggcttcag accattttct tttcttggga gccagtggaat tttccagccl500
gtgaaggggac attctctaca ctcaagatgac tctaccagtg gcccttttaa caagaagtgt1560
tacttgattg gtcatttgaa aacactgcga cagtgaactt ttgcatctca agaaaacatt1620
gaaaattctt atgaattgtt gtacgcgggt aattgagtcg tattctgtga tttctgtgcl1680
tgaagaaaaa ttggctgtcg aacattttt ctctctgact gctgcttgaa tgttcttggcl1740
ggctgtttct tatgtatggg ttttttttaa tgtgatccct tcaattgaaat attaatggct1800
ttttccattta aagaataaaa ttttttggac aatgccgata aatgtatgaa gttagtattcc1860
acatcataaaa ttccagatga tgtttagcag taaatcaata ttttgaagt attacacagat1920
gtcttttctc cccacaaact tttttaaaca aaaaaacaag cctcttttct ttagattggt1980
ccacactatgc ccaccacaac agagatttta catgaaaacc gggctcagtg agaactagt2040
tctctcccaa tttgttttct tgggctgtct ctagtgaact attattaagg aatctagctg2100
gtttatcacgt tcaaggcttt ctatgttgtt aatgaacctc aaaaatagcg ttaagcatg2160
aaatacagca gcagggttacc aatgcgaaca ggtagtctgc atttatgtaa aacattcaga2220
aaatgaagtt ttgaatttgt tggaaacattc aaaggacttg agagcatttt attgtgaact2280
aaaaaaaata atacaactgt cactaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2342
aa

```

&lt;210&gt; 80

&lt;211&gt; 1959

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 80

```

gcagttatat aataagtttg ggagacaaaa tgatacgcac acgagagaag atgaagaaga 60
tactcaaaagt tccaatctcg aagaacatca tttgtactct aatccaatca aagaagaagt 120
gactgactctc aaattctctta agtactctga aatgagttag gaaaaacgag ccaactctcg 180
tgaatttgag ctcaaaagtta tgaagtttca ggatgaattg gaactctggg aagacacata 240
aaaaaccaggc cagagtttttc agggagcaagt agaactacac agagataaac tcttccaacg 300
agagaagaag aagaagtag aagagaaacg agaagaagac aagaaagata aagaaaaaatt 360
ggaatctcgc tccaaagaca agaaggaaaa agatgagtgt actccgacaa ggaaggaaaag 420
gaagaggcga cacagtatcat ccccacagccc atctcgcagt agcagtggta gacgagttaa 480
atccccatca ccaaaatcgg agcgatcaga cgcgttcagaa agatctcata aagagagctc 540
acggtccagg tcaatctaca aagattctcc tagagatggt agcaaaaaag ccaaaagact 600
accatctggg tcaaggacac ctaaaaggct tagggcataa aggtctagat ctccataaac 660
atcaggaaaag aagtcocagat cccagtcacag atctccacac cgtgtctata aaaagtcaaa 720
gaaaaacaaa cactgacgta aatttttaag atgtgtctca ttaattggaaa tgcgatttgt 780
tttgtgcctg aacggtctgt tttttaaaaa acaaaaaaat caaatgaaag agcatctctg 840
gggttttttg tttttttgt tatgcatgtg taaactcatg agcaactgca tctgtatgct 900
tgctatttgt ttatatttgt taaattactt tctattgggc tattttctca gatgaattt 960
ttattgtctt aatggatttc atcagaatgt tgtataatgg atctgctgac agtagtagta1020
ttttgtttta ggtgtgtgtg acttagcaaaa aataatacac atgtcttccc cctttttgtal1080
gcttttgacaa ttgtgaattg atttcaaaaa aaatctgaac agaaaactat aatgttgtt1140
ttttggccca cgggtgatat taagtccctt aaagtctcac tgagtttccac actactgttg1200
tgcttttatat acctgatgca ctttataaag cccagtgctc aagttagctta agttttatat1260
tctcaatgag gactatccaa attaagggac ctgagactcc ttatttgggtg ttctgaacc1320
atttgctttt gtaagtttct tcttgggtaa tactaatacc cagatatcaa agactaggta1380
gatatggcat gacattttgt tagtggaatg cctggctaaa acattttttt cacagaagca1440
atatgattct catcatccca acccatgttc tgagcaacta cttactttta gggggaaatt1500
aaatattctt tctattctct tctctattatg aaagaagttt atttgtaaaa caaattttct1560
aacaaggttt ggccatagaa tctctttgta tgattgttga ctttttataa tctctgtag1620
gctacttttc aaacactggc atcagaatat tttttataag tttgtgttaa aacagcttag1680
ttgggtcccc cccccactcc caagagactt gggtttagtt atagctttaa gtataattt1740
aaaaataaat gtttttcagg aaacttcgta tctaattggt ttgaatttca aggtgcaaaa1800

```

```

agtgtagttaa accatttgc agagtgaac tctattatga aaataaattt gctacgggtat1860
gaggaagaaa taaaacttgt gtaattgttg tcataatact gctataataa taataaagggt1920
ttatgtagaa ttgaactgac aaaaaaaaaa 1959

```

```

<210> 81
<211> 3708
<212> DNA
<213> Homo sapiens

```

```
<400> 81
```

```

gccccatttta ctaggcacgg tagacaagct tttttttttt ttttttttta cagcttataa 60
cacaactttt ttacgaaaag ttatacataa catagcatca actattttca agaacaatat 120
taaaccogat aagcaacaaa aaccagacta acaaaatgtg taacaagaaa ctaatgacct 180
ttctaaaatc aaacattcaa ttatctacaa tgccttttta caaacgggga aaactccttg 240
gtttacagcg acatcatatt gaataataag ctgcaatagc aattttatca aattaccact 300
ctgaagaaaac tgaatcatta aaacagtaat tacgagttca caaatttaaa acatttcaca 360
taatttttaa tttttgggta tacactgaag tctgagtttc aaaagtgtatt tttttttccc 420
acaaaagtgt caacacttaa gctagaactt tctaggttaa ctttgcccta aaaagtttag 480
acataattctg ataactataa cagtcacatg atttctgatg ctactctggtc tgttaataat 540
aaagtctctta ttgggatgta ttaattttcc atcagctctg ccttgtagta ggcaggggcaa 600
tcgttggcaac gctatttaag ttccaaacca ggagtggtgca gcactggaaa aggagatcag 660
tactaaaaat tacaataaat atcagagaag ccgttagctt ttacagcatc gctgcttaa 720
aagctaagtt gaccaggtgc ataattttcc atcagctctg ccttgtagta ggcaggggcaa 780
ttttctgttt catgatcggg atactcaaat atactcaaac atctttttta aaacttgatt 840
tatagctctc agaaaagtat gttttttaat agtcaactca ctctaactcag gcctagcttt 900
cactcatcttg gagcctcact aaaataacag atttcaagta agccaagtcc atcagaaga 960
ctcaaatggg atgatttaca aaatagaaca ctttaaacca ggtcagctct atcttttgg1020
agctggaagcg tatcagtcac aacacaattt cgcgtacacc tctgctcatt atggaattac1080
acttaaaagg aatctcaaga ggggtgacct tgttggtttca gataccatcc caaaggagag1140
tgggttaacg gaagattgcc agtgttactg atggaaagaa gtgtttgttt gttttttt1200
cttggtaaac acttacacca tagtttttaa ttaaaactgtc aggcattttc tcagacaggt1260
tttcttttcc aatgcagtaa tgaagaacta agataaaaaa catgactttt gactgccatt1320
caacattatt acatgcacca atattgcaca catctgtctc gaactgttaa aactcatctt1380
tgagtctctg ggggtgctgt ttctccatca gaacacaaac acaaccccat taatcagtt1440
gggggcaatt tgtaagcact agtgaatcaa acactagcta taatgcttct agctccttat1500
aaagactttg tacagacaaa aatctaaagt ttctcaaaag gttctgtgtc cctcacacat1560
agctcaatag cttgtgctgt tttaagaacc aagaagctgt agaactttgc agctccttat1620
tttctgtctg tatttcgaca taactcaaac aaactgatag attcagctcc agtttttagca1800
agagcacgct gaagaccatg aagcatctgc tgagctcctt tgttccatct tcttttctc1860
tgatcttgat cgccccctga tgcactttca tctcttctct ctctcatctc tcttttttcc1920
ttctcttctt cctctctctt ttctggcaga agttctaaact ctgtcattag ctgacagata1980
tttggagggg cttctggggg aagctctaca ggttggtatt cccactgtct ctgggtcaat2040
ttgtccagct ttctgcttaa ctccctgagg tgggtgtgga ggcatagctg actcattct2100
gtttgtctgt ctggtctcca tcactgactc ctggagggcg cttggctctt cactaatggg2160
ctcatcgata acatcaagct gctgatgctg ctgtgtgctg tctctctctg gaacctctgg2220
atttttcaat tttttgagga attcatccaa attatctgcc tctcctctg tctcctttt2280
ctaaaggtct tctgtgtcaa gcgggtgtaa acagcgtgta aagagcttca gtatgctgt2340
attccacaaa ggtcgctgag gtaaaagaaa cagtttttct actcctcctg tctctttcca2400
catcatcaat ttctgtgtgg cgggtgccga tccaaagtat taacaatatc tgaataatca2460
ctaaagttgg ctctaattgt cttgctcatc aactccttga cactgtcaac atctagct2520
ctctctctct tggcttttgt ttctttaaca gttatatcaa taggctccaa tgc aaatgct2580
tcttctcatc ttggaacaag tgttgtttga tctgctatgg ttggcattgg atccatcatg2700
tccactgaat caggactatc agggccaccc attgatcatc tatcatctct ttaacggga2760
tcatgtcgag gctgctctgg caacatcacc cctgcctcag agagggcagg gggatcatg2760
aagatcacgc catcatctat actaataagt ttgtcatcta atattccacc atcattctct2820
ttccaaaaat tatcatcctt atattgatct tcatattcta aatggtaatt ttctcatctc2880
agattgtgtg tgcctgtgtc agactctaat agggaggttag aagttagtagt gctctataac2940
atgtgctgat ctcacaaagc actgcctctc cactattatc cagcatcacc catccaaaaa3000
tcaccaaaat cattttcttg taaaatactg atgttcccaa cttcttctct catgggtatc3060
ttctccactc tactctgatt caagctgaac tgcgtggcca catgatgct atctaagta3120

```

```

ggcagtggtgatcaaaagtc atgaaattcttc caggtgaaag taatggcatt ataagctgct3180
tcccgatctt cctcaggcag gtaaccacac cctgccgaag aagccatctt tatcttaagtg3240
aatgtcttcat tacagttctgc aagaaggtat ttggctttcc ttggtgatagtc tcgaactact3300
cccgatgaaga gatgtctctga tgcctcgtaac gccattttta cctttggtga gatgatcact3360
ttccagctgc tctcttaaat tacactcgaa cactctttta ctgagaaacaa aatgtgcgt3480
atgggcccgt agccaaattc ttgccagagg cctcttttta ctgagaaacaa aatgtgcgt3480
gaacatttgt ctggctggtc atgaaaacag tgcctctccg ttggagttgg3540
ggcgggtggtc tggcccggtg aggggaaaaa ggtcggggga ggggggtggg aaagggggga3600
cgttctcgga ggtgtagctt ccgagcagct ccccgcccc cagagccggc gctcctctcc3660
cgattcactc aaaaacaaac gatggtctgcc gttaaccccg ggctcttc 3708

```

&lt;210&gt; 82

&lt;211&gt; 3045

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 82

```

gtccattgcc caaaatccgc tatgaaagct tgaccaatcc ccagtaaat agacctctgg 60
gaaaagagct gccatatatt ccataccoca aacacccaag atcgaaactc cactatttgg 120
gatactggaa ttggaattgac caaggctgac ttgatcaata accttggtac tatgcgcaag 180
tctgggacca aagcgttcat ggaagctttg caggtctgtc cagatatctc tatgattggc 240
cagttcggtg ttggttttta tctcgtctat ttggttctgt agaaagtaac tbtgatcacc 300
aaacataaac atgatgtagca gtacgcttgg gactctccag caggggggatc attcacagt 360
aggacagaca caggtgaacc tatgggtcgt ggaacaaaag ttactctaca cctgaagaa 420
gaccaaactg agtacttgga ggaacgaaga ataaaggaga ttgtgaagaa ccctgtcag 480
ttatttgat atcccatatt tctttttgtg gagaaggaaac gtgataaaga agtaagcgat 540
gatgagggtc aagaaaaagga agacaaaaga gaagaaaaag aaaaagagagc 600
gaagacaac ctgaaattga agatgttgtt tctgatgagg aagaagaaaa gaaggatggt 660
gacaagaaga agaagaagaa gattaaggaa aagtacatcg atcaagaaga gctcaacaa 720
acaaagcccc tctggaccag aaatccccag gatattacta atgaggagta cggagaattc 780
tataagactg tgaccaatga ctgggaagat cacttggcag tgaagcattt ttcaagttgaa 840
ggacagcttg aattcagagc ccttctattt gtccacgac gtgctccttt tgactgttt 900
gaaacagaaa agaaaaagaa caatatcaaa ttgtatgtac gcagagtttt catcatggat 960
aactgtgagg agctaatccc tgaatatctg aactctatta gaggggtggt agactcggag1020
gatctccctc taaacatatc ccgtgagatg ttgcaacaaa gcaaaatttt gaaagttat1080
aggaagaatt tggctaaaaa atgcttagaa ctctttactg aactggcggg agataaagag1140
aactcaaga aattctatga cagttctctc aaaaaataa agcttggaaat acacgaaagac1200
tctcaaaatc ggaagaagct ttcagagctg ttaaggtact acactctgc cctctgtgat1260
gagatggttt cctcacaaga ctactgcacc agaattgaag agaaccagaa acatatct1320
aaacatggct tagaagtgat ctatttgatt gagccattag atgagtactg ttgtccagag1440
ctgaaggaat ttgagtggtg gactttagtg tgcagccaca aagaaggcct ggaactctca1500
gaggtatgaag aagagaaaaa gaagcaggaa gagaaaaaaa caaagtttga gaaactctgc1560
aaaatcatga aagacatatt ggagaaaaaa gttgaaaaag gttgtgtgac aaaccgattg1620
gtgacatctc catgctgtat ttgtcacaag acatatggct ggagcagaaa ctggagaga1680
atcatgagag ctcaagccct aagagacaac tcaacaatgg gttacatggt gttacatgag1740
cactcggaga taacacctga ccatccattc attgagacct taaggcaaaa ggcagaggt1800
gataagaacg caaagctctg gaaggatctg gtcatcttgc ttattgaaaa tttatgaaac1860
tctcttggtc tcaagctgga agatccccag acacatgcta acaggaatcta caggatgat1920
aaacttggtc tgggtattga tgaagatgac cctactcgtg atgataccag gtctgctgat1980
ctgagagaaa tgcacccctc tgaaggagat cagcacacat cagcgtatga agaagtagac2040
taactctctg ctgagggatg acttacctgt tcaagtactc acaattctc ttgataata2100
tctttcaagg tgtttttctt tatttttgtt aatattaaaa agtctgtatg gcatgacaa2160
tacttttaag ggaagataag atttctgtct actaagtgat gctgtgatac cttaggcact2220
aaagcagagc tagtaatgct ttttgatgtt catgttggtt tattttcaca gattggggta2280
acgtgctgac taagacgtat gtaacatgat gttactctg ttgggtcttc aagtggtct2340
tgtcaagcgc gatgctcaag tagaccaaat ctgtttatgt aagtgttctg agctgtatct2400
tgatgtttag aaaaattatc gttacatctt gttagatcta cttttgaaac ttctcatcc2460
ctgtagttag caattctgca tgtactagtc cctagaaat aggttaaacg gaagcaact2520
gatggaaaga tctctccaca gggctgtgtt atctctgtaa agtattgttt ggaagacaa2580
agttcaaaagc ctacetaagc atatcgtaaa gctgttcaaa aataactcag accagctct2640
gtggatggaa atgtagtgtc cgagtcacat tctgttataa gttgttaaaa atacagatga2700

```

```

gtttaaagat attgtgtgac agtgtcttat ttatgggggaa aggggagat ctggatgaca2760
gttagtgcca aaatgtaaaa catgaggcgc tagcaggaga tgggttaaaa cttagctgtc2820
caagggttga catggctcttc ccagcatgta ctccagcagg ttgggggttga gtgggggttag2880
gcacagaaaa caggaatgca gacaaatgac atccccctggt tccatagagt acatgtgttc2940
tcttagtgtc ccagtgtgtt tgatgtttat catggaatca ctctgtgtct aaatcacgtc3000
acttaattcc ttggccaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3045

```

&lt;210&gt; 83

&lt;211&gt; 2815

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

```

cagtgggcgc gcaaccagcc ttctaggcgc gcggaggagt ggagtcaaca tatcaatgga 60
gcaagtcaca gtcgtcgatg ccagctctct ctgaaatct acccagaatg gaatcctgac 120
aatgatacag gacacacaa ttgggtatcca ttcatgttgc agcagctcac aaatccagca 180
ccaggaatcc tgggacctcc acctccctca tttcatcttg ggggaccagg agttgggacca 240
agaggaaatc tgggtgctgg aaatggaaac ctgcaaggac ctagacacat gcagaaagcg 300
agagtggaaa ctagtcagag tgttcacatc atggattctc aacaggggaa aaactctgaa 360
taccagatat tacagctggg agaacatttt tgaatggaac caatcatct gattctaaat 420
aaaaattaat aggcatttat tgaaatggca accacagagg atgtctcagg cgcagtgga 480
tattacacaa ccacaccagg gttagtattt ggcaagccag tgagagtcca ttatccccc 540
aagtataaaa gaataaagaa acctgaagga aagcagatc agaaagtttga ctaaaaggcaa 600
gagctctggc gtgtgataca tctcagcaat ttgcgcgatt ctggctattc tgatagtgtc 660
gttctcaagc gttctgagcc ttatgggaaa ataaagaatt acatattgat gaggatgaaa 720
agtcaggctc ttatgtgatg ggagacaaga gaagtgcgaa ttggcaatgt tgaccattgt 780
ttgaaaaaag cctcttggtt tcaggggaga tgtgtgaagg ttgacctgtc tgagaaatag 840
aaaaaacctg tctctgagat tccaaacaga ggcattgatt tactgaaaaa agataaatcc 900
cgaaaaagat cttactctcc agatggcaaa gaatctccaa gtgataagaa atccaaaact 960
gatgtgtccc agaagactga gagttcaacc gaagtcaaga acaagaagag aagtcgggtg1020
aagatggtga gaaagacaca aaggatgacc agacagagca ggaacctaat atgctcttg1080
aatctggaag tagactcatt gtatgatgag aagaagcagc agcactgcta gaaagtggca1140
gttcagctgg agccagacac gatcttgcta atttaggtga tgtggcttct gatgggaaaa1200
aggaaccatc agataaagct gtgaaaaaag atggaaagtc ttccagcagca gcaaaagaaa1260
agctcaaaaa ggtggacaag atcgaggaa ctgatacaaga aaacgaagca cgcgtggaaa1320
atggaattaa aaatgaggaa aacacagaac cagggtgcta atctctgtag aacgtgtatg1380
atcccaacaa agatcacaa gtgaaacgcag atggtcctaa tgatgagaac aaggacgact1440
atcataatcc agatgagat agaattggac catatcagcc caatgttctt gttggtatag1500
actatgtgat acttaaaaca ggggtttact gtaagctgtg ttcatctctt ttcaaaatg1560
aagaagtgtc aaagataact cattgcagca gccctctcca ttatcagaaa ttaagaaat1620
ttctgaabaa attggcagaa gaacgcagac agaagaagga aacttaagat tgccaaggag1680
atttaagtat ttcaagaaa ataatgtgtc tttgttttta atgttaacct tttttaaat1740
caatactgat agttagaaga aaactattgt actctttgt tttagtgag aaataatag1800
tgtctgttca tgtgttaagt gttatagcaa aaaaaataca catatgggta agttaatgaa1860
tagtttttgt ttatcagaa ttggcaacaga cagaagtact ttgtagagat tgactctcta1920
agctaatgaa gacactattgc accactaaga gaaccatttg gaacattttg gaaaaatgaa1980
atttagtagt tccaagtttc aaagaaatgt caacatttta ttccattcaa taaagacaa2040
aaccaatagt gtttttatta ctttcatctg aaacattcca tgttttaact tggagctgtc2100
agactttcat ttggagtttg aaccgctttt ggtgtcattt catttttgga gaacttaatt2160
aacgtgagat tggcaattga aatgcagggt cagttttctg ttaatgtcat ttatgtctat ttcgatgtt2220
aggtataatg aaatattaa ttaattggct tagattttgt aatttttttc cctgagttcc2280
tgctagattt cgtatctag tagtcaatgt attttcagta aatgcacaaa atcttcccat2340
tatctttgac cagtattaat ttttgagatc ttactcgttg tcaacttgaat ccctgtgatg2400
tcatacatct cgtgtataag caacatttga tttttgaagt gtgtagacca tcttctcata2460
tttccaagat gtaattttac atttctgcac ttttaaaaca gtttggccat aatcctagat2520
gcagctctct aattcaatga cctgcacatg tgacctttgt gaacagaaat ttgcagtatg2580
aatgtgtgtt tacttctaac tttctgttta tatactgtgt atactgtgtg atccaagta2640
ctgaagtgaa taccataaaa aagaaaaccc taggcattgt taattgttta tacatgtgtg2700
gaatgttaac caaaaaaaa aacagttgtg gtttttatc gctcttaaac tttgtcatg2760
ctttaacaat ttatcgcttt taaatctaga gtgaattcct aagagctgac cgcta 2815

```

&lt;210&gt; 84

<211> 3462  
 <212> DNA  
 <213> Homo sapiens

<400> 84

```

ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaacga 60
agcggctctt tccgctatct gccgcctgtc caccggaagc gagttgcgac acggcaggtt 120
cccgcgccga agaagcgacc aaagcgccctg aggaacggga acatggtgcg gtcggggaat 180
aaggcagctg ttgtgctgtg tatggacgtg ggctttacca tgagtaactc cattcctcgtt 240
atagaatccc catttgaaca agcaaaagaag gtgataacca tgtttgtaca gcgacaggtg 300
tttgcctaga caaaggatga gattgcttta gtccctgttt gtacagatgtg cactgacaa 360
cccccttctg tgggggatga ctatcagaac atcacagtg acagacatgc gtagctacca 420
gatatttgatt tgcctggagg cattedgaaagc aaaatccaac caggttctca acaggctgac 480
ttcctggatg cactaatcgt gagcatggat gtgattcaac atgaaacaat aggaagaag 540
tttgagaaga ggcatattga aatattcact gacctcagca gccgattcag caaaagttag 600
ctggatatata taattcatag cttgaagaaa tgtgacatct ccctgcaatt cttcttgcc 660
ttctcaactg gcaaggaaaga tgggaagtg gacagaggag atggccctct tcgcttaggt 720
ggccatgggc cttcctttcc actaaaagga attaccgaac agcaaaaaga aggtcttag 780
atagtgaaaa tggtagat atctttagaa ggtgaagatg ggttgatga aattttaca 840
ttcagtgaga gtctgagaaa actgtgcgtc ttcaagaaaa ttgagaggca tcccttca 900
tggccttggc gactgacct tggctccaat tgtctcataa ggatcgacg ctaataatcg 960
attctcacgg agagagttaa aaagacttgg acagttgttg atgcaaaaac cctaaaaaa1020
gaagatatac aaaaagaaac agtttattgc ttaaatgtatg ttgaatgaac tgaagtttta1080
aaagaggata tttatcaagg gtctccgtat ggaagtgtata tagttccttt cttcaaaagt1140
gatgagaaac aaatgaataa taaactcgag ggaagtgtct tctcgtttt gggatgttgc1200
aaatctcttc aggttcagag aagattcttc atgggaaatc aagttcttaa ggtctttgca1260
cgaagagatg ataggcagc tgcagttgca cttctctccc tgattcatgc ttggatgac1320
ttagacatgtg tggccatagt tcatatgtct tatgacaaaa gagcttaacc tcaagtcggc1380
gtggcttttc ctcatatcaa gcataaactat gagtgtttat tgtatgtgca gctgctttc1440
atgggaagat tggcgcaata catgttttca tcttgaaaa acagtaagaa atagctccc1500
accgaggcac agttgaatgc tgttgatgct tttgattgact ccatgagctt ggcaagaaa1560
gatgagaaga cagacacccc tgaagacttg ttccaacca ccaaaatccc aaatctctga1620
tttcagagat ttttcagtg tctgctgcac agagctttac atccccggga gccctcacc1680
ccaattcagc agcatatttg gaatatgctg aatctcccgc ctgaggtgac aacgaaaagt1740
cagatttccc tctctaaaat aaagaccctt ttctcttga ttgaagccaa gaaaaggat1800
caagtgactg ctacgaaaat ttccaagac aacctgaag atggacctac agctaaaaa1860
ttaaagactg agcaaggggg agcccacttc agcgtctcca gtctggctga aggcagctgc1920
acctctgttg gaagtgtgaa tctgctgtaa aactctcgtg ttctagttaa accagagaag1980
gccagctttg aggaagcgag taaccagctc ataaatcaca tcgaacagt ttggatact2040
aatgaacac atgtatttat gaagagcata gactgcattc gagccttcgc ggaagaagcc2100
attaagttt cagaagagca gcgctttaac aactcctga agacccttca agagaagtgc2160
gaaatataac aattaaatca tttctgggaa attgttgtcc aggatggaat ttactctgat2220
accaaagagg aagcctctgg aagttctgtc acagctgagg aagccaaaaa gttctgccc2280
cccaagagca aaccaagtg agacacagca gctgattttg aagaaggtgg ttgtctggac2340
gatttatttg acatgatata ggtcgtggat gtatggggaa tctaaagagg ctgccatcgc2400
tgtgtgttg ggaagtctaa caaaacaagt tggatgcggc catccaaggg catccaagaa2460
ctcaagaaat tcccagcagg ttacctggag gccgatcatc taattctctg ttgaatgat2520
acacacatat atattcaag ggataattta gaccctata aagtttataa agttctgat2580
ttatttctgt gttgggtgat tattttttct gtggtcttat tgatctttgt atttacat2640
catgctttga agtttcttga aagttagatct ttctttgacc tagtatatac gtgacagt2700
cagcccttgt gatgtatta gtgtctcatg tggaaacctg gcatgggtat tgatgagt2760
cttaaccctt tccagagatc tcttttgctt gatcctcaa cagctgtcac cagctgtcac2820
gagcaagcag tagcatttgc ttctcccaa caagcagctg ggttaggaaa accatgggt2880
aggaagcga cactctctct tttagttgag gcctctagt taccacat ta cctgcctct2940
gtatataaggt ggttttcttt aagtggggtg ggaaggggag cacaatttcc ctctaatc3000
atgtaagaca gttgatttat gtggtggtct catgaagaaa agaccttttg gcccaatc3060
tgccatatca gtaacacctt agaaactcaa aaactagaaa attactaca gtagttaga3120
ttatatcact tcaactgtct ctacttgcaa gcctcaaaaga gagaagtgt cgttatatta3180
aaacacttag gtaacttttc ggtctttccc atttctacct aagtcagctt ctactctt3240
ggagtgggtc tcttttacta aataagaaaa taacaaagcc ctattctct tttttctt3300
tctctattct tgccttgagt tccagttctt ctttggtgta cagactctct ggtaccag3360
cacctctgtc ttcagcacc tcataagctg tcaataatc acagttttgt acatgtaaca3420

```

ttaaaggcat aatgactca aaaaaaaaaa aaaaaaaaaa aa

3462

<210> 85

<211> 668

<212> DNA

<213> Homo sapiens

<400> 85

atagggccgg tgctgctgc ggaagccggc ggctgagagg cagcgaactc atctttgccca 60  
gtacaggagc tcgtgccgtg gccacagcc cacagccac agccatggc tgggacctga120  
cggtgaagat gctgcggggc aacgaattcc aggtgtccct gagcagctcc atgtcggtgt180  
cagagctgaa ggcgcagatc acccagaaga tcggcgtagc cgcttccag cagcgtctgg240  
ctgtccaccc gagcggtgtg gcgctgcagg acaggggtccc ccttgccagc cagggcctgg300  
gccccggcag cagcgtcctg ctggtggtgg acaaatgcga cgaacctctg agcatcctgg360  
tgaggaaata caaggccgc agcagcacct acgaggtgcy gctgacgcag accgtggccc420  
acctgaagac gcaagtgcg gggctggagg gtgtgcaggc cgacctgttc tggctgaacct480  
tcaggggaa gcccctggag gaccagctcc cgctggggga gtacggcctc aagcccccta540  
gcacccgtgt catgaatctg cgctgcggg gaggcgccac agagcctggc gggcggagct600  
aaggggcctc accagcatcc gagcaggatc aaggcccgga aataaaggct gtgtgaagaag600  
gaaaaaaa 668

<210> 86

<211> 671

<212> DNA

<213> Homo sapiens

<400> 86

ggaaaccggt ctcatgaac tcgctgcag ctcttgggtt ttttgggtt tccttcgtta 60  
ttggagccag gccacaccc cagcaaccat gtccaaaggga cctgcagttg gtattgatct120  
tggacacccc tactcttctg tgggtgtttt ccagcacgga aaagtgcaga taattgccaa180  
tgatcagggg aacggaacca ctccaagcta tgtgcctttt accgacactg aacggttgat240  
cggtgatgcc gcaagaatc aagttgcaat gaaccccacc aacacagttt ttgatgccaa300  
acgtctgatt ggagccagat ttgatgatgc tgttgcagc tctgatata aacattggcc360  
ctttatgggt gtgaatgatg ctggcaggcc caaggtccaa gtagaatata agggagagac420  
caaaagcttc tatccagagg aggtgtcttc tatgttctg acaaatgata aggaaattgc480  
agaaagcttc cttgggaaga ctgttaccac tgcttgggtt cacagtcca ccttacttta540  
atgactctca gcgtcaggct accaaaagat gctggagact attgatggct tgcattgtca600  
tttaggaatt attaatgga gccaaacttg tgctgggtta tttctttacg ggtttgggca660  
aaaaaagggt t 671

<210> 87

<400> 87

000

<210> 88

<211> 1108

<212> DNA

<213> Homo sapiens

<400> 88

agtggaggag ggagagagc tggcccgga cccgaggggc gtgggcatcg ggaggcgggc 60  
ccgggttagg ggcgggagcc cgccctggtt aaaggcgctt atttcccagg cagccgctgc 120  
agctgcgcaca cctttgcccc tgctgcgatg accctgtcgc cacttctctg tcggacgtcc 180  
cacaggcgcc ggtgcagatc tcctctctgc aagccttaga ctctcttggg aatggggcac 240  
cagtttaact caagacagggc aatctatacc tgcggggggc cctgaagaag tccaatgcac 300  
cgcttgcata ttgacccctc tactatgaag cactgtcgg tggctgccga gccttctcga 360  
tcggggagct cttccaacaa tggctgttgg tcatggagat cctcaatgct acgctggtgc 420  
ctacgggaaa ggcacaggaa caaaatgtca gtggcaggtg ggagttcaag tgccagcatg 480  
gagaagagga gtgcacaatc aacaaggtgg aggcctgcgt gttggatgaa cttgacatgg 540  
agctagccct cctgaccatt gctgtcatgg aagagtttga ggaacatggag agaagctcgc 600

```

cactatgcct gcagctctac gccccaggcc tgtcgccaga cactatcatg gagtgtgcaa 660
tgggggagcc cgccatgcag ctcctgcacg ccaacgcccc gcgagcagat gctctccagc 720
caccgcacga gtatgtgccc tgggtcacgc tcaatgggaa acccttgaa gatcagaccc 780
agctcctcac ccttgtctgc cagttgtacc agggcaagaa gccggatgtc tgcctctctc 840
caaccagctc cctcaggagt gtttgcctca agtgcagctc ggtgagctgc ggagagctca 900
tggaaaggcga gtgggaaccc ggctgcctgc ctttttttct gatccagacc ctcggcagctc 960
gctacttacc aactggaaaa ttttatgcac cccatgaagc ccagatacac aaaattccac1020
cccatgatca agaactcctgc tccactaaga atgtgtgctaa agtaaaacta gtttaataag1080
cccaaaaaaa aaaaccgcgt cggctcgac

```

&lt;210&gt; 89

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

```

aaagcagccg ccggcgccgg gtgcctcaca gacagctgcc acgcccagcc agacccctct 60
ctgcacgccg gcccgccccc accccaccatg gccacagttc agcagctgga aggaagatgg120
cgctggtggg acagcaaaagg ctttgatgaa tacatgaagg agctaggagt gggaaatagct180
ttgcgaaaaa tgggcgcaat ggccaagcca gattgtatca tcaactgtga tggtaaaaaac240
ctcaccataa aaactgagag cactttgaaa acaaacacgat tttctgtac cctgggagag300
aagtgttgaa aaaccacagc tgatggcaga aaaactcaga ctgtctgcaa ctttacagat360
ggtgcattgg ttacgcatca ggagtgggat gggaaggaaa gcacaataac aagaaaaattg420
aaagatggga aattagtggt ggagtggtgc atgaacaatg tcacctgtac tcggatctat480
gaaaaagtag aataaaaaat ccatcatcac ttggacagag agttaattaa gagaatgacc540
aagctcagtt caatgagcaa atctccatcac tgtttcttct ttttttttct cattactgtg600
ttcaattatc ttatcataaa acattttaca tgcagctatt tcaaaagtgtg ttggattaat660
taggatcatc cctttggtta ataaataaat gtgtttgtgc taaaaaaaaa aaaaaaaaaa720

```

&lt;210&gt; 90

&lt;211&gt; 837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

ctctcgcgag gattggctgt tagcggcggt gtagttaagc tcgtgtaaac gcggcggtgt 60
cggcagctgc ttagtgcgaag agagtttgcc gcatgtcttc acaccatttt gctggtacag120
cctaccaga ggcgcagaagg cagaacttat gctgactacg aatctgtgaa tgaatgcag180
gaaggtgtct gtaaaatgta tgaagaacat ctgaaaagaa tgaatcccaa cagtcctctc240
atcacatatg acatcagtcg gttgtttgat ttcactgatg atctggcaga cctcagctgc300
ctggtttacc gagctgatac ccagacatac cagccttata acaaaactg gattaaagag360
aagatctacg tgctccttcg tcggcagggc caacagggctg ggaataaatt gtgttggaa420
cactgggggg gctgggggtg gcttggaaac cagggtgtga cagcgtgctg tagtggaa480
tttgtatcat agtaactcctg ttccactctt gtataactct agccaagatt gactgtatta540
gatgaaatgt gaggatcttg ttcaactcga aacccccgtt atccctctct tctcttctc600
tttctttttt tttttttact taaacatttt tatgatgatt tagatggaag tggttctctc660
tcacttaagt ttggttccag tccttcaact gttcatatct actttataac attcacatac720
taaccctctc tcaagatggg gtgggggggt gaaatgcagt ttagccatgt cctcaagata780
aagctcttgt aaaaataaat aaatgtcctt tagttataaa aaaaaaaaaa 837

```

&lt;210&gt; 91

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

```

gtagggtcag cgtcggaggc ggtagtgacg gtggcgcttc cttgaggaag agtgagggtt 60
ccaactcttc tgcttatctg ggaggtgttg ggcgcggaca gtcgagatgt cagagaaaaa120
gcagccggtg gacttaggtc ttttagagga agacgacgag tttagaagat tccctgccga180
agactgggct ggcttagatg aagatgaaga tgcacatgtc tgggaggaat attgggatga240

```



```

tgacaatgta gaggatgact tctctaata gttacgagct gaactagaga aacatgggtta300
taagatggag acttcatagc atccagaaga agtggtgaag taacctaaac ttgacctgtc360
taacatcttc tagggcagag aacccaggat gggacactaa aaaaatgtgt ttatttcatt420
atctgcttgg atttatttgt gtttttgtaa cacaaaaaat aaatgttttg atataaaaag480
gaaagagaaa aattgcgg

```

498

<210> 92  
 <211> 1077  
 <212> DNA  
 <213> Homo sapiens

<400> 92

```

cggctcgagc tgggtacaaca gggcacacgt gtttcacgtt gacagggttg cttgggagcg 60
tagtaaacat gggcttgctg acttagccaa agaagagtta agaagaaaa acacacaagt 120
atacagactg ttcctagttt cttagactta tctgcataatt ggataaaaa atgcaaatgt 180
tgctcttcatt tttagatgct ttcattgtct ttaagatgtg ttaggaaatg caacagagca 240
aggagaaaaa aggcagctcct ggaatcacat tcttagcaca cctacacctt ttgaaaaatg 300
aacaactctg agaatttgaga gtgatttcct tctaaaaagt gtaagaaaagc atagagattt 360
gttcgtattt agaatgggat cacgaggaaa agagaaaggaa agtgattttt tccacaaga 420
ctctgtaattg tatttccact tataaaggaa ataaaaaatg attgctaatac ttgggatac 480
aaaaagcaaat aaaaacccaa ttcagtcctc tctaagcaaa attgctaaag agagatgaac 540
cacattataa agtaactctt ggtctgaagg cattttctac ttctcttcgg gtgcgcacaa 600
tattttaaag gtaaaacatg ctggtgaacc aggggtgttg atggtgataa gggagggaata 660
tagaattgaaa gactgaattct tcttctgttg cacaataaga gtttggaaaa agcctgtgaa 720
agggtgcttc ttgactttaa tgtctttaa agtatccaga gataactcaa tattaacata 780
agaaaagatt atatatatt tctgaatcga gatgtccata gtcaaatttg taaattctat 840
tcttttgttaa tttttattta tatttattta tgacagtga cttctgatt ttcatgttaa 900
acaagaaaaa gttgaagaag atatgtgaag aaaaatgtat ttttctctaa tagaaaaaaa 960
tgatcccat ttttggtaaa aaaaagtatg tgagatttat tctgaaacgt gactactttal1020
tttctaataa agagattccc tacctgcgtc ctacaagcag tccaagaatgc catgctt 1077

```

<210> 93  
 <211> 1755  
 <212> DNA  
 <213> Homo sapiens

<400> 93

```

cgcagggtcg cttgtgatct ggtacagga ttatgcaagt ttttgaggg acctgtgaca 60
ggaatcttct ctggttatgt taattccatg ctgcaggaa acgcaaaaaa tccatctgtc 120
aaactggaaac acaagatgac agccatctac ctgagtacat cttgtgcatc aaaagcccaa 180
acacagaagc atggaattac acaagcaaat gaactgttaa acctaactga gttctttgtg 240
aatcacatct tctctgattt aaaaatcagct aatgtgaaat ttttctctgt ccttaaaagt 300
gacggatata aatatattat gatttttaga aatcaaagtc caaaagaaca ttttttagtc 360
tcgattctct tcttgattaa tcatctcaa gctgaaagta ttgtgtgtca tacttaacga 420
gctcatgctc ttgacggcct ctttactatg cgagggccta acaatgccac ttcttttaca 480
gctgcagaaa tgcacccgtt tgttgagatt ctgctaacaa accctttcaa agctcttcaa 540
cttctcggtc cttcagaaaaa tgaatatatt atgaaagcta tcatgagaag tttttctctc 600
ctacaagaag ccaatattccc ctacatccct actctcatca ctacagcttac cagaagagcta 660
tagctgttta gtaagaaccc aagcaaacct caacttcaatc actacatgtt tcgaagcaata 720
ggtttatcca taagaataac ttgcaaaagct aacctgtgtg ctgtgtgaaa ttttgaggag 780
tctgtgtttt tgggtgtttac tgaaatctta caaaatgatg tgcaagaatt tattccatc 840
gtctttcgaag tgatgctctt gcttctgaaa acacacaaaa atgacatccc gtcttctcat 900
atggccttat tctctcatct cctcagcca gtgctttggg aaagaacagg atattattct 960
gctctagtga ggctctttca agcattctta gaacgcggtt caaacacaa agcaagtgtc1020
goagctgaca aaatctctgg gttactaggt gtctttcaga agctgattgc atccaaagca1080
aatgacaccc aaggttttta tcttctaacc agtataatag agcactgccc tcttgaatca1140
gttgaccatt ataggaataa aatcttcatt ctgctattcc agagacttca gaattccaaa1200
acaaccaaag ttatcaagag ttttttagtc tttattaatt tgtattgcat aaaaataggg1260
gcactagac tacaagaata atttgatgtt atacaaccaa aatggtttgg aatggtttg1320
gaaaaatta ttattctga aattcagaag gtatctgaaa atgtagagaa aaagatctgt1380
gcggttgga taaccaaatt actaacagaa tgtcccccac tgatggacac tgagtatacc1440

```

```

aaactgtgga ctccattatt acagtctttg atgtgtcttt ttgagttacc cgaagatgat1500
accattctctg atgaggaaca ttttattgac atagaagata caccaggata tcagactgcc1560
ttctcacagt tggcatttgc tgggaaaaaa gagcatgatc ctgtaggcca aatggtgaat1620
aaccocaaaa ttacacttgc acagtcaact cacaagtgtg ctaccgcctg tccaggaagg1680
gttccatcaa tggcaagaa ctctgtgata aatggagact ttaatgggag ggcaaaaggal1740
tagtagtagt tctggg                                     1755

```

&lt;210&gt; 94

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

```

gttggcgag cgagcacctt cgacgcggtc cggggacccc tgcgtcgtgt cctccgcagc 60
cggaccgggt gccccagcct cgcgctgccc ggcagggtgc tctgtgccca ctcccgcgc 120
acgcccctcg cgcctccgg gccctcccg cgcctctctt ctgcgcgcgc gcgcagatgg 180
gcgccccgcg aggtctctgc ctgtcggtct ctgcttgcgc cgccgacgac gacttttgcc 240
gcagcttcggc aagaatgtgt ctgtgaaaa ctacaagctg cctgtaaatg ctttgtgaat 300
aataatcgct aatgccagtg tacttcagtt ggtgcacaaa atactgtcat ttgctcaaa 360
ctggctgcca aatgtttggt gatgaaggca gaaatgaatg gctcaaaact tgggagaaga 420
gcacaaacctg aaggggccct ccagacaact cgtgggcttc atgatcctga ctgcgatagg 480
agcgggctct ttaaggccaa gcagtgcac ggccactcca tgtgctgggt tgtgaacact 540
gctgggggtca gaagaacaga caaggacact gaaataacct gctctgagcg agtgagaacc 600
tactggtatca tcatgaact aaaaacacaa gcaagagaaa aacctatga tagtaaaagt 660
gtgcggactg cacttcagaa ggagatcaca acgcttacc aactggatcc aaaaatttacc 720
acgagatatt tgtatgagaa taatgtttat actattgatc tgggtcaaaa tctctctcaa 780
aaaaactcaga atgatgtgga catagctgat gtggcttatt attttgaaaa agatgttaaa 840
ggtgaactct tgtttcattc taagaaaaatg gacctgcagc taaatgggga acaactggat 900
ctggactctg gtcacaaactt aatttattat gttgatgaaa aagcacctga attctcaatg 960
cagggtctaa aagctggtgt tattgctgtt attgtgggtg tgggtgatgc agttgttct1020
ggaattgtgt gctgtgttat tccagaaag aagagaatgg caaagtatga gaagctgag1080
atagaaggaa tgggtgagat gcataggaaa ctcaatgcac aactatataa ttggaagatt1140
atagaaggaa ggaatagaca aatggacaca aattacaaat gtgtgtgcgt gggacgaaga1200
catctttgaa ggtcatgagt ttgttagttt aacatcatat atttgaata gtgaaacctg1260
tactcaaaat ataagcagct tgaactggc ttaccaatc ttgaaattg accacaagt1320
tcttatatac gcagatctaa tgaataaacc agaacttggg ctccatcgtt aaaattatt1380
atgtgttaaca tcaaatgtg tgcattaat atgcttccac agtaaaatct gaaaaactga1440
tttgtgattg aaagctgcct ttctatttac ttgagctctg tacatcata cttttttatg1500
agctatgaaa taaaactatt taaactgaaa aaaaaaaaaa aaggc                                     1545

```

&lt;210&gt; 95

&lt;211&gt; 1133

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

gcgcggtatt atcgggtaga catctcgac cgcgtctcgc aaaccggtag cgcttcgagc 60
atggctgacc aactgactga agagcagatt gcagaattca aagaagcttt ttactattt 120
gacaaaagat gtgatggaaac tataacaaca aaggaattgg gaactgtaat gagatctctt 180
gggcagaaat ccacgaagac agagtacagc gacatgatta atgaagtaga tgcgtgatgg 240
aatggcaca tgaacttctc ctgaatttct ggacaaggat ggcaagaaaa atgaagaca 300
cagacagtgga agaaagaaat agaaaagcat tccgtgtgtt tgataaggat ggaacgggct 360
atatagtgtc tgcgaactt ccactgtgga tgacaaacct tggagagaag ttcaaatgat 420
aagaagttga gaaatgatc agggaaagcag atattgatgg tgatggtcaa gtaaaactatg 480
aagagttgtg gcttactctg acagcaaaagt gaagaccttg tacagaatgt gtttaactgt 540
ttgtacaaaa ttgtttattt gccctttctt ttgttgaact ttatctgtaa aaggtttctc 600
cctactgtca aaaaaaatg catgtatagt aattaggact ctactcctcc atgtttctct 660
cccttatctt actgtcattg tctaaaaacc ttattttaga aaagtgtatc aaggttaaat 720
gttgctatgtg gcttactctg gggaaatatt taagcccttc tgcacatcta aacttagatg 780
gagttgggtca aatgagggaa catctgggtt atgccttttt taaagtagtt tctcttagga 840
actgcacaga tgttgttgtt gaagtgtgga gttgtaactc tgcgtggact atggacagtc 900

```

```

aacaatatgt acttaaaagt tgcactattg caaaacgggt gtattatcca ggtactcgta 960
cactattttt ttgtactgct ggtcctgtac cagaacatt ttcttttatt gttacttgc1020
ttttaaactt ggtttagcca cttaaaatct gcttatggca caatttgccc caaaatccat1080
tccaaagtgt atatttgttt tccaaataaa aaattacaat ttacccaaa aaa 1133

```

&lt;210&gt; 96

&lt;211&gt; 791

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

```

ggcggccgcg cggaccgggc gagaggcggc ggcgggagcg gcggtgatgg acgggtccgg 60
ggagcagccg agagcggggg ggcccaccag ctctgagcag atcatgaaga cagggggccct120
tttgcctcag ggtttcatcc aggatcgagc agggcgaaat gggggggagg caccgagct180
ggccctggag ccggtgcctc aggatcgctc caccagaag ctgagcgagt gtctcaagcg240
catcggggag gaactggaca gtaacatgga gctgcagagg atgattggcg ccgtggacac300
agaactcccc cgagaggtct ttttccgagt ggcagctgac atgttttctg acggcaact360
caactggggc cgggtgtgtc cccttttcta ctttgcagc aaactgggtg tcaaggccct420
gtgcaccaag gtgcgggaac tgatcagaac catcatgggc tggacattgg acttctccg480
ggagcggctg ttgggctgga tccaaagcca ggtgtggtgg gacggcctcc tctcctact540
tgggaacgccc acgtggcaga ccgtgacct ctttgtggcg ggagtgctca ccgcctact600
caccattcgg aagaagatgg gctgaggccc ccagctggct tggactgtgt ttctctcaa660
taaatattgg catttttctg ggaggggtgg ggtattgggg acatgggcat tttcttact720
tttgaatata ttgggggtg tggggaagag tggttctgag ggggtaataa acctcctctg780
ggacacaaaa a 791

```

&lt;210&gt; 97

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

```

tcctgccttc accatgaagt ccagcggcct cttcccttc ctggtgctgc ttgccctggg 60
aactctggca ccttgggctg tggaaaggctc tggaaagtcc ttcaaagctg gagtctgtcc120
tcctaaagaa tctgccagct gcccttagata caagaacct gagtccgaga gtactggca180
gtgtccaggg aagaagagat gttgtcctga cacttgtggc atcaaatgcc tggactcctg240
tgacacccca aaccacaaca ggagggaagcc tgggaaagtgc ccagtgcatt atggccaatg300
tttgatgctt aaccccccca atttctgtga gatggatggc cagtgcgaag gtgacttgaa360
gtgtgtgatg ggcatgtgtg ggaatcctg cgtttccctc gtgaaagctt gattcctgcc420
atatggagga ggctctggag tcctgctctg tgtgttccag gctcttcca cctgagact480
tggctccacc actgatattc tccttggggg aaaggcttgg cacacagcag gcttcaaga540
agtgcagatt gatcaatgaa taataaaagc agcctatttc tctttgcata aaaaaaaa 599

```

&lt;210&gt; 98

&lt;211&gt; 643

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

```

ggggccgcg ctcggcgcta ggaggcgggt cctctgcagc aagcgtgggg gcggggaacc 60
cgagcaggag tctccagatc tcagtcacct tggacaaaga agtgtggatc ctacagattcc120
atcttttcca actccaaggt gccatggcag agaaggtgct ggtaacagggt ggggtggct180
acattggcag ccacacgggt ctggagctgc tggaggctgg ctacttgctt gtggtcatcg240
ataacttcca taactgcctc cgtggagggg gctccctgcc tgagagctgc cggcggttcc300
aggagctgac aggcgctcct gtggagtgtt agggagatgga cattttggac cagggaagccc360
tacagcgtct cttcaaaaag tacagcttta tggcggtcat ccactttggc gggctcaagg420
ccgtggcgga gtgggtgcag aagcctctgg attattacag agttaacctg accgggacca480
tcacagctct ggagatcatg aaggccacag ggggtgaagaa cctggtgttc agcagctcag540
ccactgtgta cgggaacccc cagtacctgc ccccttgatg gaggggccacc ccacggggtg600
ggatgtaaca accttacgga agtccaaatt tctttatctt ttc 643

```

<210> 99  
 <211> 860  
 <212> DNA  
 <213> Homo sapiens

<400> 99

```
ctcgcagccgc tcgagccgat tcggctcgag tgcctccaga ggactggcca cttttgcct 60
agataaagat gcacttagag atgaatatga tgatctctca gatttgaatg cagtacaaat120
ggagagtgtt cgagaatggg aaatgcagtt taaagaaaaa tatgattatg taggcagact180
ctctaaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaactttgt aaacaaccaa agtcaggggc ctccaagaact gcaattctta300
ctccctttcca cagactgtcc ggagtctttg ggtttgattc acctgctgcg aaaaacattc360
aacaataatt gtacaagata aattaatctc actatgaaga ttgaataac tagacattat420
ttatgctgccc aaactcattt gttgcagtgt tttgtaatgt ctagtggggc ttcatcatcc480
tgaaaagaag gagacaggga tttttttaaa gagcaagaaa gtcaaatat tacttctttc540
ctctcttttt tcctctcttt ctttctcttt tctcttttaa atatattgaa600
gacaacccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagtgt ttcaggctac tgaaacatta aaagtgaat780
tcccaaatct ttctttttgg cattgtctcg gggataggga aatatcggtt ttaaggaggt840
cttggaattt ggggtggga                                     860
```

<210> 100  
 <211> 1155  
 <212> DNA  
 <213> Homo sapiens

<400> 100

```
cggggctcgc ccagcctggt ccggggagag gactggctgg gcaggggcgc cgccccgcct 60
ggggagaggc gggccgggag gggctgggag tatttgaggc tcggagccac cgccccgcct 120
cgcccgccag caccctctcg ccagcagccg tcggagagcca gccacgagc ggaaaatggc 180
agacaatttt tcgctccatt atgcgttatt tgggtcttga aaccacaaac ctcaaggatg 240
gcctggcgca tgggggaacc agcctgctgg ggcagggggc taccagggg ctccctatcc 300
tggggcctac ccggggcagg caccctcagg ggccttatct ggacaggcac ctccaggcgc 360
ctaccctgga gcactggag ctatcccg agcacctgca cctggagtct acccagggcc 420
accagcggc cctggggcct acccatcttc tggcagacca agtgccaccg gaggctacc 480
tgccactggc cccatggcg cccctgctgg gccactgatt gtgcttata acctgccttt 540
gactgctgat aacaattctg ggacgggtga agcctcaatgc 600
aacagaattt gctttagatt tccaaagagg gaatgatgtt gccttccact ttaaccacgc 660
cttcaatgag aacaacaggga gactcattgt tgaaagtggg aaaccattca aaatacaagt 780
aagggaaagaa agacagctcg ttttccatt tgaagtggg gctcacttgt tgcagtaaca 840
actgggtgaa cctgaccatt tcaaggctgc caaactggga atttctggtg acatagacct 900
ctatcggtgt aaaaaactca atgaaatcac tgaataaact agattaaaaa aaaaaaaga 960
cttcaaaactc tacatgtgta aaggtttcat gttcactgtg agtgaaaaat ttcatattca1020
tcaatatccc tcttgttaagt catctactta ataatatta cagtgaaaaa aaaaaaaaal1080
aaaaaaaaaa gtccgaaaaag gagggggaag gagagagagg gaagaagaga gagggaagg1140
aggggggggg tgggt                                     1155
```

<210> 101  
 <211> 522  
 <212> DNA  
 <213> Homo sapiens

<400> 101

```
aaaaatatatt gctggaaaatt gctgtgtagg attacaggcg tgaccactgc gcccgccac 60
attcagttctt tatcaaaagaa ataaccagaa cttaattctg aatgatacga ttatgcccaal120
tattaagttaa aaaataataa aaagggttat cttaaataga tcttaggcaa aatcaccagct180
gatgaaggca tctgatgcct tcactgttgc agtcatctcc aaaaacagta aaaataacc240
```

```

ctttttgttg ggcaaatatga aattttttaa ggagtagaat accaaatgat agaaacagac300
tgccctgaatt gagaattttg atttctttaa gtgtgtttct ttctaaatgt ctgttccctta360
atttgatttaa ttttaattcat gtattatgat taaactctgag cgagatgagc ttacaagtat420
gaaaaaatat actaattaat cacaaatgtg aagttatgca tgatgtaaaa aatacaaaa480
ttctaatttaa aggtcttgca acacaaaaaa aagaaaaaaa aa 522

```

<210> 102  
 <211> 1628  
 <212> DNA  
 <213> Homo sapiens

<400> 102

```

ccagctcgcc ctgectagcc agggcgcccc cgccccctgc ctgcccggcc accttcggga 60
gcgcgtttcca ataggcggtc gccattggct ctggcgacct ccgcgcgttg ggaggtgtag 120
cgcggtctctg aacgcgctga gggccgttga gtgtcgagcg ccgcgagggc gcgagtgagg 180
agcagaccoca ggcacgcgcg ccgcgagaagg ccggcgctcc ccacactgaa ggtccggaaa 240
ggcgacttccc gggggcttgg gcacctggcg gacctctccc gagcgtcgcc gacggaacgc 300
gagcgctctcc attgcgcgtg cgcgttgagg ggcttcccgc acctgatcgc agactggccaa 360
cgcgctgggtg cgtcgctcgc gcgtctcgcc tgagctggcc atggcgagct gtgcgggctg 420
agcgcgagcgc ggcgtgttct gccctgctgg gatcgctgct cctctctgag gtctggcgcg 480
ccgacccaga ccgcagcctc caccactctc gcctgtgtgc gaaggtggtg ggcagatgcc 540
gggctcccat gcctaggtag tggtagcaat tcactgacgg atctggccag ctgtttgtgt 600
atgggggctg tgacggaaaac agcaataatt acctgaccaa gggaggagtgc ctcaagaagt 660
gtgccactgt cacagagaat gccacgggtg acctggccac cagcaggaaat gcacgggatt 720
cctctgtccc aagtgtctcc agaaggcagg atctgaaaga ccactccagc gatatgttca 780
actatgaaga atactgcacc gccaacgcag tcactggggc ttgcccgtga tccctccac 840
gctgtactct tgacgtggag aggaactcct gcaataactt catctatgga ggctgccggg 900
gcaataagaa cagctaccgc tctgaggagg cctgcattgt ccgctgcttc gccacagcgg 960
agaatcctcc cctgcccttt ggctcaaaag tgggtgttct ggcggggctg ttctgtgagg1020
tgtgtatcct ctctcctggga gccctccatg tctacctgat ccgggtggca cggaggaaacc1080
aggagcgtgc cctgcgcacc gctctggagct ccggagatga caaggagcag ctggtgaagall140
acacatatgt cctgtgaccg cctgtgcgcc aagaggactg ggggaaggag gggagactat1200
gtgtgagctt tttttaaata gagggaattga tccggatttg agtgatcatt agggctgagg1260
tctgtttctc tgggaggtag gacggctgct tctgtgtctg gcagggatgg gtttgtttt1320
gaaatcctct aggaggtctc tctctgcgat gctctgcagc tggcagcagc ccagagtgt1380
ttctcgtctg atcgatttct ttctccagg tagagtttct tttgcttatg ttgaattcca1440
ttgcctcttt tctcatcaca gaagtgtatg tggaaatcgt tctttgtttt gtctgattta1500
tggttttttt aagtataaac aaaagttttt tattagcatt ctgaaagaag gaaagtaaaa1560
tgtacaagtt taataaaaaa gggccttccc cttagaata aaaaaaaaaa aaaaaaaaaa1620
aaaaaaa

```

<210> 103  
 <211> 605  
 <212> DNA  
 <213> Homo sapiens

<400> 103

```

cctggcgagct gtcggctgga aggaactggt ctgctcacac ttgctggctt gcgcatcagg 60
actggccttta tctgctgact cagcgtgcaa aggtgcactc tgcgaacgtt aagtcgctcc120
ccagcgcttg gaatcctacg gcccccacag ccggatcccc tcaagcttcc aggtcctcaa180
ctcccgcgga cgctgaacaa tggcctccat ggggctacag gtaatgggca tcgcgctggc240
cgtcctgggc ttgctggcgg tcatctgctg ctgcgcgctg cccatgtggc gcgtgacggc300
ctctaccgce agcaacattg tcaactcgca gacctctgg gaggggcctg gggatgaact360
cgtggtgcag agcaccggcc agatcgagtg caaggtgtac gactcgctgc tggcactgcc420
gcaggacctg caggcgggcc gcgccctcgt catcatcagc atcatcgctg ctgctctggg480
cgtgctgctg tccgtggtgg ggggcgaagt gtaacaaact tgctctggag attaaaaagc540
ccaagggcaa gaacatgatt cgttggcggg cgtgggtgtt tctgtttggg ccggcctaatt600
gggtg

```

<210> 104  
 <400> 104

000

<210> 105  
 <211> 2731  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 105

```

aggggggcgg acagacacag actatgcaga tgggagtgaa gacaaagtag tagaagtagc 60
agaggaggaa gaagtggctg aggtggagga cgatgaggat ggtgatgggg tagagaaaga 120
ggctgaggaaa cctctacgaag aaagccacaga gagacacaga gtcctgtgaaa gaggctggttc 180
gagaggtgtg gactgaaggg aagtgtgtccc cattctcttta cggcggatgt ggcggcaacc 300
accttggatgt tgacacagaa gagtactgca tggccgtgtg tggcagcgcc attcttcaaa 360
ggaaacaactt tgacacagaa gccgttgaca agtatctcga gacacctggg gatgagaatg 420
cagcagccag taccctcgat gccaaagaga ggcttgaggc caagcaccga gagagaatgt 480
aacatgccca ttccagaaaa gcaaaagaga aacctgaagc aaagaacttg cctaaagctg 540
cccaggtcat gagagaatgg gaagaggcag aacgtcaagc atctttgaaa caggaaagcag 600
ataaagaagg agttatccag catcttccagg agaaaagtga agtgaaagcc atgtctcaatg 660
ccaacgagag acagcagctg gtggagacac acatggccag agtggaagcc atgtctcaatg 660
acgcgcgcgc cctggccctg gagaactaca tcacgcctct gcaggctgtt cctctctggc 720
ctcgtcacgt gttcaatatg cttaaagaagt atgtccgcgc agaacagaga gacagacagc 780
acacctcaaa gcatttcgag catgtgcgca tgggtggatcc caagaaagcc gctcagatcc 840
ggctccagggt tatgacacac ctccgtgtga ttatgagcg catgaaatcg tctctctccc 900
tgctctcaaa cgtgcctgca gtggccgagg agtatcagga tgaagtgtat gagctgtctc 960
agaaagagca aaactattca gatgacgtct tggccaacat gattagttaa ccaaggtcal1020
gttacggaaa cgatgctctc atgccatctt tgaccgaaac gaaaaccacc gtggagctcc1080
ttcccgtagaa tggagagttc agcctggacg atctccagcc gtggcattct tttggggctg1140
actctgtgcc agccaacaca gaaaacgaag ttgagcctgt tgatgcccgc cctgctgccg1200
accggagcct gaccactcga ccagggtctg gggtgacaaa tatcaagacg gaggagatct1260
ctgaagttaa gatggatgca gaattccgac atgactcagg atatgaagt catcatcaaa1320
aatgtgtgtt ctttgcagaa gatgtgggtt caaacaaagg tgcaatcatt ggaactcatg1380
tgggcggtgt tbtcatagcg acagtgtatc tcatcacctt ggtgatgctg aagaagaaac1440
agtcacatc catctcatcat ggtgtggtgg aggttgacgc cgctgtcacc ccagaggagc1500
ggcacctgtc caagatgcag cagaacggct acgaaaaatcc aacctacaag ttctttgagc1560
agatgcagaa ctagaccccc gccacagcag cctctgaagt tggacagcaa aaccattgct1620
tcactaccct tgggtgtcca tttatagaat aatgtgggaa gaaacaacc cgttttatga1680
tttactcatt atcgctcttt gacagctgtg ctgtaacaca agtagatgc tgaacttgaa1740
tttaatccca catcagtaat gtattctatc tctctttaca ttttggcttc tatactacat1800
tatttaagtg ttttgtgtac tgtaaaagaa tttagctgtat caaaactagc atgtctgatt1860
ttctctcctg attattttac acatagcccc tttagccagt gtattattt cttgtgggtt1920
gtgacccaat taagtctctac tttacatagt ctttaagaaat cgatggggga tgcttcatg1980
gaacgtggga gttcagctgc ttctcttgcc taagtattcc tttctcgtac actatgcatt2040
ttaaagttaa aactttttaa gtatttcaga tgcttttagg agattttttt tccagtactg2100
cattttactg tacagattgc tgtcttctgt agatttttga tataggaatt aagaggatc2160
acacgcttgt ttctctgtgc ctgttttatg tgcacacatt aggcatttag acttcaagct2220
ttctcttttt tcttccacgta tctttgggtc ttgtataaag aaaagaatcg ctgtctattg2280
taagcacttt tacggggcgg gtgggggagg gtgctctgct ggtcttcaat taccaaagaa2340
tctccaaaac aattttctgc aggatgattg tacagaaatca ttgcttatga catgatcgct2400
ttctacactg tattacataa ataaattaaa taaaataacc ccgggcaaga ctttctctgt2460
aaggatgact acagacatta aataatcgaa gtaattttgg gtggggagaa gaggcagatt2520
caattttctt taagcagttc gaagtttcat ttaatgatac aaagaagatg aaaaaggaa2580
tggcaatata aggggatgag gaaggcatgc ctggacaaac ccttctttta agatgtctc2640
tcaaatttga taaattgtgt ttttcatgta aataataaca ttcttggagg agccaaaaaa2700
aactatatta ctggcaggtt tataatatgg c

```

<210> 106  
 <211> 2194  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 106

```

gaattcagaa gttaatgatg ttgggtaaga gaacaatggt aagagagcaa tctaagaata 60
tatcaccttac ttttaatttta tatgagagta ctggtgagtg ggaattgtag 120
cactgctcctt acccaacgcag atttattcca gtgaacaac aactggaact tcaagtaact 180
cctccacagag tgccctgcag ttctgggttg ccccaaatcc aactaatgcc accaccaagg 240
cggtctgtggg ttgaagagact caggccaaga aagctctctt aaatttcccc ttcttctcaa 360
ccaatcccaa atggcgtctg gaagtccaat gtggcaagga aaacacagtc atctctgaat 420
ctactaatttc cacacctttt attgacacag aatgatgtga gaatcccaaa ttgtattgat 480
ttgaagaaca ttgagagggt ttgactagat gatggatgcc aattattaaat ctgtggagt 540
ttcatgtaca agatgaaggga gaggcaacat ccaaaatagt taagacatga ttctcttgaa 600
tgtggcttga gaaatatgga cacttaatac taccttgaaa ataagaatag aaataaaggga 660
tgggatttgtg gaattggagat ccagttttca ttgggttcat taattctata agggccataaa 720
acaggtaata taaaacagctt ccagtattct atttatagt acatgagaag gaacttccag 780
gtgttactgt aattctccaa cgtattgttt cgacagcact aatttaattgc cgatatactc 840
tagatgaagt ttacatttgt tgagctattg ctgttctctt gggaactgaa ctcaactttcc 900
tcttgagggt ttgattttga cattgcattt gaccttttat gtagttaatt acatgtgcca 960
gggcaaatgt ggaatgagaat ctaccccag atccaagcat cctgagcaac ttgtgattat 1020
ccatatttga tcgaatggta ggcattttct atcacctgtt tccattcaac aagagcacta 1080
cacttcattta gctaaaacgga ttccaaaagg tagaattgca ttgaccgcga tcaattttcaa 1140
aatgcttttt attatattta ttttttagac agtctcactt tgcgcgccag ctgggagtg 1200
agtgggtgcga tctccagatca gtgtaccatt tgctcccggt gctcaagcga tctctctgcc 1260
tcagctctccg aagttagctgg gattacaggg acctgccacc atgcccggct aatttttgt 1320
attttagtag agacagggtt tcaccatggt gcccaggctg gtttcgaagt ctgactctca 1380
gtgtactccac cgcgtctggc ctcccaaggt gctgggatta ctttttcaaa tttaaaaaaa 1440
cagccatacaa aatgcttttt atttctgcat atgttgaata ctttttcaaa tttaaaaaaa 1500
tgatctgttt tgaaggcaaa attgcaaaatc tgaaaatcaa gaaggccaac atgtaaaagg 1560
tgcataaacta taatacaagt atttgggaag tgaagactgg aagctaattt gcaattaaat 1620
cacaaaactt tataactctt ctgtatatac attttttctc tatattttta tagtttagaa 1680
cagaattagcc acattttagaa cactttttgt tatcagtcac tattttttaga tagtttagaa 1740
ctggctcttaa gcttaaaaagt gggcttgatt ctgcatgtaaa ttttttcaaa ctgctctgac 1800
acacataaac ctttttaaaa atagacactc ccgaagctct ttgttgcga tgggtacaca 1860
ctgatgctta gatgttccag taatcttaata tggccacagt agctcttgat accaaagtcc 1920
tttttttcca tcttttagaaa actacatggg aacaaacaga tcgaacagtt ttgaagctac 1980
tgtgtgtgtg aatgaacact ctgtgcttat tccagaatgc tgcatactga ttttgattg 2040
tatatttgtt ttgtgtattt acgctttgat tcatagtaac tctctatgga attgatttgc 2100
attgaacaca aactgtaaat aaaaagaaat ggctgaagaa gcaaaaaaaa aggaaagaaa 2160
aaaagaaaaa aaaagaaaaa aaaagggggg agggc

```

&lt;210&gt; 107

&lt;211&gt; 1812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

```

cggaaaggtgg accttggatg aattttgacg agaacaagtt cgtggaccga agaagatggg 60
ggccgcacgac ccaggcccggt gccccgacga ggccgaggtg gacacctgcc ccttgcgcaa 120
aggaataactg aaacagaccc tacaggcagc tctgaagaac cccctatcac acacacagag 180
tcaggccagtg aaggaccggg caggcagcat tgtctgaag tgcctcatct cctttaaagg 240
taattgatata gaaaaggcag ttcaattctc ggacagaagt ggttggatgc tccatttgaa 300
gtatctttat aaaggatttg agagcccgctc tgacaaatag agtgcattgt tactgcaatg 360
gcatgaaaaa gcaacttgctg ctggaggagt aggttccatt gttcgtgctc tgactgcaag 420
aaaaactctgt tagtctggca ggaagtggat tatctgcctc gggagttggga attgctggta 480
caaaagccaa agcaaccaaa tgcccacgct gccctgtggg tagcatctgt ttctctcagc 540
ttgtctctct tgccttttca tatctgtaaa gaaaataaatt acatatcagt tgcctcttaa 600
tgaaaatttg gataaatatg aagaatttgt gttaaaaatg aagtgtttca tctcttcaaa 660
accaatttcag tgatgtttat accaatctgt atatagtata atttaccatc aagttttaatt 720
gtgcaactct taaccocctgt tggcgtgggt ttgttctgt tttgttttgt attattttta 780
actaaactct agaatatttg tcaagaatttg agggcagttt cctagctcat tgcactcag 840
gaaatgatat ttataaaaaa tatgagagac tggcagctat taacatttga aaactggacc 900
atatcttccc tattttaata gcaaaaatag ttttggaaat aagtggtggg tgaataccac 960
tgccaaagtta tagctttgtt ttgtctggcc tcttgattat ctgtactgtg ggtttaagta 1020
tgtactttc tctcagcatc caataatcat ggccctcaaa tttattttgt gtaaccagg 1080

```

```

gttcagagca agaagtcttg ctttatacaa atgtatccat aaaatatcag agcttggtgg1140
gcatgaacat caaacctttt tccactaat atggctctgt ttggaaaaaa ctgcaaatca1200
gaagaataga ttctgcagaaa gaaagaaaaa ctatggtgta atttaaacctc tgggcagcct1260
ctgaatgaaa tgctactctt tttagaataa taatagctgc cttagacatt atgagggtata1320
caactagtat ttaagatacc atttaatatg ccccgtaaat gtcttcagtg ttcttcaggg1380
tagtgggtag ctcaaaaagat ttgggtccaga tccaaaaaaa tacacattct gtgttttagc1440
tcagtgtttt ctaaaaaaaag aaactgccac acagcaaaaa attgttttct ttgtttggaca1500
aaccaaatca gtcttcaaaa aatgaccggg gcttataaaa agttataaat atcgagtagc1560
tctaaaacaa accacctgac caagagggaa gtgagcttgt gcttagtatt tacattggat1620
gccagtcttg taactactga cttatgtgca aactggtgca gaaattctat aaactctttg1680
ctgtttttga taccctgctt ttgtttcatt ttgtttttgt ttgtaaaaaa gataaaactt1740
cagaaaataa aatgtcagtg ttgaataaaa taaaaaaaac aattgaagaa gaggatggag1800
atctcgactt gg                                     1812

```

```

<210> 108
<211> 890
<212> DNA
<213> Homo sapiens
<400> 108

```

```

aacgactcct ggtaccttgc tccattact tcccgttttc tgcgtctgct gctcgtctca 60
ggctcgtagt tcgctctcaa catgccggaa ccagcgaagt ccgctcccgc gcccaagaag120
ggctcgaaag aagccgtgac taaggcgacg aaggaaggac gcaagaagcg caaggcagcc180
gcaaggagag ctactccgta tacgtgtaca aggtgctgaa gcaggtccac ccgacaccg240
gcactctctc taaggccatg ggaatcatga actcctctgt caacgacatc ttcgaaacg300
tcgccccgtg ggcttccgcg ctggcgcatc acaacaagcg ctcgaccatc acctccagg360
agatccagac ggccgtgcgc ctgctgctgc ccggggagtt ggccaagcac gccgtgcct420
agggccacaa ggcgctcacc aagtacacca gcgctaagta aacttgccaa ggaggagact480
tctctggaaat ttccgtgata gaccaagaaa gcttcttatt aaaagaagag caatgtcct540
cggttacctc attacttact gcagaaaaaa agacgagaat gcaaccatac ctgagtgga600
ttttccaaa gctaaaagctg gccctctgat ctattcaga ttccaaagag atccatttac660
aagttaattt ctgtctcctt ggtccattcc ttctctctaa taatcattta ctgttctcca720
aagaattgtc tacattaccc atctcctctt ttgcctctga gaaagagtat ataatgtctc780
gtaccccatc ggggggttgg ggtaatatc ttgtgtctct agccctgtac cttaataaat840
ttgtatgcct ttctcttaa aaaaaaaaaa aagaagaagg aagaggatgc 890

```

```

<210> 109
<400> 109
000
<210> 110
<211> 2627
<212> DNA
<213> Homo sapiens
<400> 110

```

```

ggcacgagat gtgaaaagg tttgtgtaca ccacctccaa aaataaaaaa tggaaaaaac 60
acctttagtg aagtagaagt atttgagtat cttgatgcag taacttatag ctgtgatcct 120
gcacctggagc cagatccatt ttcaactatt ggagagagca cgaattattg tggtgacaat 180
tcagttggga tctgctgctgc tccagagtgt aaagtgggta aatgtcgatt tccagtagtc 240
gaaaaatgaa aacagatata aggtatttga aaaaaatttt actacaaagc aacagttatg 300
tttgatgcg ataagggttt ttacctcgat ggcagcgaca caattgtctg tgacagtaac 360
agtactctgg atccccagtt tccaaagtgt cttaaagtgt gactctcttc cactacaaaa 420
ttccagcgt ccagtgccct aggtcctagg cctacttaca agcctccagt ctcaaatatt 480
ccaggatctc gtaaacctga ggaagggaata cttgacagtt tggatgtttg gctcatttgc 540
gtgatgttga ttgccatagt tgttggaagt gcagtaattt gtgtgtccc gtacagatat 600
ctcaaaagta ggaagaagaa agggaaagca gatggtggag ctgaatatgc cacttaccag 660
actaaatcaa ccaactccagc agagcagaga ggctgaatag attccacaac ctggtttgcc 720
agttcatctt ttgactctat taaaaatctc aatagttggt attctgtagt ttcactctca 780
tgagtgcac tgtggcttag ctaattatgc aatgtggctt gaatgtaggt agcatccttt 840
gatgtctctt tgaaacttgt atgaatttgg gtatgaacag attgctctgt tccctctaaa 900

```



```

taacacttag atttattgga ccagtcagca cagcatgcct ggttgtatta aagcagggat 960
atcgctgtat ttataaaaatt ggcaaaaatta gagaaaatata gttcacaatg aaatttatatt1020
ttctttgttaa agaaagtggc ttgaaatctt tttgtttcaa agattaatgc caactcttaa1080
gattattctt tcaccaacta tagaatgtat tttatataac gttcattgta aaaaagccctt1140
aaaaaatatgt gtatactact ttggctcttg tgcataaaaa caagaacact gaaaaattggg1200
aatatggcaca aacttggcct ctttaaccaa gaattattatt ggaataattct ctaaaagttai1260
atagggtgaaa tctctattt ttgttaattg gttcgggtgat ttcagaaagc tagaaagtgt1320
atgtgtggcca ttgtttttca ctttttaaaa catccctaac tgatcgaata taccagtta1380
tccagaatca gatgcactct ttcataagaa gtgagaggac ctgcacagcc ataacaggga1440
tgccacttca tgggtgcgaag tgaacactgt agtcttgttg tttcccaaaa gagaaactccg1500
tagttctctt taggttgagt aaccactctt gaattctggt tacatgtgtt tttctctccc1560
tccttaataa aagagagggg ttaaacatgc cctctaaaag taggtgtgtt tgaagagaat1620
aaatttcacca gataacctca agtcacatga gaattcttagt ccatttacct tgccttggct1680
agctaaagcc atctatgtat atgtcttacc tcatctccta aaaggcagag ccctctctac1860
gccatgtatc tcaggaaggt aacttccatt tgtctatttg ctgttgattg taccacaggga1800
tggaagaagt aaatatagct caggtagcac tttatactca ggcagatctc agccctctac1860
tgagtccctt agccaagcag tttctttcaa agaagccagc agggagctgc1920
cactgcattt catatcacac tgttaaaagt tgtgttttga aattttatgt ttagttgcac1980
aaattggggc aaagaacaat tgccttgagg aagatatgat tggaaaaatca agagtgtaga2040
agaataaata cttgtttact atgctttagg aagataaagg atgtttatag tgcctgttaa2100
cctttgtagt ctctggcaag ttgaagttaa taccggtttc acatgtcttt caagaatgtc2220
attctgaatt aagcacagag ttgaagttaa taccggtttc atattccaac2280
aataacttta atgataaaaa taatatattat taatatattc ataatatagc tgtatagcag2340
acatttgatt ttttcaaat taatatattat attagagatc tatatatgta taatatgta2400
ttttgtcaaa ttgtttactt aaatatattat agaccagttt tctctgggaag ttgttttaa2460
tgacagaagc gtatatgaat tcaagaaat ttaagctgca aaaaatgatt tgcataaaa2520
tgagaagctc cactgataga gggtctttat tgcctatttt ttaaaaaatg gactcttga2580
atctgttaaa ataaaattgt acatttggaa aaaaaaaaaa gccaaaaa 2627

```

&lt;210&gt; 111

&lt;211&gt; 976

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

```

ctcgcagccgc gagattccccc cgaagttctc catgaagcgc ctcaccgccg gcctcatcgc 60
gcctcatcgt ggtgctcgtg tggccctcgt cgcgcgcgat gccgtctcgt tgatcaccaa120
ccggagaaaag tcgggggaagt acagaaggt ggagatcaag gaactggggg aggttgagaa180
ggaaaccgagc ttgtaggtac ccggcggggc agggagatggg gtgggggtacc ggaattccggt240
atcgtccccag acccaagtga gtccagcttc ctgattcctc ggcgcaaaag agacgtttat300
cctttcaaat tctgtccttc cccctccctt ttgcgcacac accaggttta atagatcctg360
gcctcaggggt ctctctttct tctcacttct gctctgaagg aagcatttct aaatgtatc420
ccctttcgtgt ccaaccaaacg gaaacctgac tggggcagtg aaggaaggga tggcatagcg480
ttatgtgttaa aaaaacaagta tctgtatgac aacccgggat cggttgcaag taactgaatc540
catgtcgaca ttgtgaaggc ttaaatgagt tttagatggga aatagcgttg ttaacgcctt600
gggtttaaat tatttgatga gttccacttg tatcatggcc taccgcagga gaagaggagt660
tggttaactg ggcctatgta gttagcctcat ttaccactgt ttgtattact gaccacat720
cctgttcact gggaaagaag cctgtttcag ctgcctgaac cgagtttgga tgtctttgag780
gacagacatt gcccggaac tcagttcatt tattcttcag cttgccctta ctgccactga840
tattggttaat gttctttttt gtaaaatggt tgtacatag ttgtcttga taatgttgc900
gtaatttttt aaaaataaac acgaatttaa taaaatatgg gaaaggcaca caaaaaaa960
aaaaaaaaaa aaaaac

```

&lt;210&gt; 112

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

```

cttcgggggt gactgcctct tccagggcgg gcggtgtggt gcacgcattg ctgtgctcca 60

```

```

actccctcag ggcctgtgtt gcgcactct gctgctatga gcttctcaa aagtttccc 120
ccgcctgggg cagcgagggg gctcctgcgg cagcagccag acactagggc tgtgctgaac 180
gggaaggggc tcggcactgg taccctttac atcgctgaga gccgctgtgc ttggttagat 240
ggctctggat taggattctc actggaatcacc cccaccatta gtttacatgc attatccagg 300
gaccgaagtg actgtctagg agagcatttg tatgtttatg tgaatgccaa atttgaagaa 360
gaatcaaaag aacctgtgtc tgatgaagaa gaggaagaca gtgatgatga tgttgaacct 420
attactgaat ttagatttgt gcctagtgtat aaatcagcgt tggaggcaat gttcactgca 480
atgtggcgaat gccaggccctt gcactcagat cctgaggatg aggattcaga tgactacgat 540
ggagaagaat atgatctgga agcacatgaa caaggacagg gggacatccc tactatttac 600
acctatgaag aaggattatc ccatctaaaca gcagaaggcc aagccacact ggagagatta 660
gaaggaaatgc ttcttcagtc tgtgagcagc cagtataata tggctggggt caggacagaa 720
gattcaataaa gagattatga agatgggatg gaggtggata ccacaccaac agttgtctgga 780
cagtttgtag atgcagatgt tgatcactga aaatgattta tgcaagttta agtattctgc 840
cctaagttga ggagagaact tgggtgcctc tccactctgg agtgaagtta atgaaagtct 900
tttctctttt ccaaaaccca acctgaacca gtttttctt gagacagact atactgagac 960
aacaagtgtg caccagcaga agatagataa tatgaccttt attaacctga tgaattaaact1020
taaccagaag ggtatttgta gtttactatt taccctaaaa ctttctgtgt ctgggtacccl080
ctcgagtagg cctataaatt ctaccttgac tgtgtgcact atttgttaag tagcagattc1140
atgtggtgaa aatgcacagg agcttggtag actgcggggg aaagagagag cctctttcgl200
cagtgtttac cagctcgtcg ttataacctc ttagtgtga tcccttaatt tccagccttt1260
taggttagtt tctgtaacag aacaagttag tctgggatga agtccctaaa gttctcaaa1320
tggtaattgt ttgtttttg taatagctta acaataaac attaggtttc tatatataaa1380
aaaaaaaaa aaaaaaaga aaggtacctg cctaataat attctgc 1427

```

&lt;210&gt; 113

&lt;211&gt; 2639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

```

tccctatctt acccttccc attctccttt tttctttctt tttttatat ggctttcttc 60
ttttcttctt tttctttttc ttcccctttt tatttgacca gtgtaaataa caaacatttta 120
ttggtgtcac ttatggtaga aaaaacttcc tacaccagat gcacatgacc cagtgtgttaa 180
atagaacatt ttgaagggtga acacacacc taaccagggt tttttaccgc ctttttaaga 240
tgggcaattc ttcttctccc cccaccccaa agacattgtga gcaactgcta atgaaaagca 300
gtaaaacagcc gcttaggcta tagcagtttc aactccactc tgagggtgaag attccaatta 360
cattcgagac ttaagttctt tcaatttttt cctaaccaaa gttcctgagt ccagatttta 420
caatattaca gcactagcag atcagtgctc acaactcacc tttttctgct gtatctctct 480
caccagttgg gggaggggcct gcacttccat agagtttgct gataaattgg tgaacaattt 540
cttccagttc cttttcttct acagtctttt cctcaatgtc agcatcttgg tggctttcca 600
gccattcaat cttttcttct tctccaatct ccatgtgtct cttatcttca gaggaaagt 660
tacctcccag cttttcttct atctcatttg gctttttgtc ttctccagca tagctttcca 720
actcatttct agtatacaat gcgtccttga gctttttgtc attctgttca ttggtgattg 840
catcattaac catctcttca atttcttcag gtgtcaggcg cactcgagaa ataccattca 900
tgatcttatt ttgttctctc gtacccttgt cttcagctgt ggaagccagc aggaagcagga 960
catctatctc aaaggtgact tcaatctgtg cttttgtcag ggggtcttca ccttcataga1020
tcagatcaaa tgtaccocaga agatgatttg tgattatcag aagctgtaga aagactctga gtttcaatac1140
ccttgattgt aacagtttgt tgattatcag tgggtcatgac acctcccaca gtattcttga taccacaga1200
tagggcaccac tgtgttctctt ggaatcagtt cagggtcacc ctacagcttc atctgggttg atgccaggg1260
caaggttaag gggacataca tcaagcagta caggttcacc cagttgtgct aatctttgga ttgtggctg1320
gcacaccagc tgggacagca gcaaccatag cagacttctt caaatcagaa tttctcaaca1380
atggttctct gccatgtgaag aactctttta tcatcaatat gttgagctct tcaaatttgg1440
agccaccaac aagaacaatt tcatcaatat gttgagctct tcaattctgt1500
ctttctggag gccctctata gtgaccgga cttcatagaa ggaactcaat tcaattctgt1560
cccgagtcag ggtctcagaa aagtcttctc cttcatagaa ggaactcaat tcaattctgt1560
cttgatgctg aagaagcagg gccggtttgg cgtcttctt tttgtacagt ttgatggc1620
cagctctatt gcttctctcg acatctttgc caccagatg agtatctcca ttagtgagc1680
gttccatgag acgctgtgtca aagtcttctc caaccagatg atcgaaggtt cgcgccacca1740
caacttccaa gacaccattg tcaattggtga gaagagacac atcgaaaggtt cgaatagcag1800
ggtcaaacac caggatgttc ttctccctct cctcttctc caggccataa ccagcgtctt1860
tgcgcgtagg ctgcgttgat atctctataa cattaggcc agcaaatagtt ccagcgtctt1860
tgggtgcttg gcgttgggca tcaataaaat aggtcgtgtc agtaacaact gcatgggtaa1920

```

```

ccttcttttc caaataagcc tcagcgggtt ctttcatttt agtgagaacc atggcagaaa1980
tttcttccagg agcaaatgtc ttgtgttggc cacctccaat atcaacttga atgtatgggt2040
tagtttttttt ttcaaccacc ttgaacggca agaacttgat gtcctgtgac acagacgggt2100
cattccacgt gggcgcatg agccgcttgg cgtcaagac cgtgttctcg ggggtggagg2160
tgagctgggt cttggcgcca tcgccaatca gacgttcccc ttccaggagt aaggcgacat2220
aggacggcgt gatcggttg ccctgatcgt tggcgatgat ctccacggcg cggttcttga2280
acacggcgac gcaggagtag gtgttcccc ggctgatgac gaccacgctg cccacgttct2340
ccttcttctc ctccctctcg gcccgcgccg cgctgagcag cagcagcatc gggcgccaca2400
gggagagctt catcttgcca gccagtgggg cagcagcagg cagtcacgac acaggccgta2460
ggcgaggagc acagcgcaat ttccgacttg cagcgccgag gggcccgggg tcacaaggcg2520
ccacgaacca ggcgaaggcg aggtctagaa atacaggcgg cggcgcttcc ctctcacact2580
cgcgaaacac cccaataggt caatctgtct gtgctgtctt ggccggcatc gacccttag 2639

```

```

<210> 114
<211> 634
<212> DNA
<213> Homo sapiens

```

```
<400> 114
```

```

ctccccgcgg cgcggttaaa tccccgcacc tgagcatcgg ctacacactg caccctggcc 60
gggcatagca ccatgcctgc ttgtcgccca ggcgcgctag ccgcgcctct cctcctcagc120
ctgctgctgt tcgggttcac cctagtctca gccacaggag cagagaagac tggcgtgtgc180
cccgagctcc aggcgtgacca gaactgcacg caagagtgcg tctcggaacg cgaattgcgc240
gacaacctca agtgcctcag cgcgggctgt gccaccttct gctctctgac caatgataag300
gagggttctc gcccccagggt gaacattaac ttcccccagc tgcgcctctg tcgggaccag360
tgccagggtg acagccagtg tcttggccag atgaatgctt gccgcaatgg ctgtgggaag420
gtgtcctctg tcactcccaa ttcttgagct ccagccacca ccaggctgag cagtgaggag480
agaaaagttt tgcttggccc tgcatctgtt tccagccacc ctgcctctcc ctttttcggg540
actctgtatt cctctctggg ctgaccacag ctcttccctt tcccaaccaa taaagtaacc600
actttcagca aaaaaaaaaa aaaaaaaaaa aaaa

```

```

<210> 115
<211> 719
<212> DNA
<213> Homo sapiens

```

```
<400> 115
```

```

gtcgactttt tttttttttt tttaaacatgg aaaagtattt ttaaaaaatcg aataatccta 60
ttcaagtcac ccagtggttaa ccccgggtgt cttcctgcga gtctgttctc ccccatggga120
gtcacacaaa atgaaaatct ctagaaaaga gaagacaaaag acccgcaaaa gatgtatgcc180
accatctatg agctgaaaga agacaagagc tacaatgtca cctccgtctc gtttagggaaa240
aagaagtgtg actactggat caggactttt gtctcagggt gccagcccgcg cgagttcacg300
ctggggcaaca ttaagagtta ccttggatta acgagttacc tcgtccgagt ggtgagcacc360
aactacaacc agcatgctat ggtgttcttc aagaagaatt tctcaaacag ggagttactt420
aagatcaccc ttatcggggag aaccaaggag ctgacttcgg aactaaagga gaacttcata480
cgctcttccc aatctctggg cctccctgaa aaccacatcg tcttccctgt ccaatcgaca540
cagtgatcgc acggctgagt gcacaggctg ccgcagctgc cgcaccagac cgaaccacat600
tgaggagagt gggagacctt cccacagtg ccacccatgc agctgtctcc caggccaccc660
cgctgatgga gcccccacct gtctgtctaaa taaacatgtg ccttcaaaaa aaaaaaaa 719

```

```

<210> 116
<211> 494
<212> DNA
<213> Homo sapiens

```

```
<400> 116
```

```

gtcgataacc ccagacgcaa gacgccgggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgctttcca aggcattctgt gagccccggg agtatacacc atgacaaaag ctaccctcc120
cgagttgaaa aaatttatgg acaagaagtt atcattgaaa ttaaatgggt gcagacatgt180
ccaaggaata ttgcggggat ttgatccctt tatgaacctt gtgatagatg aatgtgtgga240

```

```

gatggcgact agtggacaac agaacaatat tgggaatggtg gtaatacagag gaaatagtat300
catcatgttta gaagcctctgg aacgaggtata aataatggctt gtccagcaga gaaacccatg360
tcctctctccc atagggcctg ttttactatg atgtaaaaat taggtcatgt accttttcac420
attagactttt ttgttaataa aactttttgta atagtcaaaa aaaagtttgg tctcatctac480
cttataatat ctgc
494

```

```

<210> 117
<211> 1065
<212> DNA
<213> Homo sapiens

```

```
<400> 117
```

```

acgcggttga ctacgtctaa agctccattg ttagatcctt tctgtctccc ttcctggctc 60
ctcctctctc cccacccttc taataggctc ataagtgggc tcaggcctct ctgcggggct 120
cactctcgcc ttaccactgg ctttcattgc caagctcttc tatgacctca gtgccatcag 180
cctggatggg gagaaggtag atttcaatac gttccggggc agggccgtgc tgattgagaa 240
tgtggcttgg ctctgaggca caaccaccgc ggacttccac cagctcaacg agctgcaatg 300
cgctcttccc aggcgcctgg tggctcttgg tctcaagatg gtccgtctgt ggggtggata 420
gaactgtcag aatgaggaga tcttgaacag tgaagtgatg gggcagaacg agcatcctgt 480
ccagcccacc ttaccctctg tccaaaaaat tgaggtgaat gggcagaacg agcatcctgt 480
cttcgcctac ctgaaggaca agctccctta cctctatgat gacccatttt ccctcatgac 540
gcatcccaag ctcatcattt ggagccctgt gcgcgcgtca gatgtggcct ggaactttga 600
gaagtctctc atagggcccg agggagagcc ctccgcagcg tacagccgca ccttcccaac 660
catcaaacat gagcctgaca tcaagcgccct cctttaaagt gccatataga tgtgaaactgc 720
tcaacacaca gatctctac tccatccagt cctgaggagc cttaggatgc agcatcctt 780
caggagacac tgcctggacct cagcattccc ttgatatcag tccccctcac tgcagagcct 840
tgcttctccc ctctgcctgt ttctttttcc tctcccaacc ctctggttgg tgattcaact 900
tgggctccaa gacttgggta agctctgggc ctccacagaa tgatggacc tctctaaact 960
ctcatgggtg gtgtctgaga ggcgtgaagg gctctggagc actctgctag aagagaccaa1020
taaaaggcgag gtgtggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1065

```

```

<210> 118
<400> 118
000

```

```

<210> 119
<400> 119
000

```

```

<210> 120
<211> 648
<212> DNA
<213> Homo sapiens

```

```
<400> 120
```

```

ggactgcggt cgtagtctc cggcgagttg ttgcctgggc tggacgtggt tttgtctgct 60
ggcccgctgc ttcgcgtctc cgtttcatth tctgcagcgc gccagcagga tggcccacaa120
gcagactctac tactcggaca agtactctga cgaacactac gagtaccggc atgttatgtt180
accagagaaa ctttccaaac aagtacctaa aactcatctg atgtctgaag agggatggag240
gagacttggt gtccacacaga gtctaggctg ggttccatcc atgattcatg agccagaacct300
acatatctct cctcttagac gacctcttcc aaaaagatcaa caaaaatgaa gtttatctgg360
ggatctgcaa atctttttca aatttaattg atatgtgtat ataaggtagt attcagttaa420
tacttgagaa atgtacaaaat ctttcatcca tactctgca tgagctgtat tcttcacagc480
aacagagctc agttaaatgc aactgcgaag aggttactgt aagatgttta agataaaagt540
tcttccagtc agtttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaag tttgtatgtt gcatttataa aaaaaaaaaa aaagtcca 648

```

```

<210> 121
<211> 1842
<212> DNA
<213> Homo sapiens

```

&lt;400&gt; 121

```

ctcgagccgc tcgagccgct gctctcttga gggggtagag atcaaaggcg gctccttccg 60
acttctcccaa gaggggccagg cactggagta cgtgtgtcct tctggcttct acccgtagcc 120
tgtgcagaca cgtacctgca gatctacggg gtctctggagc accctgaaga ctcaagacca 180
aaagactgttc aggaaggcag agtgcagagc aatccactgt ccaagaccac acgacttcca 240
gaacggggaa tactggcccc ggtctcccta ctacaatgtg agtgcagaga tctcttcca 300
ctgctatgac ggtttacact tccggggctc tgccaatcgc acctgccaag tgaatggccc 360
gtggagtggg cagacagcga tctgtgacaa cggagcgggg tactgtccca acccgggcat 420
ccccattggc acaaggaaggt tgggcagcca gtaccgcctt gaagacagcg tcactacca 480
ctgcagccgg gggcttaccct tggctggctc ccagcggcga acgtgtcagg aaggtggctc 540
ttggagccgg ccgagagcctt cctgccaaga ctctctcatg tacgacacc ctcaagaggt 600
ggccggaagt ttctgtctt ccttgacaga gaccatagaa ggagtcgatg ctgaggatgg 660
gcacggccca ggggaacaac agaagcggaa gatcgtcctg gaccttcag gctccatgaa 720
catctacctt gtgctagatg gatcagacag cattggggcc agcaactcca caggagccaa 780
aaagtgtcta gtcaacttaa ttgagaaggt ggcaagttat ggtgtgaagc caagatatgg 840
tctagtgcac tatgccacat accccaaat ttgggtcгаа gtgtctgaag cagacagcag 900
taatgcagac tgggtcacga agcagctcaa tgaatcaat tatgaagacc acaagttaa 960
cagcgggact aacaccaaga aggcctcca ggcagtgatc agcatgatga gctggccaal020
tgacgtccct cctgaagggt ggaacggc acccaattac gtccattgat gagatccggg acttgctaa1140
attgcacaac atggggcggg acccaaggga ggaattattcgt gatgtctatg ttgttggggt1200
cattggccaag gatccaaaaa tgaacatcaa tgcctttgggt tccaagaaa acaatgagca1260
cgggctctttg gtgaaccaag tgaacatcaa tgcctttgggt tccaagaaa acaatgagca1280
acatgtgttc aaagtcaagg atatggaaaa cgttgaagat gtgttctacc aaatgatcga1320
tgaagccagc tctctgagtc tctgtggcat ggtttgggaa cacaggaaag gtaccgattal1400
ccacaagcaa ccatggcagg ccaagatctc agtcattcgc ccttcaaaag gacacagag1480
ctgtatgggg gctcgtggtg ctgagtaact ttgtgtgaca gcagcacatt gtttcaactgt1500
gtgtagcaag gaacactcaa tcaaggtcag cgtaggaggg gagaagcggg acctggagat1560
agaaagtatc ctatttcacc ccaactacaa cattaattgg aaaaagagga caggaaattcc1620
tgaattttat gactatgacg ttgcccgtgat caagctcaag aataagctga aatctggcca1680
gactatcagc cccatttgct tcccctgcac caggggaaca actcgagct tgaggcttcc1740
tccaaactacc acttgcacgc aaaaaaagg aagcgtgtct cccgcagaag agcaagaaa1800
ctgtgtgttg tccgggggga gaaaaaaacc gcccccgggg gg 1842

```

&lt;210&gt; 122

&lt;211&gt; 1596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

```

ggcgggtata aaagccccac ccaggccagc cggctctgct cagcatttgg ggacgtcttc 60
agctctcggc gcacggccca gcttccctca aaatgtctac atgtccagaa atcttgccta 120
agctcagctt ggagggtgat cactctacac ccccaatgct atatgggtct ctcaagctc 180
atactaactt tgatgtctgag cgggatgctt tgaacattga aacagccatc aagaccaaa 240
gtgtggatga gcttaccatt gtcaacattt tgaccaaccg cagcaatgca cagagacagg 300
atattgcctt gcctaccagc agaaggacca aaaaggaaat tgcatcaga ctgaagtcag 360
ccttatctgt ccaactggag acggtgattt tgggcctatt gaagacactt gctcagttg 420
acgcttctga gctaaaagct tccatgaagg ggctgggaa cgcagaggac tctctcattg 480
agatcatctg ctccagaacc aaccaggagc tgacagaaat tgacagagtc tacaaggaaa 540
tgatacaagg tgatctggag aaggacatta ttccggacac atctggtgac tcccgcaag 600
tgatggttgc cctggcaaa ggtagaagag cagaggatgg ctctgtcatt gattatgaa 660
tgattagcca agatgcctgg gatctctatg acgctggagt gaagaggaaa ggaactgatg 720
ttcccaagtc cctgcagcat atgacggagc ggaggggccc cactccaga gattatttga 780
taggtacaag agttacagcc ctatgatcat gttggaagac atcaggaaa aggttaaa 840
agacactggaa aatgctttcc tgaacctggg tcaagtgcatt cagaacaagc cctgtattt 900
tgctgtcagg ctgtatgact ccatgaagg caaggggagc cgagataaag tctctgatca 960
aatcatggct tcccgcagtg aagtgacat gttgaaaatt aggtctgaat tcaagagaa1020
gtacggcgaag tctgttact attatatcca gcaagacact aagggcgact accgaagc1080
ggtgctgtac ctgtgtggtg gagatgactg aagccgaca cggcctgagc gctcagaa1140
gtgtctcacc atgctccag ctaacagggtc tagaaaacca gcttgcgaat aacagtcctc1200
gtggccatcc ctgtgagggt gacgttagca ttaccccaa cctcatttta gttgcctaag1260

```

```

cattgcctgg ccttcctgtc tagtctctcc tgtaagccaa agaaatgaac attccaaggal320
gttggaagtg aagctctatga tctgaaacac ttgcccctct gtgtactgtg tcataaacag1380
atgaataaac tgaattttgta ctttagaacc acgtactttg ttgcccctgt ttcaactgaa1440
ttgtttgaaa attaaacgtg cttgggggttc agctgggtgag gctgtccctg taggaagaaa1500
gctctgggac tgagctgtac agtatgggtg cccctatcca agtgtgcgta tttaaagttaa1560
atttaaatga aataaaataa aataaaatca aaaaaa

```

&lt;210&gt; 123

&lt;211&gt; 1033

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

```

gtcgcagctg accctcgctc cgcggccgcg ctggagtcgg acgtggaagt tgctggctga 60
ctgggcttgc gaggaaccgc cctcggagct gcagccgaag gcaaggaaac actgaagatc 120
ggcgaggagg gacagggggg tcatcatggg tggccttttc tcaagtatat tttccagtct 180
gtttggaact cgggaaatga gaattttaat ttggggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaagt tgttactact ataccctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gagcacagac 360
agagtatcagg ccaactctgga gatgttaacta ttcaaacaca gatgcagtca tttatgtagt 420
agacagttgt gaccgagacc gaattggcat ttccaaatca gagttagttg ccatgttgga 480
ggaagaagag ctgagaaaag ccatttttagt ggtgtttgca aataaacagg acatgggaca 540
ggccatgact tctctagaga tggcaaatcc acttgggtta cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaccaa aggcaccggc ctgtgatgag caatgggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagtcga ttctctctcc ctgaaatgaa 720
gactacatca cctctctccc ttgggaacaa gtcaagtgtg ctccacacta ctatagtgtta 780
aaactatatt attattggca tatactgact gactgcaata ttgttagtaa atagggaaaa 840
taagtattta gtggagggga taatttgatc gaatcacctg aatgttctat gtaagtataa 900
tatctctttt attctcttct tgtgttaagg tatatatctt atttgtagtg aattcttatt 960
caaatcacgt tctattaaag agtatactcc tatgtgatga aaaaaaccta aaaaaaaaaa1020
aaaaaaaaaa aaa

```

&lt;210&gt; 124

&lt;211&gt; 65

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

```

Ile  Cys  Leu  Leu  Val  His  Phe  Val  Ser  Arg  Ala  Lys  Thr  Val  Asn  Leu
 1      5      10      15      20      25      30      35      40      45      50      55      60      65

Thr  Phe  Ser  Tyr  Trp  Trp  Val  Ile  Thr  Glu  Asn  Lys  Asp  Leu  Phe  Ser
      20      25      30      35      40      45      50      55      60      65      70      75      80      85      90

Cys  Ser  Leu  Leu  Lys  Ser  His  Lys  Asn  Asn  Gln  Ile  Gly  Ser  Cys  Leu
      35      40      45      50      55      60      65      70      75      80      85      90      95      100      105

Leu  Ser  Cys  Val  Ser  Trp  Phe  Leu  Thr  Cys  Val  His  Thr  Pro  Val  Cys
 50      55      60      65      70      75      80      85      90      95      100      105      110      115      120

Leu
65

```

&lt;210&gt; 125

&lt;211&gt; 64

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

```

Ile  Ser  Val  Phe  Arg  Leu  Phe  Lys  Tyr  Leu  Thr  His  Phe  Gln  Thr  Cys

```

| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Phe | Tyr | Lys | Pro | Leu | Asp | Phe | Gln | Gln | His | Thr | Ile | Glu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Cys | Tyr | Ser | Lys | His | Asn | Phe | Ser | Val | Ser | Ser | Ile | Ala | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asp | Asn | Ile | Ala | Ile | Ser | Gly | Met | Leu | Gln | Ala | Phe | Lys | Ile | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

<210> 126  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

| <400> 126 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys       | Ala | Asn | Leu | Leu | Pro | Ala | Thr | Pro | Glu | Gly | Thr | Gln | Ile | Trp | Val |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly       | Pro | Val | Phe | Gln | Leu | Gly | Lys | Arg | Met | Gly | Lys | Pro | Gly | Asp | Gly |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe       | His | Lys | Phe | Ser | Ser | Gly | Leu | Trp | His | Ser | Phe | Gln | Glu | Ile | Pro |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu       | Gly | Lys | Gly | Leu | Leu | Ala | Asn | Met | His | Phe | Gln | Thr |     |     |     |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

<210> 127  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

| <400> 127 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu       | Lys | Asn | Thr | Asn | Glu | Val | Lys | Ala | Leu | Asn | Trp | Tyr | Thr | Leu | Phe |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr       | Pro | Ile | Phe | Gln | Val | Trp | Lys | Cys | Ile | Phe | Ala | Ser | Arg | Pro | Leu |
|           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro       | Arg | Gly | Ile | Ser | Trp | Lys | Glu | Cys | His | Asn | Pro | Leu | Glu | Asn | Leu |
|           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp       | Lys | Pro | Ser | Pro | Gly | Phe | Pro | Ile | Arg | Leu | Pro | Ser | Trp | Lys | Thr |
|           | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly       | Pro | Thr | His | Ile | Trp | Val | Pro | Ser | Gly | Val | Ala | Gly | Arg | Arg | Phe |
| 65        |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala       | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 128  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

| <400> 128 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His       | Thr | Trp | Asp | Pro | Tyr | Pro | Leu | Gly | Ile | Ser | Pro | Arg | Thr | Ile | Arg |
| 1         |     |     |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |     |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----|-----------|
| Pro       | Val       | Cys       | Gln<br>20 | Pro       | Lys       | Val       | Ala       | Phe<br>25 | Gly       | Met       | Leu       | Asn       | Phe<br>30 | Pro | Leu       |
| Ser       | Lys       | Lys<br>35 | Val       | His       | Leu       | Pro       | Asn<br>40 | Glu       | Val       | Thr       | Ile       | Arg<br>45 | Leu       | Asn | Pro       |
| Lys       | Lys<br>50 | Ser       | Leu       | Asp       | Phe       | Val<br>55 | Phe       | Tyr       | Lys       | Asn       | Ser<br>60 | Thr       | Phe       | Pro | Ile       |
| Lys<br>65 | Ser       | Leu       | Val       | Ile       | Lys<br>70 | Ile       | Ser       | Thr       | Leu       | Pro<br>75 | Lys       | Cys       | Asp       | Ser | Thr<br>80 |
| Ala       | Trp       | Phe       | Leu       | Ala<br>85 | Asn       | Lys       | Asn       | Pro       | Ile<br>90 |           |           |           |           |     |           |

<210> 129  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 129

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met<br>1  | Val       | Ala       | Asp       | Tyr<br>5 | Gly       | Cys       | Thr       | Ile       | Leu<br>10 | Ile       | Leu       | Gly       | Pro       | Phe<br>15 | Thr       |
| His       | Arg       | Asn       | His<br>20 | Thr      | Lys       | Trp       | Pro       | Asp<br>25 | Thr       | Tyr       | Phe       | Thr       | Glu<br>30 | Gln       | Phe       |
| Lys       | Tyr       | Tyr<br>35 | Thr       | Leu      | Ala       | Lys       | Ser<br>40 | Thr       | Tyr       | Ser       | Thr       | His<br>45 | Pro       | Gly       | Glu       |
| Gly       | Gly<br>50 | Glu       | Lys       | Thr      | His       | Thr<br>55 | Tyr       | Lys       | Thr       | Thr       | Ser<br>60 | Leu       | Asp       | Thr       | Met       |
| Cys<br>65 | Leu       | Pro       | Thr       | Ile      | Ser<br>70 | Ser       | Leu       | Asn       | Asn       | Phe<br>75 | His       | Gln       | Leu       | Arg       | Cys<br>80 |
| Leu       | Val       |           |           |          |           |           |           |           |           |           |           |           |           |           |           |

<210> 130  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 130

|           |           |           |           |          |           |           |           |           |           |     |           |           |           |           |     |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Arg<br>1  | Asn       | Leu       | Val       | Thr<br>5 | Gln       | Met       | Lys       | Ser       | Gly<br>10 | Ile | Glu       | Asp       | Pro       | Trp<br>15 | Thr |
| Trp       | Gln       | Val       | Asn<br>20 | Ala      | Asp       | Tyr       | Ser       | Leu<br>25 | Ala       | Phe | Pro       | Leu       | Tyr<br>30 | Leu       | Cys |
| Lys       | Glu       | Gly<br>35 | Tyr       | Thr      | Glu       | Leu       | Ile<br>40 | Leu       | Phe       | Gln | Ala       | Tyr<br>45 | Asn       | Phe       | Lys |
| Phe       | Tyr<br>50 | His       | Leu       | Asn      | Ser       | Ser<br>55 | Thr       | Phe       | Ala       | Ala | Glu<br>60 | Glu       | Trp       | Asn       | Gln |
| Lys<br>65 | Asn       | Val       | Val       | Ser      | Trp<br>70 |           |           |           |           |     |           |           |           |           |     |

<210> 131



<211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 131

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ile | Gln | Cys | Glu | Ala | Tyr | Phe | Ile | Ala | Thr | Leu | Val | Asp | Cys | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Asp | Ser | Ala | Thr | Val | Leu | Asp | Lys | Leu | Met | Phe | Pro | Phe | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Asn | Arg | Arg | Ala | Thr | Tyr | Ser | Ala | Gly | Ser | Arg | Ala | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Gly | Ser | Arg | Gly | Tyr | Thr | Ser | Ser | Leu | Ile | Ile |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

<210> 132  
 <211> 181  
 <212> PRT  
 <213> Homo sapiens

<400> 132

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Asn | Met | Ala | Ala | Pro | Leu | Gly | Gly | Met | Phe | Ser | Gly | Gln | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gly | Pro | Pro | Gln | Ala | Pro | Pro | Gly | Leu | Pro | Gly | Gln | Ala | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ala | Ala | Pro | Gly | Ala | Pro | Arg | Pro | Ser | Ser | Ser | Thr | Leu | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Leu | Glu | Ser | Ser | Phe | Glu | Ala | Cys | Phe | Ala | Ser | Leu | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Asp | Tyr | Val | Asn | Gly | Thr | Asp | Gln | Glu | Glu | Ile | Arg | Thr | Gly | Val |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gln | Cys | Ile | Gln | Lys | Phe | Leu | Asp | Ile | Ala | Arg | Gln | Thr | Glu | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Phe | Leu | Gln | Lys | Arg | Leu | Gln | Leu | Ser | Val | Gln | Lys | Pro | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ile | Lys | Glu | Asp | Val | Ser | Glu | Leu | Arg | Asn | Glu | Leu | Gln | Arg | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Leu | Val | Gln | Lys | His | Leu | Thr | Lys | Leu | Arg | His | Trp | Gln | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Glu | Asp | Ile | Asn | Val | Gln | His | Lys | Lys | Pro | Ala | Asp | Ile | Pro |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Gly | Ser | Leu | Ala | Tyr | Leu | Glu | Gln | Ala | Ser | Ala | Asn | Ile | Pro | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Leu | Lys | Pro | Thr |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 133  
 <211> 423

<212> PRT  
 <213> Homo sapiens

<400> 133

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu<br>1   | Ser        | Glu        | Asp        | Glu<br>5   | Ile        | Arg        | Thr        | Leu        | Lys<br>10  | Gln        | Lys        | Lys        | Ile        | Asp<br>15  | Glu        |
| Thr        | Ser        | Glu        | Gln<br>20  | Glu        | Gln        | Lys        | His        | Lys<br>25  | Glu        | Thr        | Asn        | Asn        | Ser<br>30  | Asn        | Ala        |
| Gln        | Asn        | Pro<br>35  | Ser        | Glu        | Glu        | Glu        | Gly<br>40  | Glu        | Gly        | Gln        | Asp        | Glu<br>45  | Asp        | Ile        | Leu        |
| Pro        | Leu<br>50  | Thr        | Leu        | Glu        | Glu        | Lys<br>55  | Glu        | Asn        | Lys        | Glu        | Tyr<br>60  | Leu        | Lys        | Ser        | Leu        |
| Phe<br>65  | Glu        | Ile        | Leu        | Ile        | Leu<br>70  | Met        | Gly        | Lys        | Gln        | Asn<br>75  | Ile        | Pro        | Leu        | Asp        | Gly<br>80  |
| His        | Glu        | Ala        | Asp        | Glu<br>85  | Ile        | Pro        | Glu        | Gly        | Leu<br>90  | Phe        | Thr        | Pro        | Asp        | Asn<br>95  | Phe        |
| Gln        | Ala        | Leu        | Leu<br>100 | Glu        | Cys        | Arg        | Ile        | Asn<br>105 | Ser        | Gly        | Glu        | Glu        | Val<br>110 | Leu        | Arg        |
| Lys        | Arg        | Phe<br>115 | Glu        | Thr        | Thr        | Ala        | Val<br>120 | Asn        | Thr        | Leu        | Phe        | Cys<br>125 | Ser        | Lys        | Thr        |
| Gln        | Gln<br>130 | Arg        | Gln        | Met        | Leu        | Glu<br>135 | Ile        | Cys        | Glu        | Ser        | Cys<br>140 | Ile        | Arg        | Glu        | Glu        |
| Thr<br>145 | Leu        | Arg        | Glu        | Val        | Arg<br>150 | Asp        | Ser        | His        | Phe        | Phe<br>155 | Ser        | Ile        | Ile        | Thr        | Asp<br>160 |
| Asp        | Val        | Val        | Asp        | Ile<br>165 | Ala        | Gly        | Glu        | Glu        | His<br>170 | Leu        | Pro        | Val        | Leu        | Val<br>175 | Arg        |
| Phe        | Val        | Asp        | Glu<br>180 | Ser        | His        | Asn        | Leu        | Arg<br>185 | Glu        | Glu        | Phe        | Ile        | Gly<br>190 | Phe        | Leu        |
| Pro        | Tyr<br>195 | Glu        | Ala        | Asp        | Ala        | Glu        | Ile<br>200 | Leu        | Ala        | Val        | Lys        | Phe<br>205 | His        | Thr        | Met        |
| Ile        | Thr<br>210 | Glu        | Lys        | Trp        | Gly        | Leu<br>215 | Asn        | Met        | Glu        | Tyr        | Cys<br>220 | Arg        | Gly        | Gln        | Ala        |
| Tyr<br>225 | Ile        | Val        | Ser        | Ser        | Gly<br>230 | Phe        | Ser        | Ser        | Lys        | Met<br>235 | Lys        | Val        | Val        | Ala        | Ser<br>240 |
| Arg        | Leu        | Leu        | Glu        | Lys<br>245 | Tyr        | Pro        | Gln        | Ala        | Ile<br>250 | Tyr        | Thr        | Leu        | Cys        | Ser<br>255 | Ser        |
| Cys        | Ala        | Leu        | Asn<br>260 | Met        | Trp        | Leu        | Ala        | Lys<br>265 | Ser        | Val        | Pro        | Val        | Met<br>270 | Gly        | Val        |
| Ser        | Val        | Ala<br>275 | Leu        | Gly        | Thr        | Ile        | Glu<br>280 | Glu        | Val        | Cys        | Ser        | Phe<br>285 | Phe        | His        | Arg        |
| Ser        | Pro<br>290 | Gln        | Leu        | Leu        | Leu        | Glu<br>295 | Leu        | Asp        | Asn        | Val        | Ile<br>300 | Ala        | Val        | Leu        | Phe        |
| Gln        | Asn        | Ser        | Lys        | Glu        | Arg        | Gly        | Lys        | Glu        | Leu        | Lys        | Glu        | Ile        | Cys        | His        | Ser        |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 305        |            |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            | 320        |
| Gln        | Trp        | Thr        | Gly        | Arg<br>325 | His        | Asp        | Ala        | Phe        | Glu<br>330 | Ile        | Leu        | Val        | Glu        | Leu<br>335 | Leu        |
| Gln        | Ala        | Leu        | Val<br>340 | Leu        | Cys        | Leu        | Asp        | Gly<br>345 | Ile        | Asn        | Ser        | Asp        | Thr<br>350 | Asn        | Ile        |
| Arg        | Trp        | Asn<br>355 | Asn        | Tyr        | Ile        | Ala        | Gly<br>360 | Arg        | Ala        | Phe        | Val        | Leu<br>365 | Cys        | Ser        | Ala        |
| Val        | Ser<br>370 | Asp        | Phe        | Asp        | Phe        | Ile<br>375 | Val        | Thr        | Ile        | Val        | Val<br>380 | Leu        | Lys        | Asn        | Val        |
| Leu<br>385 | Ser        | Phe        | Thr        | Arg        | Ala<br>390 | Phe        | Gly        | Lys        | Asn        | Leu<br>395 | Gln        | Gly        | Gln        | Thr        | Ser<br>400 |
| Asp        | Val        | Phe        | Phe        | Ala<br>405 | Ala        | Gly        | Ser        | Leu        | Thr<br>410 | Ala        | Val        | Leu        | His        | Ser<br>415 | Leu        |
| Asn        | Glu        | Val        | Ser<br>420 | Gly        | Lys        | Tyr        |            |            |            |            |            |            |            |            |            |

&lt;210&gt; 134

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|
| Val<br>1   | Glu        | Asn        | Ile        | Glu<br>5   | Val        | Tyr        | His        | Glu        | Phe<br>10  | Trp        | Phe        | Glu        | Glu        | Ala<br>15  | Thr       |
| Asn        | Leu        | Ala        | Thr<br>20  | Lys        | Leu        | Asp        | Ile        | Gln<br>25  | Met        | Lys        | Leu        | Pro        | Gly<br>30  | Lys        | Phe       |
| Arg        | Arg        | Ala<br>35  | His        | Gln        | Gly        | Asn        | Leu<br>40  | Glu        | Ser        | Gln        | Leu        | Thr<br>45  | Ser        | Glu        | Ser       |
| Tyr<br>50  | Tyr        | Lys        | Glu        | Thr        | Leu        | Ser<br>55  | Val        | Pro        | Thr        | Val        | Glu<br>60  | His        | Ile        | Ile        | Gln       |
| Glu<br>65  | Leu        | Lys        | Asp        | Ile        | Phe<br>70  | Ser        | Glu        | Gln        | His        | Leu<br>75  | Lys        | Ala        | Leu        | Lys        | Cys<br>80 |
| Leu        | Ser        | Leu        | Val<br>85  | Pro        | Ser        | Val        | Met        | Gly        | Gln<br>90  | Leu        | Lys        | Phe        | Asn        | Thr<br>95  | Ser       |
| Glu        | Glu        | His        | His<br>100 | Ala        | Asp        | Met        | Tyr        | Arg<br>105 | Ser        | Asp        | Leu        | Pro        | Asn<br>110 | Pro        | Asp       |
| Thr        | Leu        | Ser<br>115 | Ala        | Glu        | Leu        | His        | Cys<br>120 | Trp        | Arg        | Ile        | Lys        | Trp<br>125 | Lys        | His        | Arg       |
| Gly        | Lys<br>130 | Asp        | Ile        | Glu        | Leu        | Pro<br>135 | Ser        | Thr        | Ile        | Tyr        | Glu<br>140 | Ala        | Leu        | His        | Leu       |
| Pro<br>145 | Asp        | Ile        | Lys        | Phe        | Phe<br>150 | Pro        | Asn        | Val        | Tyr        | Ala<br>155 | Leu        | Leu        | Lys        | Val        | Leu       |
| Cys        | Ile        | Leu        | Pro        | Val<br>165 | Met        | Lys        | Val        | Glu        | Asn<br>170 | Glu        | Arg        | Tyr        | Glu        | Asn<br>175 | Gly       |

|            |            |            |            |     |            |            |            |            |     |            |            |            |            |     |     |
|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|-----|
| Arg        | Lys        | Arg        | Leu<br>180 | Lys | Ala        | Tyr        | Leu        | Arg<br>185 | Asn | Thr        | Leu        | Thr        | Asp<br>190 | Gln | Arg |
| Ser        | Ser        | Asn<br>195 | Leu        | Ala | Leu        | Leu        | Asn<br>200 | Ile        | Asn | Phe        | Asp        | Ile<br>205 | Lys        | His | Asp |
| Leu        | Asp<br>210 | Leu        | Met        | Val | Asp        | Thr<br>215 | Tyr        | Ile        | Lys | Leu        | Tyr<br>220 | Thr        | Ser        | Lys | Ser |
| Glu<br>225 | Leu        | Pro        | Thr        | Asp | Asn<br>230 | Ser        | Glu        | Thr        | Val | Glu<br>235 | Asn        | Thr        |            |     |     |

<210> 135  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 135

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Arg<br>1  | Ile       | Arg       | Ile       | Asn<br>5  | Gly       | Ser       | Leu       | Cys       | Pro<br>10 | Gln       | Thr       | Lys       | Asn       | Asn<br>15 | Leu       |
| Tyr       | Phe       | His       | Ile<br>20 | Val       | Glu       | Leu       | Ser       | Ile<br>25 | Ser       | Gly       | Ala       | Ser       | Val<br>30 | Gly       | Glu       |
| Arg       | Trp       | Tyr<br>35 | Gly       | Met       | Gly       | Glu       | Ser<br>40 | Ile       | Leu       | Pro       | Ala       | Arg<br>45 | Gly       | Glu       | Ser       |
| Gln       | Gly<br>50 | Leu       | Leu       | Cys       | Leu       | Tyr<br>55 | Phe       | Tyr       | Lys       | Glu       | Ile<br>60 | Leu       | Pro       | Leu       | Phe       |
| Leu<br>65 | Val       | Asn       | Lys       | Leu       | Arg<br>70 | Gly       | Thr       | Asp       | Val       | Gly<br>75 | Leu       | Glu       | Gln       | Gly       | Leu<br>80 |
| Ser       | Gly       | Gly       | Glu       | Gly<br>85 | Ser       | Trp       | Thr       | Ala       |           |           |           |           |           |           |           |

<210> 136  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 136

|           |     |           |           |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Glu<br>1  | Glu | Glu       | Arg       | Ala<br>5 | Lys       | Arg       | Glu       | Glu       | Leu<br>10 | Glu       | Arg       | Ile       | Leu       | Glu<br>15 | Glu       |
| Asn       | Asn | Arg       | Lys<br>20 | Ile      | Ala       | Glu       | Ala       | Gln<br>25 | Ala       | Lys       | Leu       | Ala       | Glu<br>30 | Glu       | Gln       |
| Leu       | Arg | Ile<br>35 | Val       | Glu      | Glu       | Gln       | Arg<br>40 | Lys       | Ile       | His       | Glu       | Glu<br>45 | Arg       | Met       | Lys       |
| Leu<br>50 | Glu | Gln       | Glu       | Arg      | Gln       | Arg<br>55 | Gln       | Gln       | Lys       | Glu       | Glu<br>60 | Gln       | Lys       | Ile       | Ile       |
| Leu<br>65 | Gly | Lys       | Gly       | Lys      | Ser<br>70 | Arg       | Pro       | Lys       | Leu       | Ser<br>75 | Phe       | Ser       | Leu       | Lys       | Thr<br>80 |
| Gln       | Asp |           |           |          |           |           |           |           |           |           |           |           |           |           |           |

<210> 137  
 <211> 71

<212> PRT  
 <213> Homo sapiens

<400> 137

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Leu | Lys | Val | Glu | Tyr | Leu | Leu | Ser | Cys | Pro | Val | Ser | Cys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Cys | Ser | Ser | Ala | Ala | Ile | Arg | Ala | Ser | Phe | Leu | Phe | Lys | Met | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Thr | Val | Ser | Leu | Ala | Ile | Pro | Ala | Ser | Ala | Ala | Gln | Pro | Phe | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Gln | His | Thr | Arg | Lys | Ala | Glu | Leu | Arg | Asn | Ala | Asp | Val | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Lys | Lys | Glu | Gln | Lys | Met |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

<210> 138

<211> 67

<212> PRT

<213> Homo sapiens

<400> 138

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ala | Gln | Arg | Lys | Tyr | Phe | Asn | Leu | Pro | Val | Glu | Ile | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Arg | Cys | Gln | Thr | Val | Leu | Asn | Gly | Arg | Thr | Ser | Lys | Ser | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Val | Pro | Thr | Thr | Arg | Gly | Leu | Leu | Tyr | Cys | Ser | Thr | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Tyr | Phe | Leu | Ala | Glu | Ala | Ser | Pro | Trp | Ser | Ala | Met | Tyr | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 139

<211> 49

<212> PRT

<213> Homo sapiens

<400> 139

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Glu | Lys | Val | Glu | Gln | Tyr | Lys | Ser | Pro | Arg | Val | Val | Gly | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Ser | Leu | Leu | Leu | Val | Leu | Pro | Phe | Lys | Thr | Val | Trp | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Met | Thr | Arg | Ile | Ser | Thr | Gly | Arg | Leu | Lys | Tyr | Phe | Leu | Cys | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 140

<211> 132

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | Glu | Arg | Arg | Gly | Phe | Ile | Met | Ala | Asp | Asp | Leu | Lys | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Tyr | Lys | Lys | Leu | Pro | Ser | Val | Glu | Gly | Leu | His | Ala | Ile | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Arg | Asp | Gly | Val | Pro | Val | Ile | Lys | Val | Ala | Asn | Asp | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Glu | His | Ala | Leu | Arg | Pro | Gly | Phe | Leu | Ser | Thr | Phe | Ala | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Asp | Gln | Gly | Ser | Lys | Leu | Gly | Leu | Ser | Lys | Asn | Lys | Ser | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Tyr | Tyr | Asn | Thr | Tyr | Gln | Val | Val | Gln | Phe | Asn | Arg | Leu | Pro | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Val | Ser | Phe | Ile | Ala | Ser | Ser | Ser | Ala | Asn | Thr | Gly | Leu | Ile | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Glu | Lys | Glu | Leu | Ala | Pro | Leu | Phe | Glu | Glu | Leu | Arg | Gln | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Glu | Val | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 141

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Met | Ile | Leu | Leu | Phe | Leu | Glu | Ser | Pro | Ser | Leu | Leu | Pro | Trp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Arg | Ala | Lys | Val | Asp | Lys | Lys | Pro | Gly | Arg | Lys | Ala | Cys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Leu | Ser | Phe | Ala | Thr | Leu | Ile | Thr | Gly | Thr | Pro | Ser | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Thr | Thr | Met | Ala | Trp | Ser | Pro | Ser | Thr | Leu | Gly | Asn | Phe | Leu | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asn | Arg | Phe | Arg | Ser | Ser | Ala | Met | Met | Asn | Pro | Leu | Leu | Ser | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gln | Ser | Pro | Arg | Leu | Gly | Phe | Leu | Gly | Cys | Leu | Val | Leu | Ser | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Thr | Ser | Gly | Thr | Ala | Leu | Lys | Thr | Gly | Ser | Ser | Ser | Ser | His | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Met | Ile | His | Asp | Leu | Val | Cys | Ala | Pro | Gly | Ser | Thr | Phe |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

&lt;210&gt; 142

<211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 142

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Val | Lys | Arg | Gly | Trp | Asp | Leu | Asn | Met | Ala | Ala | Val | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Ala | Leu | Lys | Gly | Arg | Gly | Ala | Arg | Asn | Ala | Arg | Val | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Leu | Ala | Gly | Ala | Thr | Ala | Asn | Lys | Ala | Ser | His | Asn | Arg | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Leu | Gln | Ser | His | Ser | Ser | Pro | Glu | Gly | Lys | Glu | Glu | Pro | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Ser | Pro | Glu | Leu | Glu | Tyr | Ile | Pro | Arg | Lys | Arg | Gly | Lys | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Met | Lys | Ala | Val | Gly | Leu | Ala | Trp | Ala | Ile | Gly | Phe | Pro | Cys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Leu | Phe | Ile | Leu | Thr | Lys | Arg | Glu | Val | Asp | Lys | Asp | Arg | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Gln | Met | Lys | Ala | Arg | Gln | Asn | Met | Arg | Leu | Ser | Asn | Thr | Gly | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Glu | Ser | Gln | Arg | Phe | Arg | Ala | Ser | Ser | Gln | Ser | Ala | Pro | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Val | Gly | Ser | Gly | Val | Gln | Thr |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

<210> 143  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 143

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Arg | Ser | Ala | Pro | Gln | Val | Cys | Thr | Pro | Asp | Pro | Thr | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Gly | Ala | Leu | Trp | Glu | Glu | Ala | Leu | Asn | Leu | Trp | Leu | Ser | Tyr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Val | Leu | Asp | Asn | Arg | Met | Phe | Cys | Arg | Ala | Phe | Ile | Cys | Phe | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ser | Leu | Ser | Thr | Ser | Arg | Leu | Val | Arg | Met | Lys | Arg | Arg | Ile | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Lys | Pro | Met | Ala | Gln | Ala | Ser | Pro | Thr | Ala | Phe | Met | Gly | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Pro | Leu | Phe | Leu | Gly | Met | Tyr | Ser | Ser | Ser | Gly | Asp | Arg | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Ser | Leu | Pro | Ser | Gly | Glu | Leu | Trp | Leu | Cys | Arg | Ala | Arg | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Leu Leu

&lt;210&gt; 144

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 144

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Glu<br>1   | Asp        | Glu        | Val        | Glu<br>5   | Glu        | Glu        | Ser        | Thr        | Ala<br>10  | Leu        | Gln        | Lys        | Thr        | Asp<br>15  | Lys        |
| Lys        | Glu        | Ile        | Leu<br>20  | Lys        | Lys        | Ser        | Glu        | Lys<br>25  | Asp        | Thr        | Asn        | Ser        | Lys<br>30  | Val        | Lys        |
| Pro        | Lys        | Gly<br>35  | Lys        | Val        | Arg        | Trp        | Thr<br>40  | Gly        | Ser        | Arg        | Thr        | Arg<br>45  | Gly        | Arg        | Trp        |
| Lys        | Tyr<br>50  | Ser        | Ser        | Asn        | Asp        | Glu<br>55  | Ser        | Glu        | Gly        | Ser        | Gly<br>60  | Ser        | Glu        | Lys        | Ser        |
| Ser<br>65  | Ala        | Ala        | Ser        | Glu        | Glu<br>70  | Glu        | Glu        | Glu        | Lys        | Glu<br>75  | Ser        | Glu        | Glu        | Ala        | Ile<br>80  |
| Leu        | Ala        | Asp        | Asp        | Asp<br>85  | Glu        | Pro        | Cys        | Lys        | Lys<br>90  | Cys        | Gly        | Leu        | Pro        | Asn<br>95  | His        |
| Pro        | Glu        | Leu        | Ile<br>100 | Leu        | Leu        | Cys        | Asp        | Ser<br>105 | Cys        | Asp        | Ser        | Gly        | Tyr<br>110 | His        | Thr        |
| Ala        | Cys        | Leu<br>115 | Arg        | Pro        | Pro        | Leu        | Met<br>120 | Ile        | Ile        | Pro        | Asp        | Gly<br>125 | Glu        | Trp        | Phe        |
| Cys        | Pro<br>130 | Pro        | Cys        | Gln        | His        | Lys<br>135 | Leu        | Leu        | Cys        | Glu        | Lys<br>140 | Leu        | Glu        | Glu        | Gln        |
| Leu<br>145 | Gln        | Asp        | Leu        | Asp        | Val<br>150 | Ala        | Leu        | Lys        | Lys<br>155 | Glu        | Arg        | Ala        | Glu        | Arg<br>160 |            |
| Arg        | Lys        | Glu        | Arg        | Leu<br>165 | Val        | Tyr        | Val        | Gly        | Ile<br>170 | Ser        | Ile        | Glu        | Asn        | Ile<br>175 | Ile        |
| Pro        | Pro        | Gln        | Glu<br>180 | Pro        | Asp        | Phe        | Ser        | Glu<br>185 | Asp        | Gln        | Glu        | Glu        | Lys<br>190 | Lys        | Lys        |
| Asp        | Ser        | Lys<br>195 | Lys        | Ser        | Lys        | Ala        | Asn<br>200 | Leu        | Leu        | Glu        | Arg        | Arg<br>205 | Ser        | Thr        | Arg        |
| Thr        | Arg<br>210 | Lys        | Cys        | Ile        | Ser        | Tyr<br>215 | Arg        | Phe        | Asp        | Glu        | Phe<br>220 | Asp        | Glu        | Ala        | Ile        |
| Asp<br>225 | Glu        | Ala        | Ile        | Glu        | Asp<br>230 | Asp        | Ile        | Lys        | Glu        | Ala<br>235 | Asp        | Gly        | Gly        | Gly        | Val<br>240 |
| Gly        | Arg        | Gly        | Lys        | Asp<br>245 | Ile        | Ser        | Thr        | Ile<br>250 | Thr        | Gly        | His        | Arg        | Gly        | Lys<br>255 | Asp        |
| Ile        | Ser        | Thr        | Ile<br>260 | Leu        | Asp        | Glu        | Lys        | Ile<br>265 | Ile        | Thr        |            |            |            |            |            |

&lt;210&gt; 145

&lt;211&gt; 185



<212> PRT  
 <213> Homo sapiens

<400> 145

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Glu | Lys | Ser | Gly | Ser | Cys | Gly | Gly | Met | Met | Phe | Ser | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Pro | Thr | Tyr | Thr | Lys | Arg | Ser | Phe | Leu | Arg | Ser | Ala | Arg | Ser | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Phe | Lys | Ala | Thr | Ser | Lys | Ser | Cys | Asn | Cys | Ser | Ser | Asn | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ser | Ser | Leu | Cys | Trp | Gln | Gly | Gly | Gln | Asn | His | Ser | Pro | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Ile | Ile | Arg | Gly | Gly | Arg | Arg | Gln | Ala | Val | Trp | Tyr | Pro | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Glu | Ser | His | Arg | Arg | Ile | Ser | Ser | Gly | Trp | Phe | Gly | Arg | Pro | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Leu | His | Gly | Ser | Ser | Ser | Ser | Ala | Arg | Met | Ala | Ser | Ser | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Ser | Ser | Ser | Ser | Glu | Ala | Ala | Asp | Asp | Phe | Ser | Ser | Leu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     | Asp |
| Pro | Ser | Leu | Ser | Ser | Leu | Leu | Glu | Tyr | Phe | His | Leu | Pro | Arg | Val | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Pro | Val | His | Arg | Thr | Leu | Pro | Leu | Gly | Phe | Thr | Leu | Glu | Phe | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Phe | Ser | Asp | Phe | Phe | Lys | Ile | Ser | Phe | Leu | Ser | Val | Phe | Cys | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Val | Asp | Ser | Ser | Ser | Thr | Ser | Ser |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

<210> 146  
 <400> 146  
 000

<210> 147  
 <400> 147  
 000

<210> 148  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 148

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Gln | Pro | Thr | Ser | Ala | Met | Lys | Asp | Pro | Ser | Arg | Ser | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Ser | Ile | Ile | Asn | Glu | Asp | Val | Ile | Ile | Asn | Gly | His | Ser | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Asp | Asp | Asn | Pro | Phe | Ala | Glu | Tyr | Met | Trp | Met | Glu | Asn | Glu | Glu |

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Phe | Asn | Arg | Gln | Ile | Glu | Glu | Glu | Leu | Trp | Glu | Glu | Glu | Phe | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Arg | Cys | Phe | Gln | Glu | Met | Leu | Glu | Glu | Glu | Glu | Glu | His | Glu | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Ile | Pro | Ala | Arg | Asp | Leu | Pro | Gln | Thr | Met | Asp | Gln | Ile | Gln | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Phe | Asn | Asp | Leu | Val | Ile | Ser | Asp | Gly | Ser | Ser | Leu | Glu | Asp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Val | Lys | Ser | Asn | Leu | Asn | Pro | Asn | Ala | Lys | Glu | Phe | Val | Pro | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Lys | Tyr | Gly | Asn | Ile |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 149

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 149

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ser | Asp | Lys | Arg | Ala | Phe | Thr | Ile | Lys | Ser | Ser | Asn | Thr | Ala | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Trp | Lys | Leu | Cys | Tyr | Ile | His | Gln | Lys | Arg | Ala | Pro | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Phe | Pro | Tyr | Phe | Thr | Pro | Gly | Thr | Asn | Ser | Phe | Ala | Phe | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Arg | Leu | Leu | Leu | Thr | Thr | Arg | Ser | Ser | Arg | Glu | Glu | Pro | Ser | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Thr | Arg | Ser | Leu | Asn | Trp | Ser | Trp | Ile | Trp | Ser | Ile | Val | Cys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ser | Arg | Ala | Gly | Ile | Asn | His | Ser | Cys | Ser | Ser | Ser | Ser | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ser | Trp | Lys | Gln | Arg | Ser | Ile | Asn | Ser | Ser | Ser | His | Asn | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ile | Cys | Leu | Leu | Asn | Ser | Ser | Ser | Phe | Ser | Ile | His | Met | Tyr | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Asn | Gly | Leu | Ser | Ser | Ser |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

&lt;210&gt; 150

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ser | Gly | Ala | Asn | Gln | Cys | Gly | Ser | Cys | Asn | Ser | Lys | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Lys | Ala | Trp | Tyr | Tyr | Arg | Val | Gly | Phe | Arg | Phe | Phe | Arg | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Phe | Asp | Phe | Asp | Phe | Phe | Phe | Phe | Tyr | Val | Ile | Phe | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | His | Ser | Glu | Leu | Tyr | Leu | Val | Ser | Thr |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 151

&lt;211&gt; 61

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 151

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Phe | Val | Leu | Lys | Ser | Leu | Leu | Val | Gly | Ala | Cys | Tyr | Trp | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Phe | Val | Gln | Lys | Leu | Gln | Ser | Glu | Ser | Leu | Cys | Ile | Thr | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Ile | Thr | Ser | Leu | Leu | Ser | Leu | Pro | Gln | Lys | Thr | Val | Gly | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Lys | Ile | Ile | Cys | Ile | Leu | Ile | Tyr | Leu | Lys | Cys | Leu |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

&lt;210&gt; 152

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Cys | Lys | Phe | Leu | Arg | Asp | Leu | Pro | Leu | Leu | Thr | Val | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Met | Tyr | Thr | Cys | Ile | Ile | Lys | Ala | Leu | Asn | Lys | Ser | Leu | Trp | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Thr | Ala | Lys | Met | Gly | Thr | Arg | His | Leu | Leu | Cys | Val | Leu | Val | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ala | Leu | Arg | Ala | Val | Arg | Pro | Cys | Leu | Ile |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

&lt;210&gt; 153

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 153

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Arg | Asp | Ile | Ile | Leu | Asn | Val | Phe | Ser | Gln | Arg | Ser | His | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Asn | Gln | Asn | Gln | Ile | Asn | His | His | Glu | Lys | Asn | Glu | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gly | Asn | Thr | Lys | Leu | Trp | Leu | Gly | Ser | Ser | Tyr | Tyr | Tyr | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

His Ile Gly Trp Arg Arg Lys Pro  
50 55

<210> 154  
<400> 154  
000

<210> 155  
<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 155

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Val | His | Arg | Leu | His | Gly | Arg | Ala | Asp | Pro | Leu | Gly | Trp | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Ser | Asp | Leu | Ile | Thr | Ser | Gly | Leu | Gly | Ala | Gly | Val | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Pro | Ala | Arg | Arg | Leu | His | Ser | Leu | Gly | Arg | Arg | Val | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Pro | Gly | Val | Trp | Leu | Glu | Arg | Leu | Gly | His | Gly | Arg | Arg | Asp | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Ala | Trp | Ser | Ala | Ala | Gln | Arg | Pro | Arg | Thr | Pro | Gly | Arg | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Cys | Val | Cys | Ala | Pro | Arg | Arg | Gly | Pro | Glu | Ser | Pro | Ser | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Val | Pro | Pro | Pro | Gly | Arg | Ala | Gly | Asp | Pro | Ser | Pro | Pro | Asp | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ala | Ser | Gly | Pro | Arg | Gly | Gly | Ala | Ala | Thr | Lys | Ala | Gly | Pro | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Asp | Pro | Gly | Gln | Leu | Arg | Pro | Glu | Leu | Arg | Val | Leu | Pro | Pro | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Arg | Gly | Asp | Arg | Glu |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

<210> 156  
<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 156

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Val | Ala | Ala | Gly | Gly | Arg | Gly | Gln | Asp | Ala | Gln | Leu | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Ser | Gly | Val | Val | Ser | Arg | Pro | Arg | Leu | Gly | Gly | Gly | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Ser | Arg | Gly | Arg | Arg | Ile | Gly | Trp | Ala | Arg | Val | Ser | Ser | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Arg | Arg | Asp | Arg | Val | Cys | Gly | Gly | Gly | Leu | Gly | Ala | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Gly Arg Ala His Ala Gly Gly Ala Ala Arg Gly Ala Gly Pro Leu Arg  
 65 70 75 80

Gly

<210> 157  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 157

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ser | Gln | Ser | Val | Thr | Pro | Pro | Met | Ala | Glu | Pro | Leu | Gln | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Pro | Gly | Ala | Ala | Glu | Asp | Ala | Ala | Ala | Gln | Ala | Val | Glu | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Trp | Lys | Ala | Pro | Glu | Asp | Ala | Gly | Pro | Gln | Pro | Gly | Ser | Tyr | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Arg | His | Tyr | Gly | Pro | Ala | Lys | Trp | Val | Ser | Thr | Ser | Val | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Asp | Trp | Asp | Ser | Ala | Ile | Gln | Thr | Gly | Phe | Thr | Lys | Leu | Asn | Ser |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Ile | Gln | Gly | Lys | Asn | Glu | Lys | Glu | Met | Lys | Ile | Lys | Met | Thr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Val | Thr | Ser | Tyr | Val | Glu | Pro | Gly | Ser | Gly | Pro | Phe | Ser | Glu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ile | Thr | Ile | Ser | Leu | Tyr | Ile | Pro | Ser | Glu | Gln | Gln | Phe | Asp | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Arg | Pro | Leu | Glu | Ser | Asp | Val | Phe | Ile | Glu | Asp | Arg | Ala | Glu | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Val | Phe | Val | Arg | Ser | Phe | Asp | Gly | Phe | Ser | Ser | Ala | Gln | Lys | Asn |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Glu | Gln | Leu | Leu | Thr | Leu | Ala | Ser | Ile | Leu | Arg | Glu | Asp | Gly | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Phe | Asp | Glu | Lys | Val | Tyr | Tyr | Thr | Ala | Gly | Tyr | Asn | Ser | Pro | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Leu | Leu | Asn | Arg | Asn | Asn | Glu | Val | Trp | Leu | Ile | Gln | Lys | Asn | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Thr | Lys | Glu | Asn | Glu |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 158  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<400> 158

Pro Asn Phe Tyr Arg Gly Phe Ile Phe Asn Leu Thr Met Cys Gly Gly



000

&lt;210&gt; 162

&lt;400&gt; 162

000

&lt;210&gt; 163

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Ile | Asp | Leu | Glu | Ala | Glu | Glu | Ser | Gln | Arg | Leu | Leu | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Met | Trp | Phe | Ser | Phe | Lys | Lys | Leu | Leu | Phe | Leu | Glu | Ser | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Tyr | Asn | Val | Cys | Ser | Leu | Phe | Val | His | Lys | Ile | Lys | Pro | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Leu | Lys | Lys | Lys | Lys | Lys | Arg | Gly | Glu | Lys | Lys | Arg | Glu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Lys | Gly | Lys | Arg | Lys | Arg | Arg | Gly | Glu | Glu |     |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |     |

&lt;210&gt; 164

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Tyr | Leu | Thr | Leu | Pro | Tyr | Lys | Leu | Leu | Val | Pro | Phe | Cys | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Ile | Thr | Leu | Thr | Lys | Gly | Ile | Phe | Tyr | Cys | Lys | Glu | Tyr | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Tyr | Ile | Thr | Ser | His | Glu | Phe | Leu | Pro | Leu | Val | Thr | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Leu | Pro | Ser | Ala | Ile | Ile | Gln | Ile | Ala | Gln | Pro | Phe | Tyr | Val | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ser | Leu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 165

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Phe | Leu | Phe | Arg | Tyr | His | Thr | Val | Pro | Leu | Pro | Pro | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Leu | Ile | His | Trp | Met | Thr | Leu | Cys | Gln | Thr | Gln | Met | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Pro | Leu | Val | Phe | Gln | Ile | Met | Phe | Gly | Ile | Leu | Asn | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Tyr | His | Tyr | Ala | Val | Phe | Glu | Glu | Thr | Leu | Glu | Lys | Thr | Ile | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 166

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 166

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Leu | Lys | Gly | Asp | Arg | Gly | Gly | Val | His | Phe | Leu | Lys | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Gly | Gly | Leu | Arg | Ala | Ser | Leu | Leu | Tyr | Leu | Leu | Glu | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Leu | Val | Phe | Leu | Leu | Ser | Ile | Cys | Val | Arg | Gly | Met | Val | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Lys | Ser | Phe | Leu | Val | Gly | Glu | Gln | Leu | Leu | Ser | Ile | Ser | Glu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Phe | Lys | Met | Ser | Val | Cys | Lys | Cys | Ser | Phe | Leu | Ser | Thr | Thr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Phe | Val | Pro | Ile | Ser | Ser | Asp | Ser | Lys | Lys | Val | Ser | Ser | Tyr | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Cys | Ser | Glu | Ser | Leu | Ala | Glu | Gln | Asn | Leu | Phe | Met | Met | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Val | Phe | Cys | Ser | Glu | Gln | Lys | Phe | Asp | Pro | Glu | Leu | Asn | Asp | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Phe | Phe | Phe | Thr | Arg | Leu | Phe | Ser | Ser | Leu | Val | Thr | Leu | Arg | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Pro | His | Ala | Pro | Ala | Ser | Glu | Met | Gln | Thr | Val | Leu | Ser | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

&lt;210&gt; 167

&lt;211&gt; 439

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 167

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Leu | Leu | Phe | Thr | Ser | Ser | Lys | Phe | Pro | Leu | Ile | Ser | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Gln | Gly | Leu | Lys | Phe | Arg | Ser | Lys | Ser | Ser | Leu | Ala | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | His | Lys | Asn | Gly | Glu | Thr | Ser | Leu | Lys | Pro | Glu | Asp | Phe | Asp | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Val | Leu | Ser | Lys | Arg | Gly | Ile | Lys | Ser | Arg | Tyr | Lys | Asp | Cys | Ser |



|         | 50      |         |         |         |         | 55      |         |         |         |         | 60      |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| Met 65  | Ala     | Ala     | Leu     | Thr     | Ser 70  | His     | Leu     | Gln     | Asn     | Gln 75  | Ser     | Asn     | Asn     | Ser     | Asn 80  |
| Trp     | Asn     | Leu     | Arg     | Thr 85  | Arg     | Ser     | Lys     | Cys     | Lys 90  | Lys     | Asp     | Val     | Phe     | Met 95  | Pro     |
| Pro     | Ser     | Ser     | Ser 100 | Ser     | Glu     | Leu     | Gln     | Glu 105 | Ser     | Arg     | Gly     | Leu     | Ser 110 | Asn     | Phe     |
| Thr     | Ser     | Thr 115 | His     | Leu     | Leu     | Leu     | Lys 120 | Glu     | Asp     | Glu     | Gly     | Val 125 | Asp     | Asp     | Val     |
| Asn     | Phe 130 | Arg     | Lys     | Val     | Arg     | Lys 135 | Pro     | Lys     | Gly     | Lys     | Val 140 | Thr     | Ile     | Leu     | Lys     |
| Gly 145 | Ile     | Pro     | Ile     | Lys     | Lys 150 | Thr     | Lys     | Lys     | Gly     | Cys 155 | Arg     | Lys     | Ser     | Cys     | Ser 160 |
| Gly     | Phe     | Val     | Gln     | Ser 165 | Asp     | Ser     | Lys     | Arg     | Glu 170 | Ser     | Val     | Cys     | Asn     | Lys 175 | Ala     |
| Asp     | Ala     | Glu     | Ser 180 | Glu     | Pro     | Val     | Ala     | Gln 185 | Lys     | Ser     | Gln     | Leu     | Asp 190 | Arg     | Thr     |
| Val     | Cys     | Ile 195 | Ser     | Asp     | Ala     | Gly     | Ala 200 | Cys     | Gly     | Glu     | Thr     | Leu 205 | Ser     | Val     | Thr     |
| Ser     | Glu 210 | Glu     | Asn     | Ser     | Leu     | Val 215 | Lys     | Lys     | Lys     | Glu     | Arg 220 | Ser     | Leu     | Ser     | Ser     |
| Gly 225 | Ser     | Asn     | Phe     | Cys     | Ser 230 | Glu     | Gln     | Lys     | Thr     | Ser 235 | Gly     | Ile     | Ile     | Asn     | Lys 240 |
| Phe     | Cys     | Ser     | Ala     | Lys 245 | Asp     | Ser     | Glu     | His     | Asn 250 | Glu     | Lys     | Tyr     | Glu     | Asp 255 | Thr     |
| Phe     | Leu     | Glu     | Ser 260 | Glu     | Glu     | Ile     | Gly     | Thr 265 | Lys     | Val     | Glu     | Val     | Val 270 | Glu     | Arg     |
| Lys     | Glu     | His 275 | Leu     | His     | Thr     | Asp     | Ile 280 | Leu     | Lys     | Arg     | Gly     | Ser 285 | Glu     | Met     | Asp     |
| Asn     | Asn 290 | Cys     | Ser     | Pro     | Thr     | Arg 295 | Lys     | Asp     | Phe     | Thr     | Glu 300 | Asp     | Thr     | Ile     | Pro     |
| Arg 305 | Thr     | Gln     | Ile     | Glu     | Arg 310 | Arg     | Lys     | Thr     | Ser     | Leu 315 | Tyr     | Phe     | Ser     | Ser     | Lys 320 |
| Tyr     | Asn     | Lys     | Glu     | Ala 325 | Leu     | Ser     | Pro     | Pro     | Arg 330 | Arg     | Lys     | Ala     | Phe     | Lys 335 | Lys     |
| Trp     | Thr     | Pro     | Pro 340 | Arg     | Ser     | Pro     | Phe     | Asn 345 | Leu     | Val     | Gln     | Glu     | Thr 350 | Leu     | Phe     |
| His     | Asp     | Pro 355 | Trp     | Lys     | Leu     | Leu     | Ile 360 | Ala     | Thr     | Ile     | Phe     | Leu 365 | Asn     | Arg     | Thr     |
| Ser     | Gly 370 | Lys     | Met     | Ala     | Ile     | Pro 375 | Val     | Leu     | Trp     | Lys     | Phe 380 | Leu     | Glu     | Lys     | Tyr     |
| Pro     | Ser     | Ala     | Glu     | Val     | Ala     | Arg     | Thr     | Ala     | Asp     | Trp     | Arg     | Asp     | Val     | Ser     | Glu     |

|     |     |            |            |            |     |     |     |            |            |     |     |     |            |            |     |
|-----|-----|------------|------------|------------|-----|-----|-----|------------|------------|-----|-----|-----|------------|------------|-----|
| 385 |     |            |            |            | 390 |     |     |            |            | 395 |     |     |            |            | 400 |
| Leu | Leu | Lys        | Pro        | Leu<br>405 | Gly | Leu | Tyr | Asp        | Leu<br>410 | Arg | Ala | Lys | Thr        | Ile<br>415 | Val |
| Lys | Phe | Ser        | Asp<br>420 | Glu        | Tyr | Leu | Thr | Lys<br>425 | Gln        | Trp | Lys | Tyr | Pro<br>430 | Ile        | Glu |
| Leu | His | Gly<br>435 | Ile        | Gly        | Ala | Pro |     |            |            |     |     |     |            |            |     |

<210> 168  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Asp<br>1  | Cys       | Gly       | Lys       | Val<br>5  | Gln       | Thr       | Gln       | Met       | Gln<br>10 | Phe       | Ala       | Leu       | Thr       | Asn<br>15 | Phe       |
| Leu       | Gly       | Leu       | Ile<br>20 | Ser       | Leu       | Cys       | Lys       | Thr<br>25 | Pro       | Val       | Leu       | Ser       | Phe<br>30 | Leu       | Pro       |
| Gln       | Asp       | Arg<br>35 | Val       | Gln       | Ser       | Phe       | Leu<br>40 | Lys       | His       | Ala       | Leu       | Arg<br>45 | Cys       | Pro       | His       |
| Leu       | Arg<br>50 | His       | Cys       | Phe       | Val       | Asp<br>55 | Thr       | Leu       | Lys       | Gly       | Val<br>60 | His       | Lys       | Ala       | Lys       |
| Lys<br>65 | Ser       | Asp       | Gln       | Met       | Leu<br>70 | Arg       | Ala       | Ser       | Asn       | Leu<br>75 | Tyr       | Leu       | Thr       | Thr       | Trp<br>80 |
| Thr       | Trp       | His       | Trp       | Gln<br>85 | Lys       | Ser       | Leu       | Gln       | His<br>90 |           |           |           |           |           |           |

<210> 169  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ser<br>1  | Asp       | Phe       | Cys       | Gln<br>5  | Cys       | His       | Val       | Gln       | Val<br>10 | Val       | Arg       | Tyr       | Lys       | Leu<br>15 | Leu       |
| Ala       | Leu       | Ser       | Ile<br>20 | Trp       | Ser       | Asp       | Phe       | Phe<br>25 | Ala       | Leu       | Trp       | Thr       | Pro<br>30 | Leu       | Arg       |
| Val       | Ser       | Thr<br>35 | Lys       | Gln       | Cys       | Leu       | Arg<br>40 | Cys       | Gly       | His       | Leu       | Arg<br>45 | Ala       | Cys       | Phe       |
| Arg       | Lys<br>50 | Leu       | Cys       | Thr       | Leu       | Ser<br>55 | Cys       | Gly       | Arg       | Lys       | Glu<br>60 | Arg       | Thr       | Gly       | Val       |
| Leu<br>65 | His       | Lys       | Glu       | Ile       | Ser<br>70 | Pro       | Arg       | Lys       | Leu       | Val<br>75 | Asn       | Ala       | Asn       | Cys       | Ile<br>80 |
| Cys       | Val       | Cys       | Thr       | Leu<br>85 | Pro       | Gln       | Ser       | Tyr       | Ile<br>90 | Val       | Phe       |           |           |           |           |

<210> 170  
 <211> 91

<212> PRT  
 <213> Homo sapiens

<400> 170

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asp | Ser | His | Gln | Asn | Tyr | Ile | Pro | Trp | Pro | Pro | Ala | Cys | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Arg | Pro | Trp | Leu | Ala | Ser | Leu | Thr | Arg | Glu | Lys | Asp | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Arg | Leu | Trp | Asp | His | Phe | Val | Cys | Ala | Leu | Gly | Met | Thr | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Pro | Thr | Pro | Gly | Lys | Pro | Leu | Gly | Leu | Ser | Glu | Thr | Leu | Trp | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Asn | His | Met | Val | Ser | Leu | Lys | Val | Glu | Arg | Leu | Ser | Asn | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Pro | Arg | Glu | Phe | Gln | Ser | Val | Asp | Val | Ile |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

<210> 171  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 171

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Gly | Leu | Asn | Ala | His | Leu | Ala | Ser | Ala | Ser | Glu | Phe | Asp | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Val | Gln | Leu | Ile | Glu | Arg | Glu | Glu | Glu | Ile | Cys | Ile | Phe | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Ile | Asn | Ile | Gln | Glu | Lys | Met | Lys | Leu | Asn | Gly | Glu | Ile | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | His | Leu | Leu | Glu | Glu | Lys | Ile | Gln | Phe | Leu | Lys | Met | Lys | Ile | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Lys | Gln | Arg | Gln | Ile | Cys | Val | Thr | Gln | Lys | Leu | Leu | Pro | Ala | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ser | Leu | Asp | Ala | Asp | Leu | Ala | Val | Leu | Gln | Ile | Gln | Phe | Ser |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

<210> 172  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 172

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Glu | Phe | Gly | Ala | Gln | Leu | Gly | Arg | His | Pro | Gly | Thr | Ser | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Val | Ile | Ser | Gly | Ser | His | Lys | Phe | Val | Phe | Ala | Ser | Gln | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Phe | Ser | Gly | Ile | Gly | Ser | Phe | Leu | Pro | Val | Asp | Val | Phe | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | His | Leu | Val | Ser | Ser | Ser | Leu | Gly | Tyr | Leu | Phe | Phe | His | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Cys | Ile | Phe | Leu | Leu | Pro | Ala | Leu | Ser | Ala | Glu | Arg | His | Tyr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Ile | Gln | Arg | Gln | Arg | Leu | Ser | Gly | His |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

&lt;210&gt; 173

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Arg | Ser | Arg | Gly | Ala | Leu | Ser | Leu | Ser | Val | Gly | Ala | Ala | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Val | Ala | Leu | Trp | Gln | Arg | Arg | Arg | Gln | Asp | Ser | Gly | Thr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Phe | Ser | Thr | Glu | Glu | Arg | Ala | Ala | Pro | Phe | Ser | Leu | Glu | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Phe | Leu | Lys | Asn | Glu | Lys | Gly | Gln | Tyr | Ile | Ser | Pro | Phe | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Pro | Ile | Tyr | Ala | Asp | Lys | Val | Arg | His | Pro | Cys | Phe | Trp | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Ser | Leu | Tyr | Ser | Asp | Gln | Leu | Val | Leu | His | Met | Asn | Phe | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Leu | Ser | Thr | Ser | Ala |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 174

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 174

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Arg | Leu | Cys | Pro | Lys | Thr | Arg | Met | Pro | Tyr | Leu | Ile | Cys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Trp | Asn | Ile | Met | Lys | Trp | Arg | Tyr | Ile | Leu | Ser | Phe | Leu | Ile | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Asp | Ser | Val | Leu | Gln | Gly | Glu | Gly | Arg | Gly | Ala | Leu | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Ala | Ala | His | Ser | Ala | Gly | Val | Leu | Pro | Pro | Pro | Leu | Pro | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | His | Gln | Pro | Ala | Arg | Gly | Ala | Asp |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 175

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 175

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Gln | Arg | Lys | Ala | Glu | Pro | Gly | Ala | Cys | Ala | Leu | Gly | Arg | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Glu | Cys | Ile | Pro | Glu | Pro | Gly | Ala | Arg | Arg | Thr | Ala | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Leu | Arg | Ser | Val | Ser | Gly | Ala | Ala | Asn | Thr | Lys | Val | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | His | Phe | Arg | Phe | Leu | Gly | Leu | Leu | Arg | Ser | Cys | Arg | Ser | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Glu | Val | Asp | Ala | Pro | Gly | Val | Asp | Gly | Arg | Asp | Gly | Leu | Arg | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Arg | Gly | Phe | Ser | Glu | Gly | Gly | Arg | Gln | Asn | Phe | Asp | Val | Arg | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ser | Gly | Ala | Asn | Gly | Leu | Pro | Lys | His | Ser | Tyr | Trp | Leu | Asp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Leu | Phe | Ile | Leu | Phe | Asp | Val | Val | Val | Phe | Leu | Phe | Val | Tyr | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 176

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Lys | Met | Ala | Thr | Asn | Phe | Leu | Asn | Lys | Glu | Asp | Arg | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Arg | Arg | Ile | Ser | His | Leu | Gln | Gly | Thr | Leu | Pro | Phe | Ile | Leu | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Thr | Asn | Leu | Gln | Asn | Ser | Ile | Asn | Trp | Val | Gly | Phe | His | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Ala | Lys | Phe | Leu | Lys | Leu | Asn | Pro | Leu | Val | Arg | Val |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

&lt;210&gt; 177

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Tyr | Cys | Ile | Leu | His | Gln | Gln | Lys | Val | Leu | Arg | Leu | Tyr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ala | Leu | Arg | His | Leu | Glu | Ser | Trp | Cys | Val | Gln | Arg | Asp | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Phe | Ala | Cys | Leu | Met | Arg | Ala | Arg | Phe | Glu | Glu | His | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Asp | Met | Ala | Lys | Ala | Thr | Gln | Leu | Leu | Lys | Glu | Ala | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Phe | Trp | Tyr | Arg | Gln | His | Pro | Gln | Pro | Tyr | Ile | Phe | Pro | Asp | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Gly | Gly | Thr | Ser | Tyr | Glu | Arg | Tyr | Asp | Cys | Tyr | Lys | Val | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Cys | Leu | Asp | Asp | Trp | His | Pro | Ser | Glu | Lys | Ala | Met | Tyr | Pro | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Phe | Ala | Lys | Arg | Glu | Gln | Trp | Lys | Lys | Leu | Arg | Arg | Glu | Ser | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Glu | Val | Lys | Gln | Leu | Gln | Glu | Glu | Thr | Pro | Pro | Gly | Gly | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Thr | Glu | Ala | Leu | Pro | Pro | Ala | Arg | Lys | Glu | Gly | Asp | Leu | Pro | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Trp | Trp | Tyr | Ile | Val | Thr | Arg | Pro | Arg | Glu | Arg | Pro | Met |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

&lt;210&gt; 178

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Leu | Val | Pro | Ser | Phe | Pro | Ser | Ala | Val | Ser | Ser | Thr | Val | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Gln | Ser | Asn | Gln | Asp | Thr | Leu | Pro | Ser | Gln | Lys | Asp | Ala | Ser | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ser | Thr | Ile | Leu | Gly | Pro | Cys | Ser | Asn | Arg | Ile | Ser | His | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Pro | Gln | Glu | Ser | Gln | Gly | Arg | Cys | Met | Ala | Val | Asp | Ala | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Arg | Ile | Leu | Pro | Arg | Pro | Pro | Ser | Ala | Ala | Gly | Trp | Pro | Ser | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Pro | Phe | His | Ser | Tyr | Val | Leu | Gln | Thr | Gly | Leu | Ser | Ser | Asn | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ser | Ile | Gly | Ile | Cys | Leu | Ser | Gly | Arg | Thr | Thr | Thr | Arg | Gly | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Pro | Ala | Tyr | Lys | Ala | Ala | Thr | Pro | Phe | Ala | Asp | Val | Val | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ile | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 179

&lt;211&gt; 80

<212> PRT  
 <213> Homo sapiens

<400> 179

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Met | Met | Thr | Ile | Tyr | Ala | Leu | Ser | Asn | Glu | Phe | Ala | Phe | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Glu | Glu | Gln | Leu | Ser | Phe | Phe | Pro | Leu | Leu | Ser | Val | Gln | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | Gln | Arg | Phe | Leu | Leu | Asp | Ser | Ser | Trp | Ser | Gly | Val | Ile | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Phe | Phe | Ser | Cys | Ser | Cys | Leu | Pro | Phe | Leu | Tyr | Pro | Pro | Lys | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gln | Ile | His | Asp | Leu | Lys | Asp | Thr | Gln | Tyr | Leu | Leu | Asn | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

<210> 180  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 180

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Leu | Arg | Lys | Leu | Lys | Gly | Pro | Glu | Glu | Ala | Ser | Gly | Gln | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gly | Ala | Gly | Pro | Thr | Met | Leu | Leu | Arg | Glu | Glu | Asn | Gly | Cys | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Arg | Gln | Ser | Ser | Ser | Ser | Ala | Gly | Asp | Ser | Asp | Gly | Glu | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Ser | Ala | Ala | Glu | Arg | Ala | Arg | Gln | Gln | Leu | Glu | Ala | Leu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Thr | Met | Arg | Ile | Arg | Met | Thr | Asp | Gly | Arg | Thr | Leu | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Phe | Leu | Cys | Thr | Asp | Arg | Asp | Cys | Asn | Val | Ile | Leu | Gly | Ser | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Glu | Phe | Leu | Lys | Pro | Ser | Asp | Ser | Phe | Ser | Ala | Gly | Glu | Pro | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Leu | Gly | Leu | Ala | Met | Val | Pro | Gly | His | His | Ile | Val | Ser | Ile | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Gln | Arg | Glu | Ser | Leu | Thr | Gly | Pro | Pro | Tyr | Leu |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

<210> 181  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 181

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Lys | Gly | Lys | Arg | His | Arg | Gly | Gln | Arg | Tyr | Gly | Gly | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|           |           |           |            |           |           |           |           |            |           |           |           |           |            |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Arg       | Leu       | Ser       | Leu<br>20  | Cys       | Thr       | Ser       | Met       | Glu<br>25  | Thr       | Met       | Trp       | Cys       | Pro<br>30  | Gly       | Thr       |
| Met       | Ala       | Arg<br>35 | Pro        | Ser       | Thr       | Arg       | Gly<br>40 | Ser        | Pro       | Ala       | Glu       | Lys<br>45 | Glu        | Ser       | Asp       |
| Gly       | Leu<br>50 | Arg       | Asn        | Ser       | Cys       | Ala<br>55 | Glu       | Pro        | Arg       | Met       | Thr<br>60 | Leu       | Gln        | Ser       | Arg       |
| Ser<br>65 | Val       | Gln       | Arg        | Lys       | Gln<br>70 | Pro       | Thr       | Ser        | Val       | Arg<br>75 | Pro       | Ser       | Val        | Met       | Arg<br>80 |
| Met       | Arg       | Ile       | Val        | Leu<br>85 | Leu       | Ser       | Ser       | Ala        | Ser<br>90 | Ser       | Cys       | Cys       | Arg        | Ala<br>95 | Arg       |
| Ser       | Ala       | Ala       | Glu<br>100 | Ser       | Ser       | Arg       | Ser       | Pro<br>105 | Ser       | Glu       | Ser       | Pro       | Ala<br>110 | Leu       | Glu       |
| Leu       | Leu       |           |            |           |           |           |           |            |           |           |           |           |            |           |           |

<210> 182  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 182

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Arg<br>1  | Leu       | Ser       | Arg       | Leu<br>5  | Thr       | Glu       | Pro       | Lys       | Glu<br>10 | Asp       | Pro       | Met       | Ala       | Gly<br>15 | Ile       |
| Ser       | Thr       | Ala       | Glu<br>20 | His       | His       | Leu       | Asp       | Pro<br>25 | Thr       | Ala       | Ala       | Leu       | Pro<br>30 | Thr       | Gln       |
| Leu       | Ser       | Arg<br>35 | Ser       | Arg       | His       | Ser       | Pro<br>40 | Gln       | Val       | Ile       | Ser       | Thr<br>45 | Asp       | Gly       | Gly       |
| Glu       | Thr<br>50 | Arg       | Gly       | Cys       | Gly       | Arg<br>55 | Gln       | Glu       | Arg       | Lys       | Ala<br>60 | Glu       | Arg       | Arg       | Val       |
| Cys<br>65 | Lys       | Asn       | Ala       | Lys       | Val<br>70 | Thr       | Phe       | Pro       | Ile       | Val<br>75 | Gly       | Gly       | Lys       | Cys       | Gln<br>80 |
| Arg       | His       | Trp       | Phe       | Cys<br>85 | Cys       | His       | Arg       | Gln       | Ser<br>90 | Glu       | His       | Leu       | Glu       | Leu<br>95 |           |

<210> 183  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<400> 183

|          |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |
|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Arg<br>1 | Arg | Val       | Gln       | His<br>5 | Pro | Pro | Phe       | Phe       | Ser<br>10 | Gln | Leu | Ile       | Arg       | Asp<br>15 | Ala |
| Ala      | Lys | Arg       | Thr<br>20 | Phe      | Arg | Ile | Thr       | Arg<br>25 | Leu       | Gln | Ala | Phe       | Ser<br>30 | Lys       | Tyr |
| Leu      | Val | Val<br>35 | Tyr       | Val      | Tyr | Leu | Asn<br>40 | Gly       | Ser       | Met | Leu | Pro<br>45 | Val       | Pro       | Ser |
| Pro      | Cys | Pro       | Leu       | Cys      | Gln | Pro | Pro       | Val       | Ala       | Leu | Val | Leu       | Val       | Ser       | Phe |



| 50        |            |            |            |           | 55        |     |            |            |           | 60        |     |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|-----|------------|------------|-----------|-----------|-----|------------|------------|-----------|-----------|
| Pro<br>65 | Ser        | Ser        | Ala        | Lys       | Arg<br>70 | Pro | Trp        | Asn        | Leu       | Asn<br>75 | Gly | Gly        | Cys        | Phe       | Ala<br>80 |
| Leu       | Gly        | Gly        | Ser        | Cys<br>85 | Trp       | Trp | Asp        | Gln        | Ser<br>90 | Phe       | Asp | Lys        | Pro        | Pro<br>95 | Ala       |
| Pro       | Trp        | Trp        | His<br>100 | Leu       | Ser       | Trp | Lys        | Asp<br>105 | Val       | Thr       | Thr | Pro        | Gly<br>110 | Ala       | Gln       |
| Thr       | Ala        | Cys<br>115 | Gly        | Ser       | Arg       | Thr | Ser<br>120 | Ala        | Phe       | Gly       | Ile | Phe<br>125 | Leu        | Pro       | Gln       |
| Trp       | Gly<br>130 | Arg        |            |           |           |     |            |            |           |           |     |            |            |           |           |

<210> 184  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens  
 <400> 184

|           |           |            |           |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Thr<br>1  | Ala       | Pro        | Cys       | Cys<br>5  | Arg       | Cys       | Pro        | Ala        | Pro<br>10 | Val       | Pro       | Ser        | Val        | Asn<br>15 | Pro       |
| Leu       | Ser       | Leu        | Trp<br>20 | Cys       | Trp       | Phe       | Arg        | Ser<br>25  | Arg       | Leu       | Gln       | Gln        | Asn<br>30  | Asp       | Leu       |
| Gly       | Thr       | Ser<br>35  | Met       | Gly       | Ala       | Ala       | Leu<br>40  | Leu        | Trp       | Glu       | Val       | Leu<br>45  | Val        | Gly       | Gly       |
| Thr       | Arg<br>50 | Ala        | Leu       | Thr       | Asn       | Leu<br>55 | Leu        | Leu        | Leu       | Gly       | Gly<br>60 | Thr        | Ser        | Pro       | Gly       |
| Arg<br>65 | Thr       | Ser        | Gln       | Leu       | Gln<br>70 | Val       | Leu        | Arg        | Leu       | Pro<br>75 | Val       | Ala        | Ala        | Glu       | Pro<br>80 |
| Val       | Pro       | Leu        | Ala       | Phe<br>85 | Ser       | Ser       | His        | Asn        | Gly<br>90 | Glu       | Gly       | Asp        | Phe        | Gly<br>95 | Ile       |
| Leu       | Thr       | Asn<br>100 | Ser       | Ser       | Leu       | Gly       | Leu        | Ser<br>105 | Leu       | Leu       | Pro       | Ser        | Thr<br>110 | Ala       | Ser       |
| Arg       | Phe       | Ser<br>115 | Ser       | Ile       | Cys       | Ala       | Tyr<br>120 | Tyr        | Leu       | Arg       | Thr       | Val<br>125 | Ser        | Ala       | Pro       |

<210> 185  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens  
 <400> 185

|          |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |
|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Asp<br>1 | Ser | Arg       | Val       | Tyr<br>5 | Cys | Phe | Ser       | Gly       | Asn<br>10 | Tyr | Arg | Lys       | Leu       | Val<br>15 | Leu |
| Pro      | Arg | Lys       | Thr<br>20 | Gly      | Ala | Ile | Arg       | Asn<br>25 | Gly       | Ser | Asn | Ile       | Ser<br>30 | Lys       | Leu |
| Arg      | Lys | Gln<br>35 | Asp       | Val      | Leu | Ser | Phe<br>40 | Ala       | His       | Leu | Gly | Phe<br>45 | Leu       | Leu       | Phe |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Phe | Ser | Leu | Phe | Ser | Leu | Arg | Ser | Leu | Phe | Gln | Phe | Pro | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Pro | Leu | Val | Pro | Leu | Glu | Ser | Gln | Arg | Leu |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

&lt;210&gt; 186

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Asp | Ser | Glu | Ser | Met | Pro | Leu | Leu | Ala | Leu | Lys | Cys | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | Leu | Gly | Thr | Leu | Glu | Pro | Ser | Glu | Ile | Leu | Ile | Ile | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Pro | Tyr | Phe | Gln | Met | Phe | Ser | Ala | Gln | His | Trp | Val | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Thr | Glu | Asn | Pro | Glu | Glu | Lys | Gly | Arg | Cys | Phe | Pro |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

&lt;210&gt; 187

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | His | Pro | Ser | Arg | Arg | Leu | Thr | Gln | Gly | Arg | Trp | Val | Arg | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Ala | Met | Glu | Lys | Ile | Pro | Val | Ser | Ala | Phe | Leu | Arg | Leu | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ser | Tyr | Asn | Leu | Ala | Arg | Asp | Ser | Thr | Val | Lys | Pro | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Asp | Arg | Lys | Glu | Ser | Arg | Ala | Lys | Leu | Arg | Gln | Thr | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ser | Trp | Gly | Glu | Gln | Leu | Ile | Trp | Thr | Gln | Thr | Tyr | Glu | Glu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Tyr | Lys | Ser | Arg | Leu | Ala | Thr | Asn |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 188

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Pro | Glu | Leu | Pro | Trp | Arg | Lys | Phe | Gln | Cys | Gln | His | Ser | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Trp | Arg | Ser | Pro | Thr | Ile | Trp | Pro | Gly | Ile | Ala | Gln | Ser | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Leu | Glu | Pro | Lys | Arg | Thr | Gly | Arg | Ser | Leu | Glu | Pro | Asn | Cys | Ala | Arg |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Pro | Ser | Pro | Glu | Val | Gly | Val | Asn | Asn | Ser | Ser | Gly | Leu | Arg | Arg | Met |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| Lys | Lys | Leu | Tyr | Ile | Asn | Arg | Asp |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |  |  |

&lt;210&gt; 189

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ser | Leu | Gly | His | Arg | Pro | Arg | Asn | Gly | Gly | His | Ser | Arg | Gly | Cys | Asp |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Gly | Gly | Leu | His | Ala | His | Ser | Pro | Asp | Pro | Arg | Leu | Gln | Gly | Ala |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Leu | Gln | Gln | Ala | Lys | Asn | Ala | Ala | Tyr | Ser | Val | Ser | Leu | Pro | Pro |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Gly | Cys | Val | Gly | His | Leu | Trp | Pro | His | Leu | Arg | Leu | His | His | Arg | Thr |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gly | Arg | Glu | His | Arg | Ala | His | Thr | Leu | Leu | Pro | Leu | Trp | Asp | Pro | Leu |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Phe | His | Leu | Leu | Leu | Pro | Ala | Gly | Ser | Cys | Cys | Gln | Ser | Asp | Gln |     |  |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Ala | Arg | Pro | Gly | Glu | Glu | Ala | Pro | Phe | Pro | Val | Gly | Asp | Ser | Gly | Ser |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Gly | Arg | Gly | Leu | Gln | Pro | Ser | Pro | Gly | Cys | Tyr | Arg | Tyr |     |     |     |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |

&lt;210&gt; 190

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Arg | Gly | Arg | Asp | Ser | Cys | Pro | Arg | Ser | Pro | Pro | Ala | Leu | Arg | Ser | Ser |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Pro | Ala | Ala | Leu | Leu | Arg | Ala | Gly | Ser | Ser | Thr | Lys | Phe | Thr | Ala | Asn |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ala | Leu | Ala | Leu | Gly | Ser | Arg | Met | Ala | Thr | Thr | Val | Pro | Asp | Gly | Cys |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Arg | Asn | Gly | Leu | Lys | Ser | Lys | Tyr | Tyr | Arg | Leu | Cys | Asp | Lys | Ala | Glu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Ala | Trp | Gly | Ile | Val | Leu | Glu | Thr | Val | Ala | Thr | Ala | Gly | Val | Val | Thr |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ser        | Val        | Ala        | Phe        | Met<br>85  | Leu        | Thr        | Leu        | Pro        | Ile<br>90  | Leu        | Val        | Cys        | Lys        | Val<br>95  | Gln        |
| Asp        | Ser        | Asn        | Arg<br>100 | Arg        | Lys        | Met        | Leu        | Pro<br>105 | Thr        | Gln        | Phe        | Leu        | Phe<br>110 | Leu        | Leu        |
| Gly        | Val        | Leu<br>115 | Gly        | Ile        | Phe        | Gly        | Leu<br>120 | Thr        | Phe        | Ala        | Phe        | Ile<br>125 | Ile        | Gly        | Leu        |
| Asp        | Gly<br>130 | Ser        | Thr        | Gly        | Pro        | Thr<br>135 | Arg        | Phe        | Phe        | Leu        | Phe<br>140 | Gly        | Ile        | Leu        | Phe        |
| Ser<br>145 | Ile        | Cys        | Phe        | Ser        | Cys<br>150 | Leu        | Leu        | Ala        | His        | Ala<br>155 | Val        | Ser        | Leu        | Thr        | Lys<br>160 |
| Leu        | Val        | Arg        | Gly        | Arg<br>165 | Lys        | Pro        | Leu        | Ser        | Arg<br>170 | Leu        | Val        | Ile        | Leu        | Gly<br>175 | Leu        |
| Ala        | Val        | Gly        | Phe<br>180 | Ser        | Leu        | Val        | Gln        | Asp<br>185 | Val        | Ile        | Ala        | Ile        | Glu<br>190 | Tyr        | Ile        |
| Val        | Leu        | Thr<br>195 | Met        | Asn        | Arg        | Thr        | Lys<br>200 |            |            |            |            |            |            |            |            |

&lt;210&gt; 191

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 191

|           |           |           |            |           |           |           |           |            |           |           |           |           |            |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Ala<br>1  | Glu       | Ala       | His        | Gly<br>5  | Gln       | Thr       | Gln       | Asn        | His<br>10 | Gln       | Pro       | Gly       | Lys        | Gly<br>15 | Leu       |
| Pro       | Pro       | Pro       | Asp<br>20  | Glu       | Leu       | Gly       | Gln       | Thr<br>25  | Asp       | Ser       | Met       | Ser       | Gln<br>30  | Gln       | Ala       |
| Gly       | Glu       | Ala<br>35 | Asp        | Gly       | Lys       | Glu       | Asp<br>40 | Pro        | Lys       | Glu       | Glu       | Glu<br>45 | Ala        | Cys       | Gly       |
| Pro       | Cys<br>50 | Ala       | Pro        | Val       | Gln       | Ser<br>55 | Asp       | Asp        | Glu       | Gly       | Glu<br>60 | Gly       | Glu        | Ala       | Lys       |
| Asp<br>65 | Ala       | Gln       | His        | Thr       | Gln<br>70 | Glu       | Glu       | Glu        | Lys       | Leu<br>75 | Ser       | Arg       | Gln        | His       | Phe<br>80 |
| Ser       | Pro       | Val       | Gly        | Val<br>85 | Leu       | His       | Leu       | Ala        | Asp<br>90 | Glu       | Asp       | Arg       | Glu        | Ser<br>95 | Glu       |
| His       | Glu       | Gly       | His<br>100 | Arg       | Gly       | His       | Asn       | Pro<br>105 | Gly       | Cys       | Gly       | His       | Arg<br>110 | Phe       |           |

&lt;210&gt; 192

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Glu<br>1 | Ile | Tyr | Trp | Glu<br>5 | Thr | Asp | Tyr | Asn | His<br>10 | Ser | Gly | Thr | Ile | Asp<br>15 | Ala |
| His      | Glu | Met | Arg | Thr      | Ala | Leu | Arg | Lys | Ala       | Gly | Phe | Thr | Leu | Asn       | Ser |

| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Gln | Val | Gln | Gln | Thr | Ile | Ala | Leu | Arg | Tyr | Ala | Cys | Ser | Lys | Leu | Gly |  |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Ile | Asn | Phe | Asp | Ser | Phe | Val | Ala | Cys | Met | Ile | Arg | Leu | Glu | Thr | Leu |  |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Phe | Lys | Leu | Phe | Ser | Leu | Leu | Asp | Glu | Asp | Lys | Asp | Gly | Met | Val | Gln |  |  |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Leu | Ser | Leu | Ala | Glu | Trp | Leu | Cys | Cys | Val | Leu | Val |     |     |     |     |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |  |  |  |  |

&lt;210&gt; 193

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 193

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Glu | Ser | Leu | Ile | Ala | Phe | Leu | Phe | Leu | His | Asp | Gln | Cys | Ala | Gln | Asp |  |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |
| Ser | Ile | Val | Leu | Thr | Met | Ile | Lys | Asp | Val | Val | Arg | Ile | Gln | Trp | Thr |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Arg | Asn | Glu | Cys | Lys | Gly | Gly | Leu | Glu | Gln | Arg | Arg | Gly | Cys | Pro | Glu |  |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Gly | Lys | Glu | Ser | Tyr | Gln | Ile | Leu | Leu | Asn | Leu | Gln | Pro | Glu | Arg | Leu |  |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Glu | Phe | His | Arg | Pro | Gln | Ser | Ala | Pro | Phe | His | Cys | Ser | Arg | His | Ile |  |  |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

&lt;210&gt; 194

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Lys | Thr | Thr | Ile | His | Gly | Pro | Cys | Gln | Asn | His | Leu | Pro | Pro | Pro | His |  |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |
| Cys | Phe | Leu | Lys | Arg | Pro | Gly | Thr | Leu | Ser | Lys | Gly | Asp | Pro | Ile | Asp |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Ser | Ser | Gln | Glu | Gly | Phe | Arg | Ala | Ser | Ile | Arg | Ala | Trp | Pro | Val | Leu |  |  |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Ala | Pro | Leu | Leu | Ser | Glu | Gln | Gln | Gly | Phe | Gln | Gly | Ser | Gly | Trp | His |  |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Glu | Ser | Leu | Ser | Leu | Pro | Ser | Cys | Ser | Phe | Met | Thr | Asn | Val | Pro | Arg |  |  |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Thr | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

&lt;210&gt; 195

<211> 25  
 <212> PRT  
 <213> Homo sapiens

<400> 195

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Pro | Pro | Ser | Ser | Arg | Ser | Ser | Leu | Ala | Gly | Gln | Thr | Asn | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | His | Ser | His | Ser | Ala | Arg | Glu | Ser |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

<210> 196  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

<400> 196

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Pro | Ser | Leu | Ser | Ser | Ser | Arg | Arg | Leu | Asn | Ser | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Arg | Arg | Ile | Ile | Gln | Ala | Thr | Lys | Leu | Ser | Lys | Leu | Met | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Leu | His | Ala | Tyr | Arg | Arg | Ala | Met | Val | Cys | Cys | Thr | Trp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Arg | Val | Lys | Pro | Ala | Phe | Leu | Arg | Ala | Val | Leu | Ile | Ser | Trp | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Met | Val | Pro | Glu | Trp | Leu |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

<210> 197  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 197

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Arg | Arg | Asn | Thr | Ser | Arg | Ile | Ser | Val | His | Thr | Trp | Arg | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Tyr | Asp | Ser | Pro | Ala | Cys | Phe | Ser | Cys | Ser | Ile | Val | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Ser | Gly | Phe | Phe | Ser | Cys | Val | Ser | Val | Phe | Phe | Ser | Phe | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Asn | Phe | Ser | Ile | Ser | Ala | Ile | Ser | Gly | Leu | Ser | Asp | Met | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Glu | Glu | Lys | Gln | Ser | Glu | Ala | His | Glu | Tyr | Glu | Arg | Gln | Phe | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ser | Arg | Arg | Ser | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

<210> 198  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 198

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Phe | Ser | Thr | Phe | Pro | Thr | Leu | Pro | Pro | Gln | Ala | Gly | Lys | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ala | Thr | Leu | Leu | Ala | Ser | Gln | Cys | Ile | Leu | Gly | Gly | Ala | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Ile | Arg | Leu | Leu | Ala | Ser | Pro | Val | Gln | Ser | Phe | Leu | Trp | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Asp | Phe | Ser | Leu | Ala | Ser | Leu | Ser | Ser | Ser | Val | Ser | Thr | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Ser | Arg | Ser | Gln | Pro | Tyr | Arg | Val | Cys | Gln | Thr | Trp | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Lys | Ser | Lys | Ala | Arg | Arg | Thr | Ser | Thr | Ser | Asp | Ser | Ser | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ala | Ala | Val | Ala |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 199

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Phe | Pro | Pro | Ser | Gln | Leu | Tyr | Pro | Leu | Lys | Gln | Val | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gln | His | Phe | Ser | His | Leu | Ser | Ala | Tyr | Leu | Ala | Ala | His | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Phe | Ala | Cys | Leu | Leu | Leu | Leu | Phe | Asn | Arg | Phe | Phe | Gly | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Trp | Ile | Phe | Leu | Leu | Arg | Leu | Cys | Leu | Leu | Gln | Phe | Arg | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Phe | Leu | Asp | Leu | Ser | His | Ile | Gly | Phe | Val | Arg | His | Gly | Cys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Lys | Ala | Lys | Arg | Gly | Ala | Arg | Val | Arg | Ala | Thr | Val | Pro | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Pro | Gln | Trp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 200

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 200

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Thr | Asp | Gln | Tyr | Leu | Glu | Leu | Asn | Ala | Leu | Gln | Glu | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Pro | Phe | Gly | Leu | Val | Ile | Leu | Gly | Phe | Pro | Ser | Asn | Gln | Phe | Gly |

| 20         |            |            |            |           |            |            | 25         |            |           |           |            | 30         |            |           |           |  |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|--|
| Lys        | Gln        | Glu<br>35  | Pro        | Gly       | Glu        | Asn        | Ser<br>40  | Glu        | Ile       | Leu       | Pro        | Ser<br>45  | Leu        | Lys       | Tyr       |  |
| Val        | Arg<br>50  | Pro        | Gly        | Gly       | Gly        | Phe<br>55  | Val        | Pro        | Asn       | Phe       | Gln<br>60  | Leu        | Phe        | Glu       | Lys       |  |
| Gly<br>65  | Asp        | Val        | Asn        | Gly       | Glu<br>70  | Lys        | Glu        | Gln        | Lys       | Phe<br>75 | Tyr        | Thr        | Phe        | Leu       | Lys<br>80 |  |
| Asn        | Ser        | Cys        | Pro        | Pro<br>85 | Thr        | Ala        | Glu        | Leu        | Leu<br>90 | Gly       | Ser        | Pro        | Gly        | Arg<br>95 | Leu       |  |
| Phe        | Trp        | Glu        | Pro<br>100 | Met       | Lys        | Ile        | His        | Asp<br>105 | Ile       | Arg       | Trp        | Asn        | Phe<br>110 | Glu       | Lys       |  |
| Phe        | Leu        | Val<br>115 | Gly        | Pro       | Asp        | Gly        | Ile<br>120 | Pro        | Val       | Met       | Arg        | Trp<br>125 | Tyr        | His       | Arg       |  |
| Thr        | Thr<br>130 | Val        | Ser        | Asn       | Val        | Lys<br>135 | Met        | Asp        | Ile       | Leu       | Ser<br>140 | Tyr        | Met        | Arg       | Arg       |  |
| Gln<br>145 | Ala        | Ala        | Leu        | Ser       | Ala<br>150 | Arg        | Gly        | Lys        |           |           |            |            |            |           |           |  |

&lt;210&gt; 201

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 201

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Leu<br>1   | Met        | Pro        | Pro        | Pro<br>5  | Tyr        | Pro        | Tyr        | Pro        | Leu<br>10 | Pro        | Ile        | Met        | Gln        | Gly<br>15 | Pro        |
| Arg        | Arg        | Gly        | Ser<br>20  | Ser       | Gly        | Arg        | Lys        | Pro<br>25  | His       | Ser        | Gln        | Ser        | Phe<br>30  | Tyr       | Pro        |
| His        | Pro        | Arg<br>35  | Phe        | Ser       | Phe        | Leu        | Leu<br>40  | His        | Lys       | Arg        | Gln        | Ala<br>45  | Trp        | His       | Asn        |
| Cys        | Val<br>50  | Ser        | Glu        | Pro       | Leu        | Trp<br>55  | Thr        | Arg        | Asp       | Asn        | Cys<br>60  | Pro        | Ser        | Val       | Cys        |
| Met<br>65  | Ala        | Thr        | Gln        | Pro       | Arg<br>70  | Ile        | Cys        | Leu        | Leu       | Glu<br>75  | Thr        | Gln        | Gly        | Trp       | Ser<br>80  |
| Ile        | Cys        | Val        | Tyr        | Gly<br>85 | Leu        | Ala        | Gln        | His        | Pro<br>90 | His        | Ile        | Phe        | Phe        | Ser<br>95 | Phe        |
| Leu        | Phe        | Gln        | Met<br>100 | Ser       | Pro        | Lys        | Glu        | Thr<br>105 | Gln       | Val        | Leu        | Gly        | Pro<br>110 | Met       | Val        |
| Leu        | Leu        | Lys<br>115 | Pro        | Glu       | His        | His        | Ser<br>120 | Trp        | Gly       | Gln        | His        | Leu<br>125 | Pro        | His       | Ala        |
| His        | Thr<br>130 | Thr        | His        | His       | Gln        | Pro<br>135 | Pro        | Ser        | Ser       | Phe        | Leu<br>140 | Lys        | Asp        | Pro       | Pro        |
| Glu<br>145 | Pro        | Pro        | Ser        | Pro       | Ser<br>150 | His        | Ser        | Ala        | Pro       | Glu<br>155 | Thr        | Ser        | Gln        | Asp       | Asn<br>160 |



|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Cys        | Glu        | Arg        | Asp        | Gly<br>165 | Arg        | Val        | Pro        | Gln        | Val<br>170 | Arg        | Gly        | Gly        | Val        | Ser<br>175 | Met        |
| Lys        | Glu        | Gly        | Pro<br>180 | Glu        | Ala        | Leu        | Val        | Gly<br>185 | Gly        | Pro        | Pro        | Leu        | Ser<br>190 | Pro        | Ser        |
| Val        | Val        | Pro<br>195 | Ala        | Leu        | Ser        | Ala        | Phe<br>200 | Arg        | Leu        | Arg        | Leu        | Pro<br>205 | Gly        | Arg        | Asp        |
| Thr        | Thr<br>210 | Pro        | Ala        | Pro        | Leu        | Glu<br>215 | Asp        | Met        | Leu        | Ser        | Ser<br>220 | His        | Ser        | Val        | His        |
| Trp<br>225 | Tyr        | Leu        | Asn        | Thr        | Pro<br>230 | Ile        | Cys        | Pro        | Val        | Lys<br>235 | Val        | Phe        | Leu        | Gln        | Gln<br>240 |
| Lys        | Lys        | Lys        | Arg        | Lys<br>245 | Lys        | Lys        | Lys        | Lys        |            |            |            |            |            |            |            |

&lt;210&gt; 202

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |           |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|
| Ala<br>1   | Gly        | Leu        | Ser        | Ala<br>5  | Pro        | Pro        | Pro        | Ala        | Pro<br>10 | Leu        | Leu        | Cys        | Arg        | Ala<br>15 | Gln       |
| Ala        | Pro        | Leu        | Ala<br>20  | Leu       | Gly        | Pro        | Asn        | Phe<br>25  | Ser       | Tyr        | Arg        | His        | Gly<br>30  | Val       | Arg       |
| Pro        | Gly        | Ser<br>35  | Ser        | Pro       | Gly        | Ala        | His<br>40  | Leu        | Pro       | Glu        | Ala        | Arg<br>45  | Cys        | Gly       | Gly       |
| Gly        | Pro<br>50  | Arg        | Gly        | Arg       | Ser        | Gln<br>55  | Ala        | Gln        | Ser       | Pro        | Gln<br>60  | Ser        | Ser        | Gly       | Pro       |
| Val<br>65  | Gly        | Gly        | Arg        | Gly       | Arg<br>70  | Ser        | Gly        | Ser        | Lys       | Ala<br>75  | Arg        | Thr        | Pro        | Gln       | Leu<br>80 |
| Phe        | Arg        | Leu        | Gln        | Gln<br>85 | Gln        | Leu        | Gln        | Arg        | Phe<br>90 | Gly        | His        | Gly        | Cys        | Glu<br>95 | Val       |
| Pro        | Arg        | Cys        | Trp<br>100 | Leu       | Gln        | Ala        | Ala        | Arg<br>105 | Glu       | His        | Pro        | Gly        | Gln<br>110 | Gly       | Gln       |
| Glu        | Ala        | Gln<br>115 | Ser        | Glu       | Glu        | Glu        | Gly<br>120 | Glu        | Gly       | Gln        | Glu        | Gly<br>125 | Glu        | Gly       | Gln       |
| Glu        | Glu<br>130 | Gly        | Gly        | Ser       | Pro        | Leu<br>135 | Lys        | Gly        | Pro       | Gly        | Gln<br>140 | Gly        | Ser        | Leu       | Asn       |
| Leu<br>145 | Pro        | Leu        | Cys        | Leu       | Arg<br>150 | Val        | Pro        | Thr        | Thr       | Trp<br>155 | Ser        |            |            |           |           |

&lt;210&gt; 203

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Thr | Ser | Leu | Thr | Ala | Met | Glu | Phe | Asp | Leu | Gly | Ala | Ala | Leu |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

| 1         |           |           |            | 5         |           |           |           | 10         |           |           |           | 15        |            |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Glu       | Pro       | Thr       | Ser<br>20  | Gln       | Lys       | Pro       | Gly       | Val<br>25  | Gly       | Ala       | Gly       | His       | Gly<br>30  | Gly       | Asp       |
| Pro       | Lys       | Leu<br>35 | Ser        | Pro       | His       | Lys       | Val<br>40 | Gln        | Gly       | Arg       | Ser       | Glu<br>45 | Ala        | Gly       | Ala       |
| Gly       | Pro<br>50 | Gly       | Pro        | Lys       | Gln       | Gly<br>55 | His       | His        | Ser       | Ser       | Ser<br>60 | Asp       | Ser        | Ser       | Ser       |
| Ser<br>65 | Ser       | Ser       | Asp        | Ser       | Asp<br>70 | Thr       | Asp       | Val        | Lys       | Ser<br>75 | His       | Ala       | Ala        | Gly       | Ser<br>80 |
| Lys       | Gln       | His       | Glu        | Ser<br>85 | Ile       | Pro       | Gly       | Lys        | Ala<br>90 | Lys       | Lys       | Pro       | Lys        | Val<br>95 | Lys       |
| Lys       | Lys       | Glu       | Lys<br>100 | Gly       | Lys       | Lys       | Glu       | Lys<br>105 | Gly       | Lys       | Lys       | Lys       | Glu<br>110 | Ala       | Pro       |

His

&lt;210&gt; 204

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Gly<br>1   | Gly        | Pro        | Pro        | Pro<br>5  | Pro        | Lys        | His        | Leu        | Ser<br>10 | Ser        | Arg        | Trp        | Leu<br>15  | Val       | Leu        |
| Val        | Gly        | Arg        | Glu<br>20  | Glu       | Gly        | Leu        | Met        | Ser<br>25  | Pro       | Val        | Gln        | Gly        | Pro<br>30  | Ser       | Val        |
| Gly        | Ser        | Leu<br>35  | Leu        | Leu       | Leu        | Ala        | Leu<br>40  | Leu        | Leu       | Leu        | Ala        | Leu<br>45  | Leu        | Leu       | Leu        |
| Leu        | His<br>50  | Phe        | Gly        | Leu       | Leu        | Gly<br>55  | Leu        | Ala        | Arg       | Asp        | Ala<br>60  | Leu        | Val        | Leu       | Leu        |
| Gly<br>65  | Ala        | Ser        | Ser        | Val       | Gly<br>70  | Leu        | His        | Ile        | Arg       | Val<br>75  | Arg        | Ile        | Ala        | Gly       | Ala<br>80  |
| Ala        | Ala        | Gly        | Val        | Gly<br>85 | Arg        | Ala        | Val        | Val        | Ser<br>90 | Leu        | Leu        | Trp        | Thr        | Arg<br>95 | Thr        |
| Cys        | Pro        | Cys        | Leu<br>100 | Arg       | Pro        | Ala        | Leu        | Asn<br>105 | Phe       | Val        | Gly        | Thr        | Glu<br>110 | Leu       | Gly        |
| Ile        | Ser        | Pro<br>115 | Val        | Ala       | Arg        | Pro        | His<br>120 | Thr        | Gly       | Leu        | Leu        | Gly<br>125 | Gly        | Gly       | Leu        |
| Gln        | Gly<br>130 | Cys        | Ser        | Gln       | Val        | Glu<br>135 | Leu        | His        | Gly       | Gly        | Lys<br>140 | Arg        | Ser        | Trp       | Val        |
| Leu<br>145 | Arg        | Pro        | Arg        | Ala       | Pro<br>150 | Gly        | Pro        | Cys        | Arg       | Gly<br>155 | Ala        | Glu        | Gln        | Gly       | Glu<br>160 |
| Glu        | Arg        |            |            |           |            |            |            |            |           |            |            |            |            |           |            |

&lt;210&gt; 205

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

|            |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |  |
|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|--|
| Val<br>1   | Glu        | Pro        | Trp        | Thr<br>5  | Thr       | Cys        | Arg        | Ala        | Ala<br>10 | Gly       | Ala        | Val        | Met        | Ala<br>15 | Asp       |  |
| Tyr        | Trp        | Lys        | Ser<br>20  | Gln       | Pro       | Lys        | Lys        | Phe<br>25  | Cys       | Asp       | Tyr        | Cys        | Lys<br>30  | Cys       | Trp       |  |
| Ile        | Ala        | Asp<br>35  | Asn        | Arg       | Pro       | Ser        | Val<br>40  | Glu        | Phe       | His       | Glu        | Arg<br>45  | Gly        | Lys       | Asn       |  |
| His        | Lys<br>50  | Glu        | Asn        | Val       | Ala       | Lys<br>55  | Arg        | Ile        | Ser       | Glu       | Ile<br>60  | Lys        | Gln        | Lys       | Ser       |  |
| Leu<br>65  | Asp        | Lys        | Ala        | Lys       | Glu<br>70 | Glu        | Glu        | Lys        | Ala       | Ser<br>75 | Lys        | Glu        | Phe        | Ala       | Ala<br>80 |  |
| Met        | Glu        | Ala        | Ala        | Ala<br>85 | Leu       | Lys        | Ala        | Tyr        | Gln<br>90 | Glu       | Asp        | Leu        | Lys        | Arg<br>95 | Leu       |  |
| Gly        | Leu        | Glu        | Ser<br>100 | Glu       | Ile       | Leu        | Glu        | Pro<br>105 | Ser       | Ile       | Thr        | Pro        | Val<br>110 | Thr       | Ser       |  |
| Thr        | Ile        | Pro<br>115 | Pro        | Thr       | Ser       | Thr        | Ser<br>120 | Asn        | Gln       | Gln       | Lys        | Glu<br>125 | Lys        | Lys       | Glu       |  |
| Lys        | Lys<br>130 | Lys        | Lys        | Arg       | Ser       | Phe<br>135 | Lys        | Gly        | Gln       | Met       | Gly<br>140 | Arg        | Arg        | His       | Asn       |  |
| Leu<br>145 |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |  |

&lt;210&gt; 206

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 206

|           |           |           |            |           |           |           |           |            |           |           |           |           |            |           |           |  |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|--|
| Pro<br>1  | Ala       | Leu       | Ser        | His<br>5  | Leu       | Pro       | Arg       | His        | Gln<br>10 | Ile       | Asn       | Arg       | Lys        | Lys<br>15 | Arg       |  |
| Lys       | Arg       | Arg       | Arg<br>20  | Lys       | Lys       | Asp       | Pro       | Ser<br>25  | Lys       | Gly       | Arg       | Trp       | Val<br>30  | Glu       | Gly       |  |
| Ile       | Thr       | Ser<br>35 | Glu        | Gly       | Tyr       | His       | Tyr<br>40 | Tyr        | Tyr       | Asp       | Leu       | Ile<br>45 | Ser        | Gly       | Ala       |  |
| Ser       | Gln<br>50 | Trp       | Glu        | Lys       | Pro       | Glu<br>55 | Gly       | Phe        | Gln       | Gly       | Asp<br>60 | Leu       | Lys        | Lys       | Thr       |  |
| Ala<br>65 | Val       | Lys       | Thr        | Val       | Trp<br>70 | Val       | Glu       | Gly        | Leu       | Ser<br>75 | Glu       | Asp       | Gly        | Phe       | Thr<br>80 |  |
| Tyr       | Tyr       | Tyr       | Asn        | Thr<br>85 | Glu       | Thr       | Gly       | Glu        | Ser<br>90 | Arg       | Trp       | Glu       | Lys        | Pro<br>95 | Asp       |  |
| Asp       | Phe       | Ile       | Pro<br>100 | His       | Thr       | Ser       | Asp       | Leu<br>105 | Pro       | Ser       | Ser       | Lys       | Val<br>110 | Asn       | Glu       |  |



| 20                 |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
|--------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Leu                | Leu | Leu | Glu | Leu | Trp | Gln | Met | Glu | Trp | Pro | Gln | Ser | Ser | Lys | Arg |  |  |
|                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Glu                | Glu | Leu | Glu | Asn | Gly | Lys | Ile | Leu | Gly | Lys | Phe | Lys | Gly | Asn | Glu |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Val                | Met | Ile | Gln |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <210> 209          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <400> 209          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 000                |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <210> 210          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <211> 194          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <212> PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <213> Homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <400> 210          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Ser                | Val | His | Cys | Phe | Arg | Glu | Asp | Lys | Met | Lys | Phe | Thr | Ile | Val | Phe |  |  |
| 1                  |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ala                | Gly | Leu | Leu | Gly | Val | Phe | Leu | Ala | Pro | Ala | Leu | Ala | Asn | Tyr | Asn |  |  |
|                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ile                | Asn | Val | Asn | Asp | Asp | Asn | Asn | Ala | Gly | Ser | Gly | Gln | Gln | Ser |     |  |  |
|                    | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |  |
| Val                | Ser | Val | Asn | Asn | Glu | His | Asn | Val | Ala | Asn | Val | Asp | Asn | Asn | Asn |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gly                | Trp | Asp | Ser | Trp | Asn | Ser | Ile | Trp | Asp | Tyr | Gly | Asn | Gly | Phe | Ala |  |  |
| 65                 |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Ala                | Thr | Arg | Leu | Phe | Gln | Lys | Lys | Thr | Cys | Ile | Val | His | Lys | Met | Asn |  |  |
|                    |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Lys                | Glu | Val | Met | Pro | Ser | Ile | Gln | Ser | Leu | Asp | Ala | Leu | Val | Lys | Glu |  |  |
|                    |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Lys                | Lys | Leu | Gln | Gly | Lys | Gly | Pro | Gly | Gly | Pro | Pro | Pro | Lys | Gly | Leu |  |  |
|                    |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Met                | Tyr | Ser | Val | Asn | Pro | Asn | Lys | Val | Asp | Asp | Leu | Ser | Lys | Phe | Gly |  |  |
|                    | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Lys                | Asn | Ile | Ala | Asn | Met | Cys | Arg | Gly | Ile | Pro | Thr | Tyr | Met | Ala | Glu |  |  |
| 145                |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Glu                | Met | Gln | Glu | Ala | Ser | Leu | Phe | Phe | Tyr | Ser | Gly | Thr | Cys | Tyr | Thr |  |  |
|                    |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Thr                | Ser | Val | Leu | Trp | Ile | Val | Asp | Ile | Ser | Phe | Cys | Gly | Asp | Thr | Val |  |  |
|                    |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Glu                | Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <210> 211          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <211> 82           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <212> PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |  |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| Val<br>1  | His       | Gln       | Ala       | Leu<br>5 | Gly       | Arg       | Trp       | Ser       | Ser<br>10 | Trp       | Ser       | Leu       | Thr       | Leu<br>15 | Lys       |  |
| Leu       | Leu       | Phe       | Leu<br>20 | Asp      | Gln       | Cys       | Ile       | Lys<br>25 | Gly       | Leu       | Asn       | Gly       | Gly<br>30 | His       | Asp       |  |
| Phe       | Leu       | Val<br>35 | His       | Phe      | Val       | His       | Asn<br>40 | Ala       | Cys       | Leu       | Leu       | Leu<br>45 | Lys       | Glu       | Ser       |  |
| Gly       | Cys<br>50 | Ser       | Lys       | Ala      | Ile       | Ser<br>55 | Ile       | Ile       | Pro       | Asp       | Gly<br>60 | Ile       | Pro       | Gly       | Val       |  |
| Pro<br>65 | Ser       | Val       | Val       | Ile      | Val<br>70 | Asn       | Ile       | Gly       | His       | Ile<br>75 | Val       | Phe       | Ile       | Val       | Asp<br>80 |  |
| Thr       | His       |           |           |          |           |           |           |           |           |           |           |           |           |           |           |  |

&lt;210&gt; 212

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 212

|           |     |            |            |           |           |           |           |            |           |           |           |           |            |           |           |  |
|-----------|-----|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|--|
| Glu<br>1  | Leu | Gly        | Leu        | Asn<br>5  | His       | Leu       | Trp       | Leu        | Arg<br>10 | Val       | Trp       | Leu       | Glu        | Pro<br>15 | Thr       |  |
| Ala       | Gln | Val        | Pro<br>20  | Asp       | Val       | Leu       | Phe       | Pro<br>25  | Glu       | Phe       | Met       | Glu       | Arg<br>30  | Glu       | Glu       |  |
| Lys       | Ala | Val<br>35  | Ser        | Leu       | Leu       | Leu       | Trp<br>40 | Phe        | Asn       | Val       | Lys       | Glu<br>45 | Pro        | Gln       | Leu       |  |
| Pro<br>50 | Pro | Leu        | Pro        | Gly       | Arg       | Glu<br>55 | Ala       | Phe        | Gly       | Phe       | Leu<br>60 | Leu       | Leu        | Leu       | Leu       |  |
| Ala<br>65 | Leu | Val        | Ala        | Gly       | Glu<br>70 | Val       | Leu       | Gln        | Asp       | His<br>75 | Arg       | Leu       | Ala        | Leu       | Gln<br>80 |  |
| Leu       | Val | Leu        | Ala        | Gly<br>85 | Leu       | Arg       | Ala       | His        | Ala<br>90 | Gly       | Arg       | Leu       | Arg        | Phe<br>95 | Arg       |  |
| Lys       | Ala | Leu        | Thr<br>100 | Lys       | Ala       | Ser       | Ala       | Arg<br>105 | Cys       | Ala       | Pro       | Glu       | Gly<br>110 | Trp       | Thr       |  |
| Ser       | Glu | Ser<br>115 | Phe        | Ala       | Ser       | Phe       |           |            |           |           |           |           |            |           |           |  |

&lt;210&gt; 213

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |  |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|--|
| Ile<br>1 | Ile | Cys | Gly | Cys<br>5 | Val | Ser | Gly | Leu | Ser<br>10 | Pro | Leu | His | Arg | Ser<br>15 | Leu |  |
| Met      | Tyr | Cys | Phe | Gln      | Ser | Ser | Trp | Arg | Gly       | Arg | Lys | Arg | Leu | Tyr       | Leu |  |

| 20        |            |            |            |           |           |            | 25         |            |           |           |           | 30         |            |           |           |  |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|--|
| Cys       | Cys        | Ser<br>35  | Gly        | Leu       | Met       | Ser        | Lys<br>40  | Ser        | Arg       | Ser       | Ser       | Leu<br>45  | Leu        | Cys       | Leu       |  |
| Ala       | Glu<br>50  | Lys        | Pro        | Leu       | Ala       | Phe<br>55  | Phe        | Phe        | Phe       | Ser       | Leu<br>60 | Arg        | Leu        | Trp       | Arg       |  |
| Val<br>65 | Lys        | Tyr        | Ser        | Arg       | Thr<br>70 | Thr        | Ala        | Leu        | Arg       | Cys<br>75 | Ser       | Trp        | Ser        | Ser       | Arg<br>80 |  |
| Ala       | Cys        | Gly        | Leu        | Met<br>85 | Arg       | Gly        | Val        | Cys        | Ala<br>90 | Ser       | Gly       | Arg        | Pro        | Ser<br>95 | Arg       |  |
| Arg       | Pro        | Arg        | Pro<br>100 | Ala       | Val       | Leu        | Leu        | Lys<br>105 | Ala       | Gly       | His       | Arg        | Ser<br>110 | His       | Ser       |  |
| Pro       | Leu        | Ser<br>115 | Glu        | Thr       | Met       | His        | Gly<br>120 | Arg        | Ser       | His       | Ser       | Ser<br>125 | Phe        | Ser       | Asp       |  |
| Arg       | Phe<br>130 | Arg        | Arg        | Ser       | Leu       | Met<br>135 | Thr        |            |           |           |           |            |            |           |           |  |

&lt;210&gt; 214

<211> 101

<212> PRT

<213> Homo sapiens

&lt;400&gt; 214

[illegible]

&lt;210&gt; 215

<211> 204

<212> PRT

<213> Homo sapiens

<400> 215

|          |     |     |           |          |     |     |     |           |           |     |     |     |           |     |     |
|----------|-----|-----|-----------|----------|-----|-----|-----|-----------|-----------|-----|-----|-----|-----------|-----|-----|
| Leu<br>1 | Arg | Cys | Pro       | Ala<br>5 | Phe | Arg | Ser | Thr       | Ala<br>10 | Gly | Arg | Gly | Leu<br>15 | Arg | Glu |
| Gly      | Leu | Pro | Glu<br>20 | Ala      | Gln | Thr | Pro | Arg<br>25 | Met       | Ser | Pro | Gln | Ala<br>30 | Arg | Glu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asp | Gln | Leu | Gln | Arg | Lys | Ala | Val | Val | Leu | Glu | Tyr | Phe | Thr | Arg | His |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Lys | Arg | Lys | Glu | Lys | Lys | Lys | Lys | Ala | Lys | Gly | Phe | Ser | Ala | Arg | Gln |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg | Arg | Glu | Leu | Arg | Leu | Phe | Asp | Ile | Lys | Pro | Glu | Gln | Gln | Arg | Tyr |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Ser | Leu | Phe | Leu | Pro | Leu | His | Glu | Leu | Trp | Lys | Gln | Tyr | Ile | Arg | Asp |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu | Cys | Ser | Gly | Leu | Lys | Pro | Asp | Thr | Gln | Pro | Gln | Met | Ile | Gln | Ala |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Lys | Leu | Leu | Lys | Ala | Asp | Leu | His | Gly | Ala | Ile | Ile | Ser | Val | Thr | Lys |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ser | Lys | Cys | Pro | Ser | Tyr | Val | Gly | Ile | Thr | Gly | Ile | Leu | Leu | Gln | Glu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Thr | Lys | His | Ile | Phe | Lys | Ile | Ile | Thr | Lys | Glu | Asp | Arg | Leu | Lys | Val |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ile | Pro | Lys | Leu | Asn | Cys | Val | Phe | Thr | Val | Glu | Thr | Asp | Gly | Phe | Ile |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Ser | Tyr | Ile | Tyr | Gly | Ser | Lys | Phe | Gln | Leu | Arg | Ser | Ser | Glu | Arg | Ser |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Ala | Lys | Lys | Phe | Lys | Ala | Lys | Gly | Thr | Ile | Asp | Leu |     |     |     |     |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |  |  |

&lt;210&gt; 216

&lt;211&gt; 645

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 216

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Pro | Thr | Arg | Pro | Val | Ala | Ala | Gly | Ser | Glu | Gln | Gln | Gln | Gln | Ser | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Phe | Ile | Gln | Glu | Arg | Gln | Pro | Val | Ala | Leu | Met | Arg | Leu | Leu | Ser | Phe |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Asn | Val | Pro | His | Ile | Lys | Asn | Ser | Thr | Gly | Glu | Pro | Ile | Trp | Lys | Val |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Leu | Ile | Tyr | Asp | Arg | Phe | Gly | Gln | Asp | Ile | Ile | Ser | Pro | Leu | Leu | Ser |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Val | Lys | Glu | Leu | Arg | Asp | Met | Gly | Ile | Thr | Leu | His | Leu | Leu | Leu | His |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Ser | Asp | Arg | Asp | Pro | Ile | Pro | Asp | Val | Pro | Ala | Val | Tyr | Phe | Val | Met |  |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Pro | Thr | Glu | Glu | Asn | Ile | Asp | Arg | Met | Cys | Gln | Asp | Leu | Arg | Asn | Gln |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Leu | Tyr | Glu | Ser | Tyr | Tyr | Leu | Asn | Phe | Ile | Ser | Ala | Ile | Ser | Arg | Ser |  |  |



| 115        |            |            |            |            |            |            | 120        |            |            |            |            | 125        |            |            |            |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Lys        | Leu<br>130 | Glu        | Asp        | Ile        | Ala        | Asn<br>135 | Ala        | Ala        | Leu        | Ala        | Ala<br>140 | Ser        | Ala        | Val        | Thr        |  |
| Gln<br>145 | Val        | Ala        | Lys        | Val        | Phe<br>150 | Asp        | Gln        | Tyr        | Leu        | Asn<br>155 | Phe        | Ile        | Thr        | Leu        | Glu<br>160 |  |
| Asp        | Asp        | Met        | Phe        | Val<br>165 | Leu        | Cys        | Asn        | Gln        | Asn<br>170 | Lys        | Glu        | Leu        | Val        | Ser<br>175 | Tyr        |  |
| Arg        | Ala        | Ile        | Asn<br>180 | Arg        | Pro        | Asp        | Ile        | Thr<br>185 | Asp        | Thr        | Glu        | Met        | Glu<br>190 | Thr        | Val        |  |
| Met        | Asp        | Thr<br>195 | Ile        | Val        | Asp        | Ser        | Leu<br>200 | Phe        | Cys        | Phe        | Phe        | Val<br>205 | Thr        | Leu        | Gly        |  |
| Ala<br>210 | Val        | Pro        | Ile        | Ile        | Arg        | Cys<br>215 | Ser        | Arg        | Gly        | Thr        | Ala<br>220 | Ala        | Glu        | Met        | Val        |  |
| Ala<br>225 | Val        | Lys        | Leu        | Asp        | Lys<br>230 | Lys        | Leu        | Arg        | Glu        | Asn<br>235 | Leu        | Arg        | Asp        | Ala        | Arg<br>240 |  |
| Asn        | Ser        | Leu        | Phe        | Thr<br>245 | Gly        | Asp        | Thr        | Leu        | Gly<br>250 | Ala        | Gly        | Gln        | Phe        | Ser<br>255 | Phe        |  |
| Gln        | Arg        | Pro        | Leu<br>260 | Leu        | Val        | Leu        | Val        | Asp<br>265 | Arg        | Asn        | Ile        | Asp        | Leu<br>270 | Ala        | Thr        |  |
| Pro        | Leu        | His<br>275 | His        | Thr        | Trp        | Thr        | Tyr<br>280 | Gln        | Ala        | Leu        | Val        | His<br>285 | Asp        | Val        | Leu        |  |
| Asp        | Phe<br>290 | His        | Leu        | Asn        | Arg        | Val<br>295 | Asn        | Leu        | Glu        | Glu        | Ser<br>300 | Ser        | Gly        | Val        | Glu        |  |
| Asn<br>305 | Ser        | Pro        | Ala        | Gly        | Ala<br>310 | Arg        | Pro        | Lys        | Arg        | Lys<br>315 | Asn        | Lys        | Lys        | Ser        | Tyr<br>320 |  |
| Asp        | Leu        | Thr        | Pro        | Val<br>325 | Asp        | Lys        | Phe        | Trp        | Gln<br>330 | Lys        | His        | Lys        | Gly        | Ser<br>335 | Pro        |  |
| Phe        | Pro        | Glu        | Val<br>340 | Ala        | Glu        | Ser        | Val        | Gln<br>345 | Gln        | Glu        | Leu        | Glu        | Ser<br>350 | Tyr        | Arg        |  |
| Ala        | Gln        | Glu<br>355 | Asp        | Glu        | Val        | Lys        | Arg<br>360 | Leu        | Lys        | Ser        | Ile        | Met<br>365 | Gly        | Leu        | Glu        |  |
| Gly        | Glu<br>370 | Asp        | Glu        | Gly        | Ala        | Ile<br>375 | Ser        | Met        | Leu        | Ser        | Asp<br>380 | Asn        | Thr        | Ala        | Lys        |  |
| Leu<br>385 | Thr        | Ser        | Ala        | Val        | Ser<br>390 | Ser        | Leu        | Pro        | Glu        | Leu<br>395 | Leu        | Glu        | Lys        | Lys        | Arg<br>400 |  |
| Leu        | Ile        | Asp        | Leu        | His<br>405 | Thr        | Asn        | Val        | Ala        | Thr<br>410 | Ala        | Val        | Leu        | Glu        | His<br>415 | Ile        |  |
| Lys        | Ala        | Arg        | Lys<br>420 | Leu        | Asp        | Val        | Tyr        | Phe<br>425 | Glu        | Tyr        | Glu        | Glu        | Lys<br>430 | Ile        | Met        |  |
| Ser        | Lys        | Thr<br>435 | Thr        | Leu        | Asp        | Lys        | Ser<br>440 | Leu        | Leu        | Asp        | Ile        | Ile<br>445 | Ser        | Asp        | Pro        |  |
| Asp        | Ala        | Gly        | Thr        | Pro        | Glu        | Asp        | Lys        | Met        | Arg        | Leu        | Phe        | Leu        | Ile        | Tyr        | Tyr        |  |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 450        |            |            |            |            | 455        |            |            |            |            | 460        |            |            |            |            |            |
| Ile<br>465 | Ser        | Thr        | Gln        | Gln        | Ala<br>470 | Pro        | Ser        | Glu        | Ala        | Asp<br>475 | Leu        | Glu        | Gln        | Tyr        | Lys<br>480 |
| Lys        | Ala        | Leu        | Thr        | Asp<br>485 | Ala        | Gly        | Cys        | Asn        | Leu<br>490 | Asn        | Pro        | Leu        | Gln        | Tyr<br>495 | Ile        |
| Lys        | Gln        | Trp        | Lys<br>500 | Ala        | Phe        | Thr        | Lys        | Met<br>505 | Ala        | Ser        | Ala        | Pro        | Ala<br>510 | Ser        | Tyr        |
| Gly        | Ser        | Thr<br>515 | Thr        | Thr        | Lys        | Pro        | Met<br>520 | Gly        | Leu        | Leu        | Ser        | Arg<br>525 | Val        | Met        | Asn        |
| Thr        | Gly<br>530 | Ser        | Gln        | Phe        | Val        | Met<br>535 | Glu        | Gly        | Val        | Lys        | Asn<br>540 | Leu        | Val        | Leu        | Lys        |
| Gln<br>545 | Gln        | Asn        | Leu        | Pro        | Val<br>550 | Thr        | Arg        | Ile        | Leu        | Asp<br>555 | Asn        | Leu        | Met        | Glu        | Met<br>560 |
| Lys        | Ser        | Asn        | Pro        | Glu<br>565 | Thr        | Asp        | Asp        | Tyr        | Arg<br>570 | Tyr        | Phe        | Asp        | Pro        | Lys<br>575 | Met        |
| Leu        | Arg        | Gly        | Asn<br>580 | Asp        | Ser        | Ser        | Val        | Pro<br>585 | Arg        | Asn        | Lys        | Asn        | Pro<br>590 | Phe        | Gln        |
| Glu        | Ala        | Ile<br>595 | Val        | Phe        | Val        | Val        | Gly<br>600 | Gly        | Gly        | Asn        | Tyr        | Ile<br>605 | Glu        | Tyr        | Gln        |
| Asn        | Leu<br>610 | Val        | Asp        | Tyr        | Ile        | Lys<br>615 | Gly        | Lys        | Gln        | Gly        | Lys<br>620 | His        | Ile        | Leu        | Tyr        |
| Gly<br>625 | Cys        | Ser        | Glu        | Leu        | Phe<br>630 | Asn        | Ala        | Thr        | Gln        | Phe<br>635 | Ile        | Lys        | Gln        | Leu        | Ser<br>640 |
| Gln        | Leu        | Gly        | Gln        | Lys<br>645 |            |            |            |            |            |            |            |            |            |            |            |

<210> 217  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens  
 <400> 217

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Gly<br>1  | Ala       | Gly       | Pro       | Ser<br>5  | Gln       | Leu       | Arg       | Leu       | His<br>10 | Tyr       | Pro       | Arg       | Ile       | Ser<br>15 | Met       |
| Ala       | Val       | Arg       | Gln<br>20 | Trp       | Val       | Ile       | Ala       | Leu<br>25 | Ala       | Leu       | Ala       | Ala       | Leu<br>30 | Leu       | Val       |
| Val       | Asp       | Arg<br>35 | Glu       | Val       | Pro       | Val       | Ala<br>40 | Ala       | Gly       | Lys       | Leu       | Pro<br>45 | Phe       | Ser       | Arg       |
| Met       | Pro<br>50 | Ile       | Cys       | Glu       | His       | Met<br>55 | Val       | Glu       | Ser       | Pro       | Thr<br>60 | Cys       | Ser       | Gln       | Met       |
| Ser<br>65 | Asn       | Leu       | Val       | Cys       | Gly<br>70 | Thr       | Asp       | Gly       | Leu       | Thr<br>75 | Tyr       | Thr       | Asn       | Glu       | Cys<br>80 |
| Gln       | Leu       | Cys       | Leu       | Ala<br>85 | Arg       | Ile       | Lys       | Thr       | Lys<br>90 | Gln       | Asp       | Ile       | Gln       | Ile<br>95 | Met       |

Lys Asp Gly Lys Cys  
100

<210> 218  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 218

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Gly | Trp | Ile | Phe | Tyr | Phe | Met | Ser | Tyr | Pro | Leu | His | Ala | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Cys | Ser | Pro | Ala | Asp | Thr | Ser | Trp | Leu | Glu | Val | Leu | Leu | Trp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | His | Leu | Pro | Ser | Phe | Met | Ile | Trp | Met | Ser | Cys | Leu | Val | Phe | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Lys | Gln | Ser | Trp | His | Ser | Phe | Val | Tyr | Val | Ser | Pro | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gln | Thr | Arg | Leu | Asp | Ile | Trp | Glu | Gln | Val | Gly | Asp | Ser | Thr | Met |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Ser | Gln | Met | Gly | Ile | Leu | Glu | Lys | Gly | Ser | Phe | Pro | Ala | Ala | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Thr | Ser | Leu | Ser | Thr | Thr | Arg | Arg | Ala | Ala | Lys | Ala | Arg | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | His | Trp | Arg | Thr | Ala | Met | Leu | Ile | Leu | Gly |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

<210> 219  
<211> 64  
<212> PRT  
<213> Homo sapiens

<400> 219

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Ala | Lys | Phe | Asn | Leu | Asn | Ala | Phe | Phe | Phe | Phe | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ser | Glu | Ile | Gly | Thr | Val | Ile | Leu | Ser | Thr | Glu | Arg | Gln | Thr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Trp | Ala | Met | Lys | Gly | Gly | Gly | Lys | Val | Leu | Ser | Ile | Val | Arg | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gln | Pro | Glu | Ile | Lys | Pro | Ile | Tyr | Lys | His | Val | Cys | Ser | Ser | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

<210> 220  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 220

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Ala | Ile | Pro | Phe | Pro | Trp | His | Cys | Thr | Ile | Ser | Pro | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | Ser | Leu | Gly | Phe | Leu | Gly | Phe | Thr | Met | Val | Ala | Thr | Thr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Leu | Ile | Asp | Gly | Ser | Asn | Leu | Lys | Lys | Lys | Val | Met | Val | Met | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Ser | Arg | Ser | Arg | Glu | Val | Cys | Tyr | His | Lys | Ile | Thr | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 221

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Ile | Ser | Ser | Ile | Thr | Asp | Ser | Gln | Leu | Gln | Glu | Val | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | Glu | Ile | Phe | Ala | Ala | Leu | His | Glu | Val | Leu | His | Ile | Ile | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Arg | Lys | Asn | Leu | Lys | Gly | Gly | Leu | Gln | Glu | Val | Ala | Glu | Gln | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Glu | Arg | Ile | Gly | Pro | Gln | His | Gln | Ala | Gly | Ser | Asp | Ser | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Gly | Met | Ala | Phe | Phe | Lys | Met | Arg | Glu | Met | Phe | Phe | Glu | Asp |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Ile | Asp | Asp | Ala | Lys | Tyr | Cys | Gly | His | Leu | Tyr | Gly | Leu | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Ser | Tyr | Val | Gln | Asn | Gly | Thr | Gly | Asn | Ala | Tyr | Glu | Glu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asn | Lys | Gln | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 222

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Cys | Pro | Ile | Gln | His | Phe | Ile | Met | Met | Lys | Leu | Trp | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Ser | Leu | Pro | Asn | Ser | Pro | Asn | His | Tyr | Arg | Ser | Phe | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Thr | Leu | His | Ile | Arg | Tyr | Asn | Asn | Ser | Leu | Phe | Ile | Ser | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Leu | Ser | Arg | Arg | Lys | Leu | Arg | Val | Thr | Asn | Pro | Ile | Tyr | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Ser | Leu | Asn | Ile | Phe | Tyr | Leu | Leu | Ile | Pro | Ser | Cys | Arg | Thr |

| 65                 |            |            |            | 70         |            |            |            | 75         |            |            |            | 80         |            |            |            |
|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg                | Leu        | Ile        | Leu        | Trp<br>85  | Ile        | Ile        | Tyr        | Ile        | Tyr<br>90  | Arg        | Asn        | Leu        | Lys        | His<br>95  | Trp        |
| Ser                | Thr        | Ser        | Thr        | Val<br>100 | Arg        | Ser        | His        | Ser<br>105 | His        | Ser        | Ile        | Tyr        | Arg<br>110 | Leu        | Arg        |
| Pro                | Ser        | Met<br>115 | Arg        | Thr        | Asn        | Ile        | Ile<br>120 | Leu        | Arg        | Cys        | His        | Ser<br>125 | Tyr        | Tyr        | Lys        |
| Pro                | Pro<br>130 | Ile        | Ser        | His        | Pro        | Ile<br>135 | Tyr        | Trp        | Asn        | Asn        | Pro<br>140 | Ser        | Arg        | Met        | Asn        |
| Leu<br>145         | Arg        | Gly        | Leu        | Leu        | Ser<br>150 | Arg        | Gln        | Ser        | His        | Leu<br>155 | Asp        | Pro        | Ile        | Leu        | Arg<br>160 |
| Phe                | Pro        | Leu        | His        | Leu<br>165 | Thr        | Ile        | Tyr        | Tyr        | Arg<br>170 | Gly        | Pro        | Ser        | Asn        | Arg<br>175 | Ser        |
| Pro                | Pro        | Leu        | Pro<br>180 | Pro        | Arg        | Asn        | Arg        | Ile<br>185 | Lys        | Gln        | Pro        | Asn        | Arg<br>190 | Ile        | Lys        |
| Leu                | Arg        | Cys<br>195 | Arg        |            |            |            |            |            |            |            |            |            |            |            |            |
| <210> 223          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <211> 174          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <212> PRT          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <213> Homo sapiens |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <400> 223          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| Leu<br>1           | Pro        | Ser        | Ala        | Ile<br>5   | Glu        | Gly        | Pro        | Thr        | Pro<br>10  | Val        | Ser        | Ala        | Leu        | Leu<br>15  | His        |
| Ser                | Ser        | Thr        | Ile<br>20  | Val        | Val        | Ala        | Gly        | Ile<br>25  | Phe        | Leu        | Leu        | Val        | Arg<br>30  | Phe        | His        |
| Pro                | Leu        | Thr<br>35  | Thr        | Asn        | Asn        | Asn        | Phe<br>40  | Ile        | Leu        | Thr        | Thr        | Ile<br>45  | Leu        | Cys        | Leu        |
| Gly<br>50          | Ala        | Leu        | Thr        | Thr        | Leu        | Phe<br>55  | Thr        | Ala        | Ile        | Cys        | Ala<br>60  | Leu        | Thr        | Gln        | Asn        |
| Asp<br>65          | Ile        | Lys        | Lys        | Ile        | Ile<br>70  | Ala        | Phe        | Ser        | Thr        | Ser<br>75  | Ser        | Gln        | Leu        | Gly        | Leu<br>80  |
| Ile                | Ile        | Val        | Thr        | Leu<br>85  | Gly        | Ile        | Asn        | Gln        | Pro<br>90  | His        | Leu        | Ala        | Phe        | Leu<br>95  | His        |
| Ile                | Cys        | Thr        | His<br>100 | Ala        | Phe        | Phe        | Lys        | Ala<br>105 | Ile        | Leu        | Phe        | Ile        | Cys<br>110 | Ser        | Gly        |
| Ser                | Ile        | Ile<br>115 | His        | Ser        | Leu        | Ala        | Asp<br>120 | Glu        | Gln        | Asp        | Ile        | Arg<br>125 | Lys        | Ile        | Gly        |
| Asn                | Ile<br>130 | Thr        | Lys        | Ile        | Ile        | Pro<br>135 | Phe        | Thr        | Ser        | Ser        | Cys<br>140 | Leu        | Val        | Ile        | Gly        |
| Ser<br>145         | Leu        | Ala        | Leu        | Thr        | Gly<br>150 | Ile        | Pro        | Phe        | Leu        | Thr<br>155 | Gly        | Phe        | Tyr        | Ser        | Lys<br>160 |

Asp Leu Ile Ile Glu Ala Ile Asn Thr Cys Asn Thr Asn Ala  
165 170

<210> 224

<211> 123

<212> PRT

<213> Homo sapiens

<400> 224

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Lys | Thr | Thr | Ala | Leu | Ile | Ile | Ser | Val | Leu | Gly | Phe | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Glu | Leu | Asn | Asn | Leu | Thr | Ile | Lys | Leu | Ser | Ile | Asn | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Pro | Tyr | Ser | Ser | Phe | Ser | Thr | Leu | Leu | Gly | Phe | Phe | Pro | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | His | Arg | Ile | Thr | Pro | Ile | Lys | Ser | Leu | Asn | Leu | Ser | Leu | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Thr | Leu | Leu | Asp | Leu | Ile | Trp | Leu | Glu | Lys | Thr | Ile | Pro | Lys |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Thr | Ser | Thr | Leu | His | Thr | Asn | Ile | Thr | Thr | Leu | Thr | Thr | Asn | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Gly | Leu | Ile | Lys | Leu | Tyr | Phe | Ile | Ser | Phe | Leu | Ile | Asn | Ile | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ile | Ile | Ile | Leu | Tyr | Ser | Ile | Asn | Leu | Glu |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

<210> 225

<211> 129

<212> PRT

<213> Homo sapiens

<400> 225

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Met | Leu | Leu | Ala | Glu | Val | Arg | Ile | Ser | Met | Val | Ile | Arg | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Arg | Tyr | Leu | Met | Asn | Arg | Leu | Met | Phe | Gly | Ser | Glu | Cys | Ile | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Glu | Glu | Asn | Cys | Ile | Ile | Asp | His | Val | Thr | Lys | Arg | Ala | Thr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asn | Arg | Ile | Glu | Lys | Lys | Ser | Val | Leu | Lys | Leu | Ile | Leu | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Phe | Met | Val | Thr | Gln | Cys | Gln | Val | Val | Ile | Ile | Tyr | Ser | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Trp | Lys | Asn | Ile | Asn | Arg | Gly | Lys | Arg | Leu | Ile | Met | Lys | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Leu | Ile | Asp | Val | Val | Val | Tyr | Ser | Gly | Lys | Leu | Met | Cys | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Phe | Asp | Ile | Glu | Ile | Arg | Ile | Gly | Asp | Ser | Arg | Arg | Met | Lys | Ile |

115

120

125

Lys

<210> 226  
 <211> 83  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 226

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Phe<br>1  | Phe       | Phe       | Phe       | Phe<br>5 | Phe       | Phe       | Ala       | Ile       | Gln<br>10 | Met       | Asn       | Val       | Tyr       | Phe<br>15 | Leu       |
| Asn       | Pro       | His       | Arg<br>20 | Val      | Arg       | Ala       | Glu       | Leu<br>25 | Arg       | Asp       | Ala       | Trp       | His<br>30 | Ser       | Ile       |
| Ser       | His       | Pro<br>35 | Gly       | Ser      | Leu       | Pro       | Arg<br>40 | Ser       | Phe       | Phe       | Phe       | Ala<br>45 | Gly       | Ser       | Ile       |
| Leu       | Asp<br>50 | Leu       | Tyr       | His      | Phe       | Leu<br>55 | Gln       | Arg       | Gln       | Tyr       | Pro<br>60 | Glu       | Trp       | Gln       | Ser       |
| Gln<br>65 | Val       | Tyr       | Phe       | Lys      | Val<br>70 | Gly       | Val       | Phe       | Ser       | Gly<br>75 | Ser       | Arg       | Gly       | Asp       | Trp<br>80 |
| Ile       | Pro       | Ser       |           |          |           |           |           |           |           |           |           |           |           |           |           |

<210> 227  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 227

|           |           |            |            |           |           |           |            |            |           |           |           |           |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Ser<br>1  | Met       | Met        | Leu        | Phe<br>5  | Lys       | Val       | Leu        | Val        | Ile<br>10 | Thr       | Val       | Phe       | Cys        | Gly<br>15 | Leu       |
| Thr       | Val       | Ala        | Phe<br>20  | Pro       | Leu       | Ser       | Glu        | Leu<br>25  | Val       | Ser       | Ile       | Asn       | Lys<br>30  | Glu       | Leu       |
| Gln       | Asn       | Ser<br>35  | Ile        | Ile       | Asp       | Leu       | Leu<br>40  | Asn        | Ser       | Val       | Phe       | Asp<br>45 | Gln        | Leu       | Gly       |
| Ser       | Tyr<br>50 | Arg        | Gly        | Thr       | Lys       | Ala<br>55 | Pro        | Leu        | Glu       | Asp       | Tyr<br>60 | Thr       | Asp        | Asp       | Asp       |
| Leu<br>65 | Ser       | Thr        | Asp        | Ser       | Glu<br>70 | Gln       | Ile        | Met        | Asp       | Phe<br>75 | Thr       | Pro       | Ala        | Ala       | Asn<br>80 |
| Lys       | Gln       | Asn        | Ser        | Glu<br>85 | Phe       | Ser       | Thr        | Asp        | Val<br>90 | Glu       | Thr       | Val       | Ser        | Ser<br>95 | Gly       |
| Phe       | Leu       | Glu        | Glu<br>100 | Phe       | Thr       | Glu       | Asn        | Thr<br>105 | Asp       | Ile       | Thr       | Val       | Lys<br>110 | Ile       | Pro       |
| Leu       | Ala       | Gly<br>115 | Asn        | Pro       | Val       | Ser       | Pro<br>120 | Thr        | Ser       |           |           |           |            |           |           |

<210> 228  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 228

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Thr<br>1 | Ser       | Thr       | Thr       | Val<br>5 | Phe | Phe       | Phe       | Pro       | Phe<br>10 | His | Leu       | Ser       | Leu       | Pro<br>15 | Val |
| Gly      | Cys       | Thr       | Val<br>20 | Cys      | Ser | His       | Ala       | Leu<br>25 | Cys       | Ile | Asn       | Ile       | Leu<br>30 | Glu       | Ile |
| Tyr      | Arg       | Ser<br>35 | Val       | Leu      | Tyr | Phe       | Leu<br>40 | Tyr       | Cys       | Trp | Ile       | Leu<br>45 | Ile       | Ile       | Lys |
| Thr      | Phe<br>50 | Thr       | Arg       | Val      | Leu | Asn<br>55 | Lys       | Ser       | Ser       | Leu | Thr<br>60 | Arg       | Lys       |           |     |

&lt;210&gt; 229

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ala<br>1  | Arg       | Pro       | Cys       | Met<br>5  | Asn       | Ser       | Thr       | Lys       | Ala<br>10 | Leu       | Pro       | His       | Gly       | Arg<br>15 | Glu       |
| His       | Thr       | Arg       | Leu<br>20 | Lys       | Met       | Leu       | Ser       | Tyr<br>25 | Leu       | Lys       | Asn       | Lys       | Met<br>30 | Cys       | Lys       |
| Ser       | Ser       | Gly<br>35 | Trp       | His       | Lys       | Thr       | Lys<br>40 | Val       | Asn       | Ala       | Ser       | Trp<br>45 | Gly       | Thr       | Phe       |
| Leu       | Arg<br>50 | Gly       | Leu       | Ala       | Glu       | Cys<br>55 | Val       | Asn       | Ile       | Ile       | Asp<br>60 | Phe       | Cys       | Leu       | Cys       |
| Tyr<br>65 | Met       | Thr       | Ser       | Val       | Thr<br>70 | Ser       | Leu       | Lys       | Ile       | Cys<br>75 | Thr       | Ile       | Gln       | Phe       | Gln<br>80 |
| Leu       | Trp       | Ile       | Thr       | Ser<br>85 | Val       | Asp       | Leu       | Cys       | Glu<br>90 | Gly       | Phe       | Tyr       | Leu       | Cys<br>95 | Arg       |
| Met       | Gly       | Val       |           |           |           |           |           |           |           |           |           |           |           |           |           |

&lt;210&gt; 230

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Gly<br>1 | Glu       | Leu       | Gln       | Lys<br>5 | Ser | Ser       | His       | Tyr       | His<br>10 | Pro | Pro       | Glu       | Leu       | Phe<br>15 | Glu |
| Met      | Ile       | Phe       | Phe<br>20 | Val      | His | Phe       | Gly       | Cys<br>25 | Ser       | Ile | Gly       | Gly       | Arg<br>30 | Ile       | Tyr |
| Tyr      | Asn       | Met<br>35 | Asp       | His      | Leu | Tyr       | Phe<br>40 | Cys       | Ile       | Tyr | Leu       | Phe<br>45 | Ile       | Thr       | Arg |
| Pro      | Gln<br>50 | Pro       | Gln       | Ser      | Ser | Phe<br>55 | Ser       | Pro       | Ser       | Thr | Ser<br>60 | Leu       | Cys       | Leu       |     |

&lt;210&gt; 231

&lt;211&gt; 64



<212> PRT  
 <213> Homo sapiens

<400> 231

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Ile<br>1 | Asn       | Lys       | Tyr       | Arg<br>5 | Ser | Arg       | Asp       | Asp       | Pro<br>10 | Tyr | Tyr       | Ser       | Ile       | Phe<br>15 | Tyr |
| His      | Gln       | Tyr       | Cys<br>20 | Ser      | Gln | Asn       | Val       | Gln<br>25 | Lys       | Lys | Ser       | Phe       | Gln<br>30 | Ile       | Thr |
| Gln      | Glu       | Asp<br>35 | Asp       | Asn      | Gly | Trp       | Thr<br>40 | Phe       | Val       | Ile | His       | Leu<br>45 | Lys       | Asp       | Cys |
| Gly      | Arg<br>50 | Ala       | Asn       | Ser      | Thr | His<br>55 | Cys       | Ile       | Val       | Cys | Ala<br>60 | Tyr       | Gly       | Gly       | Leu |

<210> 232  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 232

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Pro<br>1  | Leu       | Phe       | Cys       | Ala<br>5  | Ile       | Leu       | Lys       | Thr       | Cys<br>10 | Thr       | Phe       | Tyr       | Phe       | Ser<br>15 | Asp       |
| Ser       | Leu       | Thr       | Phe<br>20 | Leu       | Ile       | Glu       | Cys       | Val<br>25 | Leu       | Tyr       | His       | Ala       | Val<br>30 | Met       | Leu       |
| Trp       | Tyr       | Tyr<br>35 | Ser       | Tyr       | Arg       | Val       | Leu<br>40 | Pro       | Ile       | Leu       | Lys       | Thr<br>45 | Cys       | His       | Phe       |
| Pro       | Lys<br>50 | Arg       | Ser       | Phe       | Asp       | Ser<br>55 | Ala       | Leu       | Glu       | Val       | Leu<br>60 | His       | Lys       | Leu       | Lys       |
| Ser<br>65 | Leu       | Ser       | Asn       | Ile       | Asn<br>70 | Met       | Lys       | Gly       | Gly       | Thr<br>75 | Gly       | Cys       | Asn       | Ile       | Tyr<br>80 |
| Ser       | Gln       | Val       | Thr       | Ser<br>85 | Leu       | Tyr       | Ile       |           |           |           |           |           |           |           |           |

<210> 233  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 233

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ala<br>1  | Ser       | Thr       | Ile       | Met<br>5 | Asp       | Leu       | Leu       | Phe       | Gly<br>10 | Arg       | Arg       | Lys       | Thr       | Pro<br>15 | Glu       |
| Glu       | Leu       | Leu       | Arg<br>20 | Gln      | Asn       | Gln       | Arg       | Ala<br>25 | Leu       | Asn       | Arg       | Ala       | Met<br>30 | Arg       | Glu       |
| Leu       | Asp       | Arg<br>35 | Glu       | Arg      | Gln       | Lys       | Leu<br>40 | Glu       | Thr       | Gln       | Glu       | Lys<br>45 | Lys       | Ile       | Ile       |
| Ala       | Asp<br>50 | Ile       | Lys       | Lys      | Met       | Ala<br>55 | Lys       | Gln       | Gly       | Gln       | Met<br>60 | Asp       | Ala       | Val       | Arg       |
| Ile<br>65 | Met       | Ala       | Lys       | Asp      | Leu<br>70 | Val       | Arg       | Thr       | Arg       | Arg<br>75 | Tyr       | Val       | Arg       | Lys       | Phe<br>80 |

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |  |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|--|
| Val        | Leu        | Met        | Arg        | Ala<br>85 | Asn        | Ile        | Gln        | Ala        | Val<br>90 | Ser        | Leu        | Lys        | Ile        | Gln<br>95 | Thr        |  |
| Leu        | Lys        | Ser        | Asn<br>100 | Asn       | Ser        | Met        | Ala        | Gln<br>105 | Ala       | Met        | Lys        | Gly        | Val<br>110 | Thr       | Lys        |  |
| Ala        | Met        | Gly<br>115 | Thr        | Met       | Asn        | Arg        | Gln<br>120 | Leu        | Lys       | Leu        | Pro        | Gln<br>125 | Ile        | Gln       | Lys        |  |
| Ile        | Met<br>130 | Met        | Glu        | Phe       | Glu        | Arg<br>135 | Gln        | Ala        | Glu       | Ile        | Met<br>140 | Asp        | Met        | Lys       | Glu        |  |
| Glu<br>145 | Arg        | Ile        | Glu        | Leu       | Leu<br>150 | His        | Leu        | Met        | Ile       | Pro<br>155 | Trp        | Val        | Leu        | Gly       | Lys<br>160 |  |
| Phe        |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |  |

&lt;210&gt; 234

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 234

|           |           |            |            |           |           |           |            |            |           |           |           |           |            |           |           |  |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|--|
| Arg<br>1  | Arg       | Val        | Arg        | Thr<br>5  | Lys       | Ser       | Phe        | Ala        | Met<br>10 | Met       | Arg       | Thr       | Ala        | Ser<br>15 | Ile       |  |
| Trp       | Pro       | Cys        | Leu<br>20  | Ala       | Ile       | Phe       | Leu        | Met<br>25  | Ser       | Ala       | Met       | Ile       | Phe<br>30  | Phe       | Ser       |  |
| Trp       | Val       | Ser<br>35  | Ser        | Phe       | Cys       | Arg       | Ser<br>40  | Arg        | Ser       | Ser       | Ser       | Arg<br>45 | Met        | Ala       | Arg       |  |
| Phe       | Arg<br>50 | Ala        | Leu        | Trp       | Phe       | Cys<br>55 | Arg        | Ser        | Ser       | Ser       | Ser<br>60 | Gly       | Val        | Phe       | Arg       |  |
| Arg<br>65 | Pro       | Asn        | Asn        | Arg       | Ser<br>70 | Met       | Met        | Val        | Glu       | Ala<br>75 | His       | Trp       | Gln        | Ala       | Gly<br>80 |  |
| Ala       | Gly       | Thr        | Asp        | Thr<br>85 | Arg       | Phe       | Arg        | Phe        | Arg<br>90 | Val       | Thr       | Leu       | Leu        | Phe<br>95 | Leu       |  |
| Gly       | Ser       | Pro        | Thr<br>100 | Cys       | Pro       | Pro       | Thr        | Lys<br>105 | Ala       | Pro       | Arg       | Ser       | Cys<br>110 | Arg       | Arg       |  |
| Arg       | Arg       | Arg<br>115 | Phe        | Arg       | Gly       | Arg       | Val<br>120 |            |           |           |           |           |            |           |           |  |

&lt;210&gt; 235

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 235

|          |     |     |           |          |     |     |     |           |           |     |     |     |           |           |     |  |
|----------|-----|-----|-----------|----------|-----|-----|-----|-----------|-----------|-----|-----|-----|-----------|-----------|-----|--|
| Lys<br>1 | Leu | Pro | Gln       | Asn<br>5 | Pro | Arg | Asp | His       | Gln<br>10 | Met | Gln | Gln | Phe       | Asn<br>15 | Pro |  |
| Leu      | Leu | Leu | His<br>20 | Ile      | His | Asp | Leu | Cys<br>25 | Leu       | Pro | Leu | Lys | Leu<br>30 | His       | His |  |
| Asp      | Leu | Leu | Asp       | Leu      | Gly | Gln | Leu | Gln       | Leu       | Ser | Val | His | Gly       | Ala       | His |  |

| 35  |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Gly | Leu | Gly | Asp | Thr | Leu | His | Gly | Leu | Cys | His | Arg | Val | Val | Gly | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Glu | Cys | Leu | Asp | Leu | Glu | Gly | His | Ser | Leu | Asp | Val | Gly | Pro | His | Gln |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Tyr | Lys | Leu | Ala | His | Ile | Ala | Pro | Gly | Ala | His | Gln | Val | Phe | Cys | His |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Asp | Ala | Asn | Ser | Ile | His | Leu | Ala | Leu | Leu | Gly | His | Leu | Leu | Asn | Val |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Cys | Asn | Asp | Phe | Leu | Leu | Leu | Gly | Leu |     |     |     |     |     |     |     |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |  |  |

<210> 236  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens  
 <400> 236

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Lys | Arg | Ser | Val | Lys | Asp | Ala | Ala | Lys | Lys | Gly | Gln | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Cys | Ile | Val | Leu | Ala | Lys | Glu | Met | Ile | Arg | Ser | Arg | Lys | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Leu | Tyr | Ala | Ser | Lys | Ala | His | Met | Asn | Ser | Val | Leu | Met | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Lys | Asn | Gln | Leu | Ala | Val | Leu | Arg | Val | Ala | Gly | Ser | Leu | Gln | Lys |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Glu | Val | Met | Lys | Ala | Met | Gln | Ser | Leu | Val | Lys | Ile | Pro | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Gln | Ala | Thr | Met | Arg | Glu | Leu | Ser | Lys | Glu | Met | Met | Lys | Ala | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ile | Glu | Glu | Met | Leu | Glu | Asp | Thr | Phe | Glu | Ser | Met | Asp | Asp | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Glu | Met | Glu | Glu | Glu | Ala | Glu | Met | Glu | Ile | Asp | Arg | Ile | Leu | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Ile | Thr | Ala | Gly | Ala | Leu | Gly | Lys | Ala | Pro | Ser | Lys | Val | Thr | Asp |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Leu | Pro | Glu | Pro | Glu | Pro | Pro | Gly | Ala | Met | Ala | Ala | Ser | Glu | Asp |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Gly | Glu | Glu | Glu | Glu | Ala | Leu | Glu | Ala | Met | Gln | Ser | Arg | Leu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Leu | Arg | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 237  
 <211> 111  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

|           |           |           |            |           |           |           |           |            |           |           |           |           |            |           |           |  |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|--|
| Leu<br>1  | Met       | Pro       | Phe        | Gln<br>5  | Ser       | Gln       | Asn       | Leu        | Gln<br>10 | Glu       | Arg       | Trp       | Leu        | Pro<br>15 | Gln       |  |
| Arg       | Met       | Arg       | Gly<br>20  | Arg       | Arg       | Lys       | Arg       | Leu<br>25  | Trp       | Arg       | Pro       | Cys       | Ser<br>30  | Pro       | Gly       |  |
| Trp       | Pro       | His<br>35 | Ser        | Ala       | Ala       | Arg       | Gly<br>40 | Cys        | Leu       | Pro       | Arg       | Trp<br>45 | Val        | Cys       | Thr       |  |
| His       | Ser<br>50 | Ser       | Gln        | Glu       | Leu       | Pro<br>55 | Phe       | Tyr        | Val       | Ser       | Leu<br>60 | Ala       | Leu        | His       | Leu       |  |
| Cys<br>65 | Cys       | Glu       | Asp        | Tyr       | His<br>70 | Phe       | Gly       | Glu        | Gly       | Ser<br>75 | Val       | Cys       | Leu        | Phe       | Ser<br>80 |  |
| Phe       | Ser       | Ala       | Gln        | Val<br>85 | Leu       | Gly       | Ser       | Gln        | Arg<br>90 | Asp       | Cys       | Ser       | Tyr        | Lys<br>95 | Ser       |  |
| Gly       | Ile       | Asn       | Lys<br>100 | Cys       | Ile       | Ile       | Phe       | Arg<br>105 | Lys       | Lys       | Lys       | Lys       | Lys<br>110 | Lys       |           |  |

&lt;210&gt; 238

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

|           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |  |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|--|
| Lys<br>1  | Ile       | Cys       | Glu        | Arg<br>5  | Cys       | Cys       | Gln       | Glu       | Gly<br>10 | Pro       | Glu       | Gly       | Cys       | Leu<br>15 | His       |  |
| Ser       | Ser       | Gly       | Gln<br>20  | Gly       | Asp       | Asp       | Gln       | Val<br>25 | Lys       | Glu       | Gly       | Cys       | Glu<br>30 | Gln       | Ala       |  |
| Val       | Cys       | Ile<br>35 | Gln        | Ser       | Thr       | His       | Glu<br>40 | Leu       | Ser       | Ala       | His       | Gly<br>45 | Asp       | Glu       | Glu       |  |
| Pro       | Ala<br>50 | Arg       | Gly        | Leu       | Ala       | Ser<br>55 | Gly       | Trp       | Phe       | Pro       | Ala<br>60 | Glu       | Glu       | His       | Arg       |  |
| Ser<br>65 | Asp       | Glu       | Gly        | His       | Ala<br>70 | Lys       | Ser       | Cys       | Glu       | Asp<br>75 | Ser       | Arg       | Asp       | Ser       | Gly<br>80 |  |
| His       | His       | Glu       | Gly        | Val<br>85 | Val       | Gln       | Arg       | Asn       | Asp<br>90 | Glu       | Gly       | Trp       | Asp       | His<br>95 | Arg       |  |
| Gly       | Asp       | Val       | Arg<br>100 | Gly       | His       | Phe       |           |           |           |           |           |           |           |           |           |  |

&lt;210&gt; 239

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

|          |     |     |     |          |     |     |     |           |     |     |     |     |           |     |  |  |
|----------|-----|-----|-----|----------|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|--|--|
| Thr<br>1 | Trp | Cys | Thr | Thr<br>5 | Met | Leu | Ala | Ala<br>10 | Arg | Leu | Val | Cys | Leu<br>15 | Arg |  |  |
|----------|-----|-----|-----|----------|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|--|--|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Pro | Ser | Arg | Val | Phe | His | Pro | Ala | Phe | Thr | Lys | Ala | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Lys | Asn | Ser | Ile | Thr | Lys | Asn | Gln | Trp | Leu | Leu | Thr | Pro | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Tyr | Ala | Thr | Lys | Thr | Arg | Ile | Gly | Ile | Arg | Arg | Gly | Arg | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gln | Glu | Leu | Lys | Glu | Ala | Ala | Leu | Glu | Pro | Ser | Met | Glu | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Phe | Lys | Ile | Asp | Gln | Met | Gly | Arg | Trp | Phe | Val | Ala | Gly | Gly | Ala | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gly | Leu | Gly | Ala | Leu | Cys | Tyr | Tyr | Gly | Leu | Gly | Leu | Ser | Asn | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ile | Gly | Ala | Ile | Glu | Lys | Ala | Val | Ile | Trp | Pro | Gln | Tyr | Val | Lys | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ile | His | Ser | Thr | Tyr | Met | Tyr | Leu | Ala | Gly | Ser | Ile | Gly | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Leu | Ser | Ala | Ile | Ala | Ile | Ser | Arg | Thr | Pro | Val | Leu | Met | Asn | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Met | Arg | Gly | Ser | Trp | Val | Thr | Ile | Gly | Val | Thr | Phe | Ala | Ala | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Val | Gly | Ala | Gly | Met | Leu | Val | Arg | Ser | Ile | Pro | Tyr | Asp | Gln | Ser | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Pro | Lys | His | Leu | Ala | Trp | Leu | Leu | His | Ser | Gly | Val | Met | Gly | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Val | Ala | Pro | Leu | Thr | Ile | Leu | Gly | Gly | Pro | Leu | Leu | Ile | Arg | Ala |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Trp | Tyr | Thr | Ala | Gly | Ile | Val | Gly | Gly | Leu | Ser | Thr | Val | Ala | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Ala | Pro | Ser | Glu | Lys | Phe | Leu | Asn | Met | Gly | Ala | Pro | Leu | Gly | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Leu | Gly | Leu | Val | Phe | Val | Ser | Ser | Leu | Gly | Ser | Met | Phe | Leu | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Thr | Thr | Val | Ala | Gly | Ala | Thr | Leu | Tyr | Ser | Val | Ala | Met | Tyr | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Leu | Val | Leu | Phe | Ser | Met | Phe | Leu | Leu | Tyr | Asp | Thr | Gln | Lys | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Lys | Arg | Ala | Glu | Val | Ser | Pro | Met | Tyr | Gly | Val | Gln | Lys | Tyr | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Ile | Asn | Ser | Met | Leu | Ser | Ile | Tyr | Met | Asp | Thr | Leu | Asn | Ile | Phe |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Met | Arg | Val | Ala | Thr | Met | Leu | Ala | Thr | Gly | Gly | Asn | Arg | Lys | Lys |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

<210> 240  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 240

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Ala | Pro | Ala | Thr | Val | Val | Gly | Gly | Arg | Asn | Ile | Asp | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Thr | Lys | Thr | Arg | Pro | Arg | Pro | Thr | Pro | Arg | Gly | Ala | Pro | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Arg | Asn | Phe | Ser | Leu | Gly | Ala | His | Met | Ala | Thr | Val | Glu | Arg | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Met | Pro | Ala | Val | Tyr | His | Ala | Ala | Leu | Met | Arg | Arg | Gly | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asn | Ile | Val | Arg | Gly | Ala | Thr | Thr | Ala | Pro | Ile | Thr | Pro | Glu | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Asn | Gln | Ala | Arg | Cys | Phe | Gly | Pro | Gly | Leu | Trp | Ser | Tyr | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Arg | Thr | Ser | Ile | Pro | Ala | Pro | Thr | Met | Ala | Ala | Lys | Val | Thr | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Thr | Gln | Glu | Pro | Leu | Ile | Met | Lys | Phe | Met | Arg | Thr | Gly | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Ile | Ala | Met | Ala | Asp | Lys | Ala | Val | Lys | Pro | Ile | Leu | Pro | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Tyr | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 241  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens

<400> 241

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Arg | Arg | Arg | Gly | Thr | Met | Ala | Ala | Ala | Ala | Asp | Glu | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Glu | Asp | Gly | Glu | Asp | Glu | Glu | Glu | Glu | Gln | Leu | Val | Leu | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Glu | Leu | Ser | Gly | Ile | Ile | Asp | Ser | Asp | Phe | Leu | Ser | Lys | Cys | Glu | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Cys | Lys | Val | Leu | Gly | Ile | Asp | Thr | Glu | Arg | Pro | Ile | Leu | Gln | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Cys | Val | Phe | Ala | Gly | Glu | Tyr | Glu | Asp | Thr | Leu | Gly | Thr | Cys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Ile | Phe | Glu | Glu | Asn | Val | Glu | His | Ala | Asp | Thr | Glu | Gly | Asn | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Val | Leu | Lys | Tyr | Lys | Cys | His | Thr | Met | Lys | Lys | Leu | Ser | Met |

| 100 |     |     |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Arg | Thr | Leu | Leu | Thr | Glu | Lys | Lys | Glu | Gly | Glu | Glu | Asn | Ile | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Val | Glu | Trp | Leu | Gln | Ile | Lys | Asp | Asn | Asp | Phe | Ser | Tyr | Arg | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Ile | Cys | Asn | Phe | Leu | His | Glu | Asn | Glu | Asp | Glu | Glu | Val | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Ser | Ala | Pro | Asp | Lys | Ser | Leu | Glu | Leu | Glu | Glu | Glu | Glu | Ile | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Asn | His | Arg | Phe | Lys | Pro | Gly | Phe | Val | Glu | Pro | Gly | Glu | Pro | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Pro | Trp | Glu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 242

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Ala | Pro | Ala | Leu | Arg | His | Arg | Glu | Thr | Arg | Arg | Pro | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | His | Val | Gly | Thr | Gly | Ala | Leu | Gly | Ala | Arg | Ser | His | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Ser | Arg | His | Leu | Glu | Phe | Trp | Gln | Lys | Gln | Phe | Ala | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Asp | Gly | Gln | Glu | Pro | Asn | Lys | Leu | Leu | Arg | Leu | Gly | Ala | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Thr | Gln | Asp | Gly | Gly | Ser | Gly | Arg | Ala | Trp | Pro | Val | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Arg | Gly | Ala | Ala | Gly | Pro | Trp | Arg | Arg | Arg | Arg | Thr | Ser | Gly | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Arg | Thr | Glu | Lys | Thr | Arg | Lys | Arg | Arg | Ser | Ser | Trp | Phe | Trp | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Tyr | Gln | Glu | Leu | Leu | Ile | Gln | Thr | Ser | Ser | Gln | Asn | Val | Lys | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ala | Arg | Phe | Trp | Ala | Leu | Thr | Leu | Arg | Gly | Pro | Phe | Cys | Lys | Trp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Ala | Val | Ser | Leu | Leu | Gly | Ser | Met | Lys | Thr | Leu |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

&lt;210&gt; 243

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

|           |            |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Arg<br>1  | Arg        | Leu        | Glu        | Val<br>5  | Ser       | Tyr       | Arg        | Gln        | His<br>10 | His       | Phe       | Arg        | Val        | Ser<br>15 | Leu       |
| Ala       | Pro        | Trp        | Ser<br>20  | Lys       | Met       | Ala       | Asp        | Glu<br>25  | Ala       | Thr       | Arg       | Arg        | Val<br>30  | Val       | Ser       |
| Glu       | Ile        | Pro<br>35  | Val        | Leu       | Lys       | Thr       | Asn<br>40  | Ala        | Gly       | Pro       | Arg       | Asp<br>45  | Arg        | Glu       | Leu       |
| Trp       | Val<br>50  | Gln        | Arg        | Leu       | Lys       | Glu<br>55 | Glu        | Tyr        | Gln       | Ser       | Leu<br>60 | Ile        | Arg        | Tyr       | Val       |
| Glu<br>65 | Asn        | Asn        | Lys        | Asn       | Ala<br>70 | Asp       | Asn        | Asp        | Trp       | Phe<br>75 | Arg       | Leu        | Glu        | Ser       | Asn<br>80 |
| Lys       | Glu        | Gly        | Thr        | Arg<br>85 | Trp       | Phe       | Gly        | Lys        | Cys<br>90 | Trp       | Tyr       | Ile        | His        | Asp<br>95 | Leu       |
| Leu       | Lys        | Tyr        | Glu<br>100 | Phe       | Asp       | Ile       | Glu        | Phe<br>105 | Asp       | Ile       | Pro       | Ile        | Thr<br>110 | Tyr       | Pro       |
| Thr       | Thr        | Ala<br>115 | Pro        | Glu       | Ile       | Ala       | Val<br>120 | Pro        | Glu       | Leu       | Asp       | Gly<br>125 | Lys        | Thr       | Ala       |
| Lys       | Met<br>130 | Tyr        | Arg        |           |           |           |            |            |           |           |           |            |            |           |           |

&lt;210&gt; 244

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Leu<br>1  | Phe        | Ala        | Ile        | Ser<br>5  | Tyr       | Ser        | Val        | Leu        | Pro<br>10 | Val       | His        | Leu        | Cys<br>15  | Cys       | Leu       |
| Ser       | Ile        | Gln        | Leu<br>20  | Arg       | Asn       | Cys        | Asn        | Phe<br>25  | Trp       | Gly       | Ser        | Ser        | Arg<br>30  | Ile       | Cys       |
| Asp       | Arg        | Asn<br>35  | Val        | Lys       | Leu       | Asp        | Val<br>40  | Lys        | Leu       | Ile       | Phe        | Gln<br>45  | Glu        | Val       | Met       |
| Asp       | Ile<br>50  | Pro        | Ala        | Phe       | Ser       | Lys<br>55  | Pro        | Pro        | Ser       | Ser       | Phe<br>60  | Leu        | Val        | Gly       | Leu       |
| Gln<br>65 | Ser        | Glu        | Pro        | Ile       | Val<br>70 | Val        | Ser        | Ile        | Leu       | Val<br>75 | Val        | Leu        | His        | Ile       | Pro<br>80 |
| Asp       | Lys        | Gly        | Leu        | Ile<br>85 | Phe       | Leu        | Leu        | Gln        | Ser<br>90 | Leu       | His        | Pro        | Gln        | Leu<br>95 | Thr       |
| Ile       | Ser        | Gly        | Ser<br>100 | Gly       | Val       | Ser        | Leu        | Gln<br>105 | His       | Arg       | Asp        | Leu        | Arg<br>110 | His       | Asn       |
| Thr       | Ser        | Arg<br>115 | Gly        | Phe       | Ile       | Arg        | His<br>120 | Leu        | Gly       | Pro       | Gly        | Arg<br>125 | Lys        | Arg       | Asn       |
| Ala       | Glu<br>130 | Val        | Val        | Leu       | Pro       | Val<br>135 | Ala        | Tyr        | Leu       | Lys       | Ala<br>140 | Pro        | Ser        | Ser       | Leu       |
| Leu       | Trp        | Glu        | Asp        | Glu       | Thr       | Leu        | Gly        | Cys        | Cys       | Lys       | Thr        | Ser        | Phe        | Glu       |           |



145  
 <210> 245  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

150

155

&lt;400&gt; 245

|           |           |           |            |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ala<br>1  | Thr       | Leu       | Pro        | Asp<br>5  | Ala       | Leu       | Pro       | Pro       | Ala<br>10 | Thr       | Lys       | Phe       | Phe       | Leu<br>15 | Lys       |
| Ala       | Phe       | Phe       | Asp<br>20  | Ser       | Leu       | Pro       | Ser       | Pro<br>25 | Ile       | Gln       | Ser       | Tyr       | Leu<br>30 | Tyr       | Ile       |
| Phe       | Ala       | Val<br>35 | Phe        | Pro       | Ser       | Ser       | Ser<br>40 | Gly       | Thr       | Ala       | Ile       | Ser<br>45 | Gly       | Ala       | Val       |
| Val       | Gly<br>50 | Tyr       | Val        | Ile       | Gly       | Met<br>55 | Ser       | Asn       | Ser       | Met       | Ser<br>60 | Asn       | Ser       | Tyr       | Phe       |
| Arg<br>65 | Arg       | Ser       | Trp        | Ile       | Tyr<br>70 | Gln       | His       | Phe       | Pro       | Asn<br>75 | His       | Arg       | Val       | Pro       | Ser<br>80 |
| Leu       | Leu       | Asp       | Ser        | Ser<br>85 | Arg       | Asn       | Gln       | Ser       | Leu<br>90 | Ser       | Ala       | Phe       | Leu       | Leu<br>95 | Phe       |
| Ser       | Thr       | Tyr       | Arg<br>100 | Ile       | Arg       | Asp       |           |           |           |           |           |           |           |           |           |

<210> 246  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 246

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|
| Ala<br>1  | Val        | Arg        | Arg        | Arg<br>5  | Gly       | Ala        | Leu        | Ser        | Leu<br>10 | Ser       | Val        | Gly        | Ala<br>15  | Cys       |
| Gly       | Leu        | Val        | Ala<br>20  | Leu       | Trp       | Gln        | Arg        | Arg<br>25  | Arg       | Gln       | Asp        | Ser        | Gly<br>30  | Thr       |
| Ser       | Gly        | Phe<br>35  | Ser        | Thr       | Glu       | Glu        | Arg<br>40  | Ala        | Ala       | Pro       | Phe        | Ser<br>45  | Leu        | Tyr       |
| Arg       | Val<br>50  | Phe        | Leu        | Lys       | Asn       | Glu<br>55  | Lys        | Gly        | Gln       | Tyr       | Ile<br>60  | Ser        | Pro        | His       |
| Asp<br>65 | Ile        | Pro        | Ile        | Tyr       | Ala<br>70 | Asp        | Lys        | Asp        | Val       | Phe<br>75 | His        | Met        | Val        | Glu<br>80 |
| Val       | Pro        | Arg        | Trp        | Ser<br>85 | Asn       | Ala        | Lys        | Met        | Glu<br>90 | Ile       | Ala        | Thr        | Lys        | Asp<br>95 |
| Leu       | Asn        | Pro        | Ile<br>100 | Lys       | Gln       | Asp        | Val        | Lys<br>105 | Lys       | Gly       | Lys        | Leu        | Arg<br>110 | Val       |
| Ala       | Asn        | Leu<br>115 | Phe        | Pro       | Tyr       | Lys        | Gly<br>120 | Tyr        | Ile       | Trp       | Asn        | Tyr<br>125 | Gly        | Ile       |
| Pro       | Gln<br>130 | Thr        | Trp        | Glu       | Asp       | Pro<br>135 | Gly        | His        | Asn       | Asp       | Lys<br>140 | His        | Thr        | Cys       |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Cys<br>145 | Gly        | Asp        | Asn        | Asp        | Pro<br>150 | Ile        | Asp        | Val        | Cys        | Glu<br>155 | Ile        | Gly        | Ser        | Lys        | Val<br>160 |
| Cys        | Ala        | Arg        | Gly        | Glu<br>165 | Ile        | Ile        | Gly        | Val        | Lys<br>170 | Val        | Leu        | Gly        | Ile        | Leu<br>175 | Ala        |
| Met        | Ile        | Asp        | Glu<br>180 | Gly        | Glu        | Thr        | Asp        | Trp<br>185 | Lys        | Val        | Ile        | Ala        | Ile<br>190 | Asn        | Val        |
| Asp        | Asp        | Pro<br>195 | Asp        | Ala        | Ala        | Asn        | Tyr<br>200 | Asn        | Asp        | Ile        | Asn        | Asp<br>205 | Val        | Lys        | Arg        |
| Leu        | Lys<br>210 | Pro        | Gly        | Tyr        | Leu        | Glu<br>215 | Ala        | Thr        | Val        | Asp        | Trp<br>220 | Phe        | Arg        | Arg        | Tyr        |
| Lys<br>225 | Val        | Pro        | Asp        | Gly        | Lys<br>230 | Pro        | Glu        | Asn        | Glu        | Phe<br>235 | Ala        | Phe        | Asn        | Ala        | Glu<br>240 |
| Phe        | Lys        | Asp        | Lys        | Asp<br>245 | Phe        | Ala        | Ile        | Asp        | Ile<br>250 | Ile        | Lys        | Ser        | Thr        | His<br>255 | Asp        |
| His        | Trp        | Lys        | Ala<br>260 | Leu        | Val        | Thr        | Lys        | Lys<br>265 | Thr        | Asn        | Gly        | Lys        | Arg<br>270 | Ile        | Met        |
| Leu        | Ile        | Val<br>275 | Gln        | Leu        | Phe        | Val        | Gly<br>280 | Pro        | Leu        | Lys        | Val        | Cys<br>285 |            |            |            |

&lt;210&gt; 247

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 247

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Thr<br>1  | Lys       | Gly       | Leu       | Arg<br>5  | Ile       | Ala       | Gln       | Ala       | Gln<br>10 | Leu       | Cys       | Pro       | Gly       | Ser<br>15 | Pro       |
| Arg       | Cys       | Arg       | Ser<br>20 | Gln       | Ser       | Ile       | Ser       | Arg<br>25 | Arg       | Ala       | Cys       | Ala       | Leu<br>30 | Cys       | Leu       |
| Arg       | Pro       | Ser<br>35 | Thr       | Gln       | Pro       | Asn       | Thr<br>40 | Thr       | Tyr       | Leu       | Arg       | Lys<br>45 | Pro       | Gly       | Gly       |
| Arg       | Lys<br>50 | Arg       | Ala       | Val       | Gly       | His<br>55 | Lys       | Ser       | Pro       | Ala       | Glu<br>60 | Thr       | Arg       | Val       | Pro       |
| Ala<br>65 | Ser       | Val       | Gln       | Arg       | Ser<br>70 | Gln       | Pro       | Pro       | Arg       | Ala<br>75 | His       | Arg       | Lys       | Ser       | Cys<br>80 |
| Leu       | Ala       | Ser       | Leu       | Gly<br>85 | Leu       | Cys       | Lys       | Asn       | Asn<br>90 | Lys       | Cys       | Leu       | Ser       |           |           |

&lt;210&gt; 248

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Asp<br>1 | Pro | Arg | Pro | Ser<br>5 | Arg | Ile | Gln | His | Ile<br>10 | Ser | Gly | Asn | Pro | Ala<br>15 | Gly |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Glu | Arg | Leu | Ala | Ile | Arg | Ala | Gln | Leu | Lys | Arg | Glu | Tyr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Tyr | Asn | Asp | Pro | Asn | Arg | Arg | Gly | Leu | Ile | Glu | Asn | Pro | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Arg | Trp | Ala | Tyr | Ala | Arg | Thr | Ile | Asn | Val | Tyr | Pro | Asn | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Thr | Pro | Lys | Asn | Ser | Leu | Met | Gly | Ala | Leu | Cys | Gly | Phe | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Leu | Ile | Phe | Ile | Tyr | Tyr | Ile | Ile | Lys | Thr | Glu | Arg | Asp | Arg | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Ile | Gln | Glu | Gly | Lys | Leu | Asp | Arg | Thr | Phe | His | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Tyr

&lt;210&gt; 249

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 249

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Arg | Ser | Gly | Ser | Glu | Ile | Arg | Ile | Asp | Ile | Tyr | Cys | Ser | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Gly | Pro | Thr | Lys | Gln | Gly | Arg | Ile | Phe | Asp | Glu | Pro | Ser | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Val | Val | Leu | Lys | Gln | Val | Leu | Ser | Phe | Gln | Leu | Gly | Ser | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Pro | Leu | Ala | Cys | Ala | Arg | Arg | Val | Ser | Gly | Asp | Met | Leu | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Gly | Ser | Arg | Val | Ser | Gly | Arg | Val | Arg | Arg | Leu | Asp | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Phe | Gly | Asn | Asp | Ile | Leu | Ala | Asn | Gln | Gly | Thr | Ile | Ala | Pro | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Arg Phe

&lt;210&gt; 250

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gln | Val | Met | Val | Gln | Ser | Met | Phe | Ala | Pro | Thr | Asp | Thr | Ser | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Ala | Val | Trp | Lys | Glu | Ala | Lys | Pro | Glu | Asp | Leu | Met | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Leu | Arg | Cys | Val | Phe | Glu | Leu | Pro | Ala | Glu | Asn | Asp | Lys | Pro | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Glu | Ile | Asn | Lys | Ile | Ile | Ser | Thr | Thr | Ala | Ser | Lys | Thr | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Pro | Ile | Val | Ser | Lys | Ser | Leu | Ser | Ser | Ser | Leu | Asp | Asp | Thr | Glu |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Lys | Lys | Val | Met | Glu | Glu | Cys | Lys | Arg | Leu | Gln | Gly | Glu | Val | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Leu | Arg | Glu | Asn | Lys | Gln | Phe | Lys | Glu | Glu | Asp | Gly | Leu | Arg |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Met | Arg | Lys | Thr | Val | Gln | Ser | Asn | Ser | Pro | Ile | Ser | Ala | Leu | Ala | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Gly | Lys | Glu | Glu | Gly | Leu | Ser | Thr | Arg | Leu | Leu | Ala | Leu | Val | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Phe | Phe | Ile | Val | Gly | Val | Ile | Ile | Gly | Lys | Ile | Ala | Leu |     |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

&lt;210&gt; 251

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Lys | Ala | Leu | Pro | Phe | Ile | Ser | Lys | Ala | Leu | Gly | Gln | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Thr | Arg | Leu | Ser | Leu | Met | Thr | Ser | Thr | Ser | Asp | Ala | Ala | Thr | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Phe | Leu | Trp | Ala | Ser | Asp | Ser | Val | His | Gln | Ser | Gln | Gly | Ala | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Asp | Arg | Thr | Glu | Asp | Thr | Glu | Ser | Ser | Leu | Gly | Arg | Glu | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Trp | Gly | Leu | Leu | Cys | Gly | Ala | Asp | Arg | Thr | Pro | Gln | His | Ala |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Leu | Gln | Leu | Pro | Lys | Gly | Gln | His | Gln | Gln | Ala | Arg | Lys | Gly | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Arg | Glu | Val | Ile | Gln | His | His | Val | Pro | Arg | Pro | Thr | Asn | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

&lt;210&gt; 252

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Gly | Cys | Ser | Ile | Thr | Glu | Thr | Val | Thr | Val | Asp | Pro | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Pro | Leu | Leu | Gly | Leu | Thr | Gln | Tyr | Arg | Arg | Gly | Ala | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Thr | Leu | Lys | His | Thr | Phe | Leu | Ser | Asp | Gly | Phe | Arg | Asn | Leu | Arg |

$$\begin{aligned} \frac{\partial \mathcal{L}}{\partial \mathbf{W}_1} &= \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_1} \mathbf{W}_2 + \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_1} \mathbf{W}_1 \mathbf{W}_2^T \\ \frac{\partial \mathcal{L}}{\partial \mathbf{W}_2} &= \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_2} \mathbf{W}_3 + \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_2} \mathbf{W}_2 \mathbf{W}_3^T \\ \frac{\partial \mathcal{L}}{\partial \mathbf{W}_3} &= \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_3} \mathbf{W}_4 + \frac{\partial \mathcal{L}}{\partial \mathbf{Z}_3} \mathbf{W}_3 \mathbf{W}_4^T \end{aligned}$$

<210> 254  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 254

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Ile | Trp | Lys | Gln | Ile | Cys | Gln | His | Lys | Asn | Val | Val | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Thr | Arg | Lys | Arg | Arg | Asp | Ala | Asn | Ser | Leu | Pro | Leu | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | His | Arg | Pro | Pro | Pro | Pro | Ala | Ser | Lys | Pro | Pro | Pro | Ala | Leu | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Leu | Ser | Asp | Gly | Val | Arg | Leu | Arg | Gly | His | Gly | Glu | Asp | Glu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Val | Leu | Asp | Pro | Pro | Thr | Asp | Leu | Lys | Phe | Lys | Gly | Pro | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Asp | Val | Val | Thr | Thr | Asn | Leu | Lys | Leu | Arg | Asn | Pro | Ser | Asp | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Val | Cys | Phe | Lys | Val | Lys | Thr | Thr | Ala | Pro | Arg | Arg | Tyr | Cys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Asn | Ser | Gly | Ile | Ile | Asp | Pro | Gly | Ser | Thr | Val | Thr | Val | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Met | Leu | Gln | Pro | Phe | Asp | Tyr | Asp | Pro | Asn | Glu | Lys | Ser | Lys | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Phe | Met | Val | Gln | Thr | Ile | Phe | Ala | Pro | Pro | Asn | Thr | Ser | Asp | Met |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Glu | Ala | Val | Trp | Lys | Glu | Ala | Lys | Pro | Asp | Glu | Leu | Met | Asp | Ser | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Arg | Cys | Val | Phe | Glu | Met | Pro | Asn | Glu | Asn | Asp | Lys | Leu | Asn | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Glu | Pro | Ser | Lys | Ala | Val | Pro | Leu | Asn | Ala | Ser | Lys | Gln | Asp | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Met | Pro | Lys | Pro | His | Ser | Val | Ser | Leu | Asn | Asp | Thr | Glu | Thr | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Met | Glu | Glu | Cys | Lys | Arg | Leu | Gln | Gly | Glu | Met | Met | Lys | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Glu | Glu | Asn | Arg | His | Leu | Arg | Asp | Glu | Gly | Leu | Arg | Leu | Arg | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ala | His | Ser | Asp | Lys | Pro | Gly | Ser | Thr | Ser | Thr | Ala | Ser | Phe | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Asn | Val | Thr | Ser | Pro | Leu | Pro | Ser | Leu | Leu | Val | Val | Ile | Ala | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Phe | Ile | Gly | Phe | Phe | Leu | Gly | Lys | Phe | Ile | Leu |     |     |     |     |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

<210> 255  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 255

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gly<br>1   | Ser        | Ser        | Gly        | Ser<br>5   | Arg        | Phe        | Glu        | Val        | Val<br>10  | Val        | Val        | Leu        | Glu        | Glu<br>15  | Arg        |
| Arg        | Gly        | Gly        | Arg<br>20  | Gly        | Arg        | Gly        | Met        | Gly<br>25  | Arg        | Gly        | Asp        | Gly        | Phe<br>30  | Asp        | Ser        |
| Arg        | Gly        | Lys<br>35  | Arg        | Glu        | Phe        | Asp        | Arg<br>40  | His        | Ser        | Gly        | Ser        | Asp<br>45  | Arg        | Ser        | Gly        |
| Leu        | Lys<br>50  | His        | Glu        | Asp        | Lys        | Arg<br>55  | Gly        | Gly        | Ser        | Gly        | Ser<br>60  | His        | Asn        | Trp        | Gly        |
| Thr<br>65  | Val        | Lys        | Asp        | Glu        | Leu<br>70  | Thr        | Glu        | Ser        | Pro        | Lys<br>75  | Tyr        | Ile        | Gln        | Lys        | Gln<br>80  |
| Ile        | Ser        | Tyr        | Asn        | Tyr<br>85  | Ser        | Asp        | Leu        | Asp        | Gln<br>90  | Ser        | Asn        | Val        | Thr        | Glu<br>95  | Glu        |
| Thr        | Pro        | Glu        | Gly<br>100 | Glu        | Glu        | His        | His        | Pro<br>105 | Val        | Ala        | Asp        | Thr        | Glu<br>110 | Asn        | Lys        |
| Glu        | Asn        | Glu        | Val        | Glu        | Glu        | Val        | Lys<br>120 | Glu        | Glu        | Gly        | Pro        | Lys<br>125 | Glu        | Met        | Thr        |
| Leu        | Asp<br>130 | Glu        | Trp        | Lys        | Ala        | Ile<br>135 | Gln        | Asn        | Lys        | Asp        | Arg<br>140 | Ala        | Lys        | Val        | Glu        |
| Phe<br>145 | Asn        | Ile        | Arg        | Lys        | Pro<br>150 | Asn        | Glu        | Gly        | Ala        | Asp<br>155 | Gly        | Gln        | Trp        | Lys        | Lys<br>160 |
| Gly        | Phe        | Val        | Leu        | His<br>165 | Lys        | Ser        | Lys        | Ser        | Glu<br>170 | Glu        | Ala        | His        | Ala        | Glu<br>175 | Asp        |
| Ser        | Val        | Met        | Asp<br>180 | His        | His        | Phe        | Arg        | Lys<br>185 | Pro        | Ala        | Asn        | Asp        | Ile<br>190 | Thr        | Ser        |
| Gln        | Leu        | Glu<br>195 | Ile        | Asn        | Phe        | Gly        | Asp<br>200 | Leu        | Gly        | Arg        | Pro        | Gly<br>205 | Arg        | Gly        | Gly        |
| Arg        | Gly<br>210 | Gly        | Arg        | Gly        | Gly        | Arg<br>215 | Gly        | Arg        | Gly        | Gly        | Arg<br>220 | Pro        | Asn        | Arg        | Gly        |
| Ser<br>225 | Arg        | Thr        | Asp        | Lys        | Ser<br>230 | Ser        | Ala        | Ser        | Ala        | Pro<br>235 | Asp        | Val        | Asp        | Asp        | Pro<br>240 |
| Glu        | Ala        | Phe        | Pro        | Ala<br>245 | Leu        | Ala        |            |            |            |            |            |            |            |            |            |

<210> 256  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 256

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Val | Phe | Asp | Ser | Ser | Pro | Val | Val | Arg | Ser | Ala | Thr | Ser | Thr | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Val | Leu | Gln | Ala | Arg | Ser | Ile | Thr | Ser | Thr | Met | Pro | Ile | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Thr | Phe | Ala | Thr | Arg | Ile | Lys | Ser | Ile | Ser | Ser | Ala | His | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Ala | Pro | Ser | Thr | Leu | Phe | Gln | Asp | His | His | Asp | Leu | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ala | Ala | Arg | Ala |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 257

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 257

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Arg | Gly | Ser | Met | Tyr | Asp | Arg | Met | Arg | Arg | Gly | Gly | Asp | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Asp | Gly | Gly | Tyr | Gly | Gly | Phe | Asp | Asp | Tyr | Gly | Gly | Tyr | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Tyr | Gly | Asn | Asp | Gly | Phe | Asp | Asp | Arg | Met | Arg | Asp | Gly | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Met | Gly | Gly | His | Gly | Tyr | Gly | Gly | Ala | Gly | Asp | Ala | Ser | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | His | Gly | Gly | His | Phe | Val | His | Met | Arg | Gly | Leu | Pro | Phe | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Glu | Asn | Asp | Ile | Ala | Asn | Phe | Phe | Ser | Pro | Leu | Asn | Pro | Ile | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | His | Ile | Asp | Ile | Gly | Ala | Asp | Gly | Arg | Ala | Thr | Gly | Glu | Ala | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Glu | Phe | Val | Thr | His | Glu | Asp | Ala | Val | Ala | Ala | Met | Ser | Lys | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Asn | Asn | Met | Gln | His | Arg | Tyr | Ile | Glu | Leu | Phe | Leu | Asn | Ser | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Gly | Gly | Ser | Gly | Met | Gly | Gly | Ser | Gly | Met | Gly | Gly | Tyr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Asp | Gly | Met | Asp | Asn | Gln | Gly | Gly | Tyr | Gly | Ser | Val | Gly | Arg | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Met | Gly | Asn | Asn | Tyr | Ser | Gly | Gly | Tyr | Gly | Thr | Pro | Asp | Gly | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gly | Tyr | Gly | Arg | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Tyr | Tyr | Gly | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Met | Ser | Gly | Gly | Gly | Trp | Arg | Gly | Met | Tyr |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |



<210> 258  
 <211> 1105  
 <212> DNA  
 <213> Homo sapiens

<400> 258

```

aatgagcctg gtgtagatg agttttacag ctccactcagg gtggtgggtg tctctgctgt 60
ctctgggtact ggattagatg aactctttgt gcaagtgtacc agtgctgcgc aagaatatga 120
aagggagtat cgtcctgaat atgaacgtct gaaaaaatca ctggccaaag cagagagcca 180
acagcagaga gaacaactgg aacgccttcg aaaaagatat ggttctgtag ccttggatcg 240
agggactccc aaagacagct tatctcctgt gctgcaccct tctgatttga tcttgactcg 300
accaacattg aaagcagaca gcatatactg tgacattgac cacagagtta cagaggaag 360
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag 420
aaacaataaa taggagactt tagcacactt cacttgtttc tagaagtcca gaattttgga 480
cctccacgtg aaagaactgt tcttaccctt gaactggggg ctccataaag gataatttt 540
cttcagagta gcaaaagtct tcttattaga gaaactctgt gactcagatg aagtcaggga 600
tagaagacc ttggacctgg caggttaaat ctgattatc cttggccttt cctctgtatt 660
tatgcaagga aggatatact gagctgatac tcttccaagc ctacaacttc aagttttatc 720
atttgaacct aagtaacttt gctgctgagg aatggaatca aaagaacgta gtctcctggt 780
aaccacctca gattcttatt attaggctag atgtatagcc tctactcccc cagctctctg 840
ctcttgacc ttgcactgtaa gttgcctctc tattagcagc caaggaaaag ggaacatga 900
gcttatccag aacggtggca ggtctctctt ggcaatcaac caactgtgct atgaaatatg 960
cttcacactg tatagctcat tataggacgt caggttttgt gaaaaaagtg gccaagacat1020
gattaatgaa tcagaatctt gtttcattgg tgacttggat aaagactttt taattttaaa1080
aaaaaaaaa aaaaaaaaaa aaaaaa

```

<210> 259  
 <211> 1088  
 <212> DNA  
 <213> Homo sapiens

<400> 259

```

attccaaaca tggcggtctc actagggggt atgtttttct ggcagccacc cgggtccccct 60
caggccccgc cgggcctctc gggccaagct tgcctttctt aggcagctcc aggcgtctct 120
agaccctcca gcagtacttt ggtggcagag ttggagtcat ctctcgaggc ttgcttttga 180
tctctgggtg gtcaggacta tgtcaatggc accgatcagg aagaattctg aaccggtggt 240
gatcagtgta tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttaca 300
aaaagattgc agttatctgt ccagaaacca gagcaagtta tcaaaaggga ttggtcagaa 360
ctaaagaaat aattatcagc gaaagatgca ctagtccaga agcacttgac aaagctgagg 420
cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagccccg cgacatccct 480
cagggctctc tggccttacc ggagcaggca tctgccaca tccctgcacc cctgaagcca 540
acgtgagcaa agggcagagg cagttggcct atgagtggtg tgatgctgta ggttggccac 600
acattctctt cttgggactt gacatttttg aagaactctt tgccagataa tgagttcatt 660
ttagttttat gttccatttg aaaaattttt cactattttt ataagctggt aatttcttga 720
gtactttata acatgtctgt agcttggata aaccaagtaa gtattttttt tttgcttta 780
gcgaagttta gactgtgaat atgatgacac agattctttt ttatggtggt tttgcttgt 840
ttaaattttt gcatgacttt tcatcttttt atgtgtgttt cctgtagttt gatccgaag 900
aaaagagtat agtagcctga gaatcaggag atgggagttt tagtcgtagg ccttatgata 960
attacccccc ggtggtgtgt agaaaagtat gtaattttgc tctgttttaa gactttgaac1020
tacctcaaga agaggaatct aatacaatat ttgtaatggt aaaaaaaaaa aaaaaaaaaa1080
aaaaaaaaa

```

<210> 260  
 <211> 3292  
 <212> DNA  
 <213> Homo sapiens

<400> 260

atgccgaact tctgcgtgc ccccaactgc acgcggaaga gcacgcagtc cgacttggcc 60

```

ttcttcagggt tcccgcgga cctgccaga tgcacgaagt gggtagagaa ctgtaggaga 120
gcagacttag aagataaaac acctgatcag ctaataaac attatcgatt atgtgccaaa 180
cattttgaga cctctatgat ctgtagaact agtccttata ggacagttct tcgagataat 240
gcaataccaa caatatttga tcttaccagt catttgaaca accccatag tagacacaga 300
acagcaatga aagaactgag tgaagatgaa atcaggacac tgaacagaaa aaaaattgat 360
gaaactctct agcaggaaca aaaacataaa gaaaccaaca atagcaatgc tcgaaccccc 420
agcgagaaga agggtagaag gcaagatgag gacattttac ctctaacctc tgaagagaag 480
gaaaaaaag aatacctaaa atctctattt gaaatcttga ttctgtatgg aaagcaaaa 540
atacctctgg ttgacatga ggctgatgaa atcccaaga gtctctttac tcagataaac 600
tttcaggcac tgcgtgagtg tcggataaat tctggtaga aggttctgag aaagcggttt 660
gagacaacag cagttaaac ctgtgtttgt tcaaaaacac agcagggaga gatgctagag 720
atctgtgaga gctgtattct agaagaaact ctacaggga tgagagactc acctctctt 780
tccattatca ctgacatgt agtgacata gcaggggaag agcactacc ttgtgttggt 840
aggtttgttg atgaatctca taacctaaaga gaggaattta taggctctct gccctatgaa 900
ccggtatcag aaattttggc tgtgaaattt cacactatga taactgagaa gtggggatta 960
aatatggagt attgtcgtgg ccaggcttac attgtctcta gtggattttc ttccaaaatg 1020
aaagtgtgtt ctctagact tttagagaaa tatcccaag ctatctacac acctgtctct 1080
tcctgtgctt taatatgtg gttggcaaaa tcagtacctg ttatgggagt actgtgtgca 1140
ttagacaaca ttgagaagt ttgttctttt tccatcnga tccacacaa tgcttttagal 1200
acttgacaac gtaattgctg ttctttttca gaacagtaaa gaaaggggtt aagaactgaa 1260
ggaaactctc cattctcagt ggacaggcag gcatgatgct tttgaaattt ttgggaact 1320
cctgcaagca ctgtttttat gtttagatgg atctatagat gacacaaatt ttagnatgg 1380
aataactata tagctggcgg agcatcttngt actctcgagt cgagtgtagc attttgat 1440
cattgtctact attgtgttct ttaaaaatgt cctactctttt acagagcctc ttgggaaaaa 1500
cctnccangg ggcaaacctc gtgatgtctt ctttggggcc ggtagcttga ctngcagta 1560
tgnnctcaga cntcaacgaa gtgagtggga aaatatnga agtttatcat gaattttgtt 1620
ttgaggagac cacaaatttg gcaaccaaac ttgatattca aatgaaactc cctgggaaat 1680
tcgcgagcgc taccnnagg gtaacttgga atctcagcta acnctctgag agttactata 1740
aagaaacccn taagtgtccc aacagtgagg cacattattc aggaacttaa agatatattc 1800
tcagaagacg acctcaaaagc ttctaaatgc ttatctctgg tacctcagc catgggaca 1860
ctcaaatcca atacgntcng gaggaacacc atgctgacat gtatagaagt gacttaccal 1920
atctgcacac cctgtcagct gagcttcatt ttgtggaga caaatggaaa cacaggggaa 1980
aagataatga gcttccgtcc acctctatct aagccctcca cctgctcgac atcaagttt 2040
ttctaatagt gtatgcattg ctgaaggctc ttgttatctt tctgtgatg aaagttgaga 2100
atgagcggtg tgaataatgn acgaaagcgt ctttaagaga tatttgaggg aacacttga 2160
cagaccctaaa ggtcaagtaa ctggctcttt gctttaacat aaattttgga tattaaaa 2220
cgactcggtt ttaattgttg acatatatat taaactctat acaagtaagt cagagact 2280
tacagataat tccgaaactg tggnaaaata cctaagagac ttttaaaaat aggccttct 2340
atatttgata tttggaagaa aaagccgttaa ggtgtatgta gacctataa tcaataa 2400
tctttgccta taggactcca ttgaatacat tagccattga taactacct gtttaaat 2460
ccccctgttg aactctcaag ctttgaagac ctacctgttc ttccagaaga gaacgtt 2520
agtgccatgt ttctnttttg cgtgatctct gtgtatggca ctctggaatt gtctcagt 2580
agtcatttta gacatgcat ttattatcac ttgtggnatc ctactgtgtt ggtgtatga 2640
attctttgga agnaaatata ttttngaaga ggtgtgggna ggnaaggaat acmatttat 2700
naaaattgtt gtgtgnaagn cccacaattn gacacttnga ctaatangga gttttaag 2760
tngttaaaaa tntctatact gnnacagntt acaagaaatt accggagaaa agcttggag 2820
ctcacnnaa caaggnattt ncagtgtaga ttgtgtntt tcttgaactc tnaagaaa 2880
caaatganca aagtctngttt catgggttag tgcgtgtgtt cncacatct nggtgtgt 2940
nntacantct cnnntttgtg gagnctacn atcttnccta agctttttna gcanggtat 3000
tngttagaca cttctngttt catgggttag acgatacag aggcctgga cactgaca 3060
tgatttgtct gttttttttc tctgtctttn tccatgact ctatatact gcctcatct 3120
gatttataag cnaaaanctt ggaanaacct ancaaaaatg gtgtgtgtgt tcatctaga 3180
aaatatggaa aatatgtcgt ttatttttgg tgaagaaat cnaattttgt atgtattat 3240
tcaatctaaa taaatgtgga attttgttta aaaaaaaaaa aaaaaaaaaa aa 3292

```

&lt;210&gt; 261

&lt;211&gt; 1196

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 261

ggtagaaaat gcaataaatt ctgggacaaat gccacagact ctggcataga ggagcctttc 60

```

gagacaaagg ttcttatgca aaaaagcaaa ttcaaatata agtggtgtcc tgaagaagaa 120
accactgcct cgagaaatcac agagataaac tctgaaaggg agaaagaggg catcaaatca 180
acaatcagga tatcaagtcg gaaaagaag cccgattctc ccccaaaagt tctagaacca 240
gaaaacaagc aagagaagac agaaaaggaa gaggagaaaa caaatgtggg tctactctta 300
agaagatctc caagaatcac tagaccact gcaaaagtgg ctgagatcag catcagaaaa 360
gctgataaaa aaagaggggg aggagaagat gagggtggaag aagagtcacac agcttttgcaa 420
aaaaactgaca aaagggaat ttgaaaaaa tcagagaaag atacaaattc taaagtgaagc 480
aaggttcaaac ccaaaggcaa agttctgatgg actggttctc ggacacgtgg cagatggaaa 540
tattccagca atgatgaaag tgaagggtct gccagtgaaa aatcatctgc agcttcagaa 600
gaggagaaag aaaggaaaag tgaagaagcc atcttcagag atgatgatga accatcgaaa 660
aaatgtggcc ttccaaaacca tcttgagcta attctctctg gtgactcttg cagatgtgga 720
taccatactg cctgcctctg cctctctctg atgatcatcc cagatggaga atggtttctg 780
ccactctgac caataataat gctctgtgaa aaatagagg aacagttgca ggaatttgag 840
gttgctttaa agaagaagaa gctgtgcgaa cgaagaagaa aacgcttggt gtatgttggt 900
atcagattg aaacatcat tctccacaaa gaggcagact ttctgaaga tcagaagaa 960
aagaaaaaag attcaaaaaa atccaaagca aacttgcttg aaaggaggtc aacaagaaca 1020
aggaattgta taagctacag atttgatgag ttgtatgaa caattgatga agctattgaa 1080
gatgacata aagaagcoga tggaggagga ctggccgag ttggccgag aacaaagatc cccaccatcc 1140
acaggtctac gtgggaaaag catctctact attttggatg aaaaaaatat aacggc 1196

```

```

<210> 262
<211> 1467
<212> DNA
<213> Homo sapiens

```

```
<400> 262
```

```

aaggacgctt gcctttttcc ggtcggggaa gggggaagaa ggtaacttcc ggtgacgggg 60
ttgcatacact tctctctcaag ctggggcggt tgtttggtgg ggttacacgc ggttcaacca 120
tgocgtatcga aaagtgttat ttctgtctcg gcccactcta tcttgagcac gccatgatgt 180
tcgtccgcaa cgtatgcaag gtgttcagat ttgcaaatc taaatgtcat aaaaacttta 240
aaaagaaagc caatccctgc aaagttaggt ggaaccaagc attccggaaa gcagctgtgta 300
aagagcttacc agtggataat tcatttgaat ttgaaaaagc tagaaatgaa cctatcaaat 360
accagcgaga gctatggaaat aaaactattg atgcgatgaa gagagtggaa gaatcaaac 420
agaagcgcca agctaaatct ataatgaaca gattgaagaa aaataaaagc ctacagaaa 480
ttcaggatata caaagaagtc aagcaaaaaca tccactctat ccgagccctc ctgcagggca 540
aagggaaaaa gttggaagag aaaaatgtac agcagttaca agagatgatg gacatgggaa 600
attgctcctta aaaaatctctg taaccaattc ttttatgtac attgaaaaat gccctttgga 660
tacttggaac ttgctaaatta ttttattttt tacataaggt cacttaaatg aaaaagcatt 720
aaaagacata ttctctgcat tgccatctac ataatatcag atattacgga tgttagattg 780
catctcagtg ttaaatcttt actgatagat gtacttaagt aaatcatgaa aattctact 840
gtaaactatag aagtgaattg tggacgtaaa atggttgctg tatttggaata atggcactag 900
cgacattttg tatagttaact aatggcaaaa attcatggct agtgatgtat aaaaaaaa 960
attctttgca gtaaaatatt ccttttgta atgttataga atgggggata aaaaaggaa 1020
ctaaacaatt gtagggcagt gtacagatatt tttattttag tatttctctg tttggtttat 1080
ttgcatctta gaagagcata atgacattgt atgtatgag ctaattatgc tggagcttt 1140
tgacattggt taacctctct gataggtagt ttgtgatgtc ggggatgaga actgaaatca 1200
ctttgctcgg agtgacacata cactctagaa ttccacttt ggagaatact cagttccaac 1260
ttgtgtatcc tttatagaaca gactttact ttctagcccc ctatgtatct agaagcagag 1320
gaatcccgag gcccttttaa agttgttatg ttgtttctct ttaaaaagct cctgtttttg 1380
gaagtagaaa tttatgggta caacgtatgt tactattttg tacaataaat aaaaacttt 1440
aaaaagttaa aaaaaaaaaa aaaaaaac

```

```

<210> 263
<211> 739
<212> DNA
<213> Homo sapiens

```

```
<400> 263
```

```

cggctcagac cccgctcagt caccgcagc aggcgtgcag ttcccggtc ctcgcgcgg 60
cggggaaagg tcagcgccgt aatggcgttc ttggcgctcg gacctactg gacctatcag 120
caaaagggtg tcaggcgctta taagcgggag ctacgccacc ctcagctcgt gtcgctccag 180

```

```

agagacaaat accgatactt tgcttggttg atgagagccc gggttgaaga acataagaat240
gaaaaggatc tggcgagggc caccagctgt ctgaaggagg ccgagggaaga attctgggtac300
cgtagcagc cagcagccata catcttccct gactctcctt ggggcaccctc ctatgagaga360
tacgattgct acaagggtccc agaattggtgc ctgagtagact ggcattcctt tagatgact aactcggagg ggaagagctgg480
atgtatcctt attactttgc caagagagaaa acgcccactgt gtggctcctt aactgaagct540
gaacgagagg ttaagcagct gcagagaggaa acgcccactgt gtggctcctt aactgaagct540
ttgccccctg ccgaaaggga aggtgatgtt gccccactgt ggtgggtat tgtgaccaga600
ccccggggag ggcacatgta gaaagagaga gacctcatct ttcattgctt caagtgaatt660
atgttacaga acatgcacct gccctaataa aaatcagtg aaatggaaaa aaaaaaaa720
aaaaaaaaa aaaaaaaaaa

```

&lt;210&gt; 264

&lt;211&gt; 2146

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 264

```

tttttttttt tttttttttt tcccaggccc tctttttatt tacagtata ccaaacctac 60
cactttgcaaa ttttctgttc tcccatcagc tgggaattaa taggtactgt gtatctttga 120
gatcatgata tcttctgccc ctgttggtgat acagaaagg aaggcacgaa cagctgaaaa 180
agaaggggtat cacaccgctc cagctggaat ccagcaggaa cctctgagca tgccacagct 240
gaacactcaa aagagggaag atcagaagct gctcttcaat tatttgtaaa gcaaatctac 300
ttgaaagtgc ataaattggtc atcataagtc aaacgtatca attagacctt caacctaggc 360
tattttaataa taacaccacac tgaattattt tgccaatgaa tcccaaatga ttggtacaaa 420
tagtacaaat cgattttgct ttctctcttc ctttcttcag acaaacacca aataaaatgc 480
aggtgaaaga gatgaaccac gttatggttaa gcttaacctc tctaaaaatc attatgctg 540
aaaaaaatga tgttggttaa cgttaacctc atatacagct agaaaagtcg ggcctcttcg gcaagccttt 600
caagggaggt caagtcacag aaaccttttca ttctccataa aatcctccct ccatactgct gcattatggc 720
gaagtataat aaccttttca ttctccataa aatcctccct ttccgattat aaacaatgat 840
gtcatgaaga ctatcccat cagacagaaa ggaccagagt catgatgaa ctcgagccga 900
acaaaagact ctaagtgcga gaacattgga tatggaatgt tctcatttaa acattacca 960
ctggggtaatt gtttaaatga tgacctcca tatccaatgt cctctgtctt ggtggcactt agagtcttt 1020
attcggctcg agctttcatc tgacctcca tatccaatgt ttttatggag aaatggggg agtcttcctg 1080
gcatcattgt ttataatcag aaactctggt cctctgtctt ggtggcactt tttgaaaagg ttattatact 1140
tcttaacaat ttttttttca gggacttttc tagctgatg actgttactt aaactatctal 1200
aaatagagca ttttggtatc ttcatctgta ccatccatatt tctcatttaa catttaacca 1260
tatccagaca ctatgtttta taatcagaaa ctctggtcct tctgtctggt ggcacttaga 1320
gtcttttggg ccatatgaga gcagatgaga gggaggattt tatgagaaaa tggggatagt 1380
ctctatgacc acaataaatt aaaggaaaac taagctgcatt tgtgggtttt gaaaagggtta 1440
ttatacttct taacaaatct ttttttcagg gacttttcta gctgtatgac ttttacttga 1500
cctcttttga aaagcatctc caaaatgctc tatattagat agattaaact taaccaacat 1560
aatttttttt atgctgagtc agcataaatt tctaagtcag cctctagtcg tggttcatct 1620
ctttcacctg catttttatt ggtgtttgtc tgaagaaaag aagaggaaaa ccaaatcaga 1680
attgactatg tgtaccacaa tctttgggat tcatttgcaa ataatttcag tgtggtgtat 1740
tattaaatag aaaaaaaaaa ttttggttcc taggtgaaag gtctaataa gtaagttgac 1800
ttatgatgac catttatgca ctttcaaatg aatgtcctt tgtaggctgc caaaataat ctagaggttc 1920
ttctctcttt tctcttttca agtgttcagc tgtggcctgc cagctggag gtgcttctct cttctgtatc 1980
ccagctggag cgtgttgata ccttcttttt aagatacaca gtacctactt aatccagct 2040
gattgggagc caaagaattt gcaagtgatg ggttggtat cactgttaat aaaaaggagg 2100
cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 2146

```

&lt;210&gt; 265

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 265

```

caagtaaatg cagcactagt ggggtggatt gaggtatgc cctgggtgat aaatagagac 60

```

```

tcagctgtgc tggcacactc agcggctctg gaccgcattc tagccgccga ctcacacaag 120
cgaggtgggt gaggaaaatc agagttggca tggagaaaat tccagtgcca gcatctctgc 180
tcctgtgggc cctctcttac actctggcca gagataccac agtcaaacct ggagccaaaa 240
aggacacaaa ggactctcga cccaactgc cccagaccct ctccagaggt tggggtgacc 300
aaactcatctg gactcagaca tatgaagaag ctctatataa atccaagaca agcaacaaac 360
ccttgatgat tattcatcac ttggatgagt gccacacag tcaagcttta aagaaaagtg 420
ttgctgaaaa taagaataat cagaaattgg cagagcaggt tgtctctccc aatctggttt 480
atgaaaacac tgacaaacac ctttctctctg ttgcccaagta attagtgttt 540
ttgaccctac tctgacaggt agagccgata tccctggaag atattcaaac cgtctctatgt 600
cttacgaacc tcgacataca gctctgttgc tcgacaacct gaagaaagct ccaagtgtgc 660
tgaagactga attgtaaaaga aaaaaaatct ccaagccctt ctgtctgtca ggccttgaga 720
cttagaaacca gaagaatgtt gagaagactg gctagtgtgg aagcatagtg aacacactga 780
ttaggtttgt gttttaatgtt acacaactta ttttttaaga aaaacaagtt ttagaatttt 840
ggtttcaagt gtacatgtgt gaaaaacaata ttgtataact ccatgatggag ccatgatttt 900
ctaaaaaaaa aaataaatgt tttgggggtg ttctgttttc tccaaaaaaa aaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaattgcc cccaagggga cgggtttaca ttggggggcg 1020

```

&lt;210&gt; 266

&lt;211&gt; 1652

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 266

```

aattcggatc catggggccac agtggatggc ttgaaatgtg gtgagcgtc tcggacaatt 60
cggatccatg nnnngtggcc accccaagac ggcgccacgc ccgcatcggc cggatccctn 120
nccgggnntc ctgcctctctg tccctgctcc tggccggngt ttgttccgcc gggccgggga 180
caagagaagt ctaagacaga ctgccatggc ggtnatgagt ggtaccatct acgagtattg 240
agccctcacc atcgatgggg aggaatacat cctctttaaag cagtatcgag caactatat 300
cctcttgtct aacgtagcca gctactgagg tctgacagac caataccttg cactgaatgc 360
actacaagaa gaactctggc catttggtcn ttgtctctct gggctctccc tccaaccaat 420
ttggcaaaa caaggccagg gagaaactcg agatactccc agatactccc tcttctgaga 480
accaggttng ggggctttgt gncctaatin mnttccagnc tcntttgaga aanngganga 540
tngtngaacn gggggagaaa gagcnagaaa ttttacaact tcttgaagaa ccttgcctct 600
cccactcgag naactcctgg gncctcancct ggcgcgncct ttttgggaac ccatgaagat 660
ccatgacatn cgcctgggaa tttgagaagt tectggtngg ggccnagant ggcataccgg 720
ttatgcgctg gtaccaccgg accacagtcn agcaacgtcn aagatggaca tcttgntct 780
tacatgaggg ggcaggcang ccttgangcg ccnagggggn aagtaactga ntgcnnnnc 840
caccctaccc ctaccccctg cccatcatng caagggccga nggaggggct cttncaggaa 900
ggaagccaca ttcccagtc ttctnanccc ccaccccaga ttctcttnc ttnattacat 960
aaaagacaag cnttggcaca actgtgtgtc tgaaccactg tnggacacgt gacaattgt 1020
cccgatgtgt gcatggctac acagnccag tatctgcctg cnttgaaccc cangggngat 1080
gtccatcntt tngtttacgg ncttggcaca acacccnntc atatttttt cagctttct 1140
gttccaaann tgcagnncca aannggaaac acnaangttc atnngttctg 1200
ctcaaanccn tganaatcnc attcnttggg gnccangcat cntcccacat ngccccacac 1260
tacacacacc cnagcctcct tctctcttnc ctgnaaggac ctcnccnnnn tgagccccal 1320
agccnctatc cacagtgcnt ctgagacca gccaaagaaa ctgtgagcgc gatggcctg 1380
tancccaagg tncaggggnt ggtgtctcta tgaagganng gnnncccgna agcccttgt 1440
ggngcggngc ctcccctgag ccngtctgt ggtgccnagc ccttagtgca ttcaggctta 1500
ggctcccag gcanggggaca cctcccgcgc gctctggag gacatggag ctctcaactc 1560
gtctcactgg tatctcaaca ccccatctg cccagtaag gtctttctgc agcaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gg 1652

```

&lt;210&gt; 267

&lt;211&gt; 1409

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 267

```

ggagtggccc tctgtgagg gctcaaatgt ttgcaattca tggcgcgtta cgacttggct 60
cacttaacta aatccctacc aactctaaat tgccgaagga agaacttgac ctcttgagga 120
accctcgatt ggtttttcct gccatttaga ttttgagta ccccatgaag agctgcaaaa 180

```

```

attctcaaa  gtggattaca  ggaggtggca  gaacagttag  agctggaacg  gataggacca  240
caacatcagg  caggatctga  ttcattgctc  acaggaaatgg  cctttttcaa  aatgagagaa  300
atgtctcttg  aagatcatat  tgatgatgcc  aaatattgtg  gtcatttgta  tggccttggt  360
tctggttcat  cctatgtaca  gaatggcaca  gggaaatcgat  atgaagagga  agccaaacaag  420
cagtcatgac  atgaaatagt  ccttttattt  ttatttcgat  ctacacacat  gctctgtat  480
aggtttttat  tctggttgaa  tccctcgaac  aatagacagt  acccttcccc  cccctttcat  540
ggcccatttt  attgtctgcc  tttcagtact  aagtatgacc  gtctctatct  cagactctaa  600
taaaaaaaga  aaaaaaacg  cattcaggtt  aaatttggcc  ttaatttaat  atacttgta  660
gcaagcgtgt  gtgacagaga  gtggggaaag  ctacatcatt  gaatttttg  ataaacttta  720
ccgacttgag  tttggtttat  ttttcccttt  tcctaaat  actagcactg  actgtaatt  780
atttccctgt  ttacagcttc  tcccttccat  tctgcaggag  ttttagctat  tttagatcgt  840
ggaccatcag  ttttgacatt  tagagagtgt  tctgactct  aaacctgttt  tatcagaaaa  900
ttgttttttt  tcttgactta  gctggaaaaa  tctgccaact  ttacacagta  ttacttggt  960
tttgaccac  agaatatagc  acgttgtgca  aactgtcgat  tcagcgaaac  ttaaaaaaga  1020
caagaaacta  ctgaggagct  tagtaactgc  tgtttctgta  cgtagtgttt  aatcttccaal  1080
gcacatctag  tgtctgtcag  tttctaattg  gcattgttag  gctgctctgt  gactgaagaal  1140
ttttcaaac  agctttacac  ccttcaggaa  aaatccctgt  gattggatgg  ttactatctg  1200
ccaggaaact  gtaccagat  gtgaagcaca  gttattatga  tagacacttc  ctgagtgtal  1260
ttgatccac  accattacct  ttttttttaa  attggagcca  tctatgagcc  tgattgtgtt  1320
cgcaaccatt  gtaaaacca  gaaagcctag  ggattggcca  ataattgggg  aaatggtgcat  1380
gtgccaaaga  aatgggatgg  caaaagaag

```

```

<210> 268
<211> 900
<212> DNA
<213> Homo sapiens

```

```

<400> 268

```

```

ccacgcgtc  ccggaacag  cggcgccgc  gacaggacg  aggggcctta  gttggtgggc  60
aactcgggga  tcccgaaag  agaagcgtga  cccggaagcg  gaaacggggt  tccgtccag  120
ctcgccctgt  ccagtgcgt  tctaccatca  tggacctatt  gttcggcgcc  cgggaagcgc  180
cagaggagct  actcgccag  aaccagaggg  cctcgaaagg  tgccatgccc  gagctggacc  240
gcgagcgaca  gaaactagag  acccaggaga  agaaaaatcat  tgcagacatt  aagaagatgg  300
ccaagcaagg  ccagatggat  gctgttcgca  tcatggcaaa  agacttggtg  gcgacccggc  360
gctatgtgcg  caagtgtgta  ttgatgcggg  ccaacatcca  ggctgtgtcc  ctcaagatcc  420
agacactcaa  gtccaacaac  tcgatggcac  aagccatgaa  ggggtgtcacc  aaggccatgg  480
gcaccatgaa  cagacagctg  aagttgcccc  agatccagaa  gatcatgatg  gagtttagcg  540
ggcaggcgaga  gatcatggat  atgaaggagg  agatgatgaa  tgatgccatt  gatgatccca  600
tgggtgatga  gaaagatgaa  gaggagagtg  atgctgtggt  gtccagggtt  ctggatgagc  660
tgggacttag  cctaaccagat  gagctgtcga  accctccctc  aactgggggg  tcgcttagtg  720
tggctgtggt  tgggaaaaaa  gcagaggccg  cagcctcagc  cctagctgat  gctgatgcag  780
acctggagga  accgtttaag  aacctgcgga  gggactgagt  gccctgcaca  ctccgagata  840
accagtggat  gccccaggatc  ttttaccaca  acccctctgt  aataaaagag  atttgacact  900

```

```

<210> 269
<211> 1145
<212> DNA
<213> Homo sapiens

```

```

<400> 269

```

```

gggccccgcc  caggcggtg  cccgtgacct  gcttggggcg  ggggaactga  aagccggaag  60
gggcaagcag  ggttcagttc  gtcattgggg  tgtttggaaa  gaccacaggag  aagccgcaca  120
aagaactggt  caatgagtgg  tcaattgaaga  taagaaagga  atgagaggtt  gttgacaggc  180
aaataaggga  tatccaaaga  gaagaaagaa  aagtgaaacg  atctgtgaaa  gatgctgcca  240
aagaaggcca  gaagggtgct  tgcatagttc  tggccaaagg  gatgatcagg  tcaaggaagg  300
ctgtgagcaa  gctgtatgca  tccaaagcac  acatgaactc  agtgctcatg  gggatgaaga  360
accagctcga  ggtcttgcca  gtggctgggt  cctgcagaaa  gggcacagaa  gttgatgaag  420
ccatgcacaa  tcttggtgaag  attccagaga  ttcaggccac  catgagggag  tctgtccaaag  480
aaatgatgaa  ggctgggatc  atagaggaga  tggtagggga  cacttttgaa  agcatggagc  540
atcaggagaa  aatggaggaa  gaagcagaaa  tggaaattga  cagaattctc  tttgaatta  600
cagcaggggc  cttgggcaaa  gcaccacgta  aagtgaactga  tggccttcca  gagccagaac  660

```

```

ctccaggagc gatggctgccc tcagaggatg agggggaggga ggaagaggct ctggaggcca 720
tgcagtcgcc gctgggcccaca ctcgcagct aggggctgcc taccgccgt ggtgtgcaca 780
cactcctctc aagagctgcc attttatgtg tctcttgccc tacacctctg ttgtgaggac 840
taccattttg gagaaggctc tggttgtctc tttctattct ctgccaggtg ttgtggatcg 900
caaagggatt gttcttataa aagtggcata aataaatgca tcatttttag tagtatagac 960
agatatatct tattgtgggg aggggaaaga aatccatctg ctcatgaagc actcttgaaa1020
atataggatg ttgctggaat gtcgaagact ctacttttgg ctataaaaaa ctataaaaa1080
gaatttttaat aaatttttgc tttagcactt ggccccattg tagattgccc tgtgcagta1140
acttt 1145

```

&lt;210&gt; 270

&lt;211&gt; 1836

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 270

```

gttgccacat gcagtgccgc ggaggaaactg tgetctttga ggccgacgt aggggcccg 60
aagggaatac gcgagggcgaa ggtgaccggg gaccgagcat ttcagatctg ctggtagac 120
ctgggtgccc ccaccacctgt tggctgcgaag gctggtgtgt ctccggacac taccctctag 180
ggttttccac ccagcttttca ccaaggccct cctctgtgtg aagaattcca tcacgaaga 240
tcaatggctg ttaacaccta gcagggaata tgcaccacaa acaagaattg ggaatccgg 300
ggggagacat ggccaagaac tcaagagggc agcattggaa ccatcgatgg aaaaaatatt 360
taaaattgat ccagatgggaa gatggtttgt tgcgtggagg gctgctgttg gctctggagc 420
atttgctcac tatggcttgg gactgtctaa tgagattgga gctattgaaa aggctgtaat 480
ttggcctcag tatgtcgaag atagaattca ttcaccctat atgtacttag caggagatatt 540
tggtttaaca gctttgtctg ccatagcaat cagcagaacg cctgtctcca tgaacttcat 600
gatgagagcg tctttgggtg caattggtgt gacctttgca gccatgggtt gactctggaat 660
ctgggtacga tcaataccat atgaccagag cccaggccca aagcatcttg ctgtgttgtc 720
acattcttgt gtgatgggtg cagtgggtgc tectctgaca atattagggg gctctctctc 780
catcagagct gcattgttaca cagtggcat tgtgggaggg ctctccactg tggccatgtg 840
tgcccccagc gaaaagtctt tgaacatggg tgcaacctct ggagtgggct tgggtctctg 900
ctttgtgtcc tcaattgggt ctatgtttct tccacctacc acgctggctg gtgcccactc 960
ttaactcgtg gcaatgagta tctacatgga tacattaaat atatttatgc gacttgcaac1140
ccagaagata atcaagcgtg cagaagtatc accaatgtat ggagtccaaa aatatgatcc1080
cattaaactc atgctgagta tctacatgga tacattaaat atatttatgc gacttgcaac1140
tatcgtggca actggaggca acagaagaag atgaagtgtc ttagcttctg gcttctctgc1200
tcgttgaagt ttagaagata agaaacatgt catcatattt aaatgttccc gtaattgtat1320
gctccagggt tgcctttttt tctggagaat aaatgcagta atctctccc aaataagcac1380
acacattttc aattctcatg tttgagtgat tttaaaatgt tttgttgaat gtgaaaaacta1440
aagtttgtgt catgagaatg taagtctttt tctactttta aaatttagta ggttcaactga1500
gtaaactaaa ttagcaaac ctgtgtttgc atattttttt ggagtgcaga atattgtaat1560
taattgtcat agtgatttgg agctttggta aaggagccag agagaaggag taccctgcag1620
tcttttgttt ttttaaatc ttagaactta gcacttgtgt tattgattag tgaggagccat1680
gtaaagaaac tctgggtatt tggaaacagg caggttgtaa tgcattcttc ctgcggttgg1800
taacaaaact ggttctatcc tggaaacagg cagagtgtaa tgcattcttc ctgcggttgg1800
ctccccagtg gccgccttc catatagga tgtggg 1836

```

&lt;210&gt; 271

&lt;211&gt; 1220

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 271

```

tgaagtctta agagctttcc aagtttggga aggtgtccgg gttttctcgg attacttctc 60
tgagcatgaa cggaagtcac cctttgtgcc ttatgctggg attttaatga taggtgtcat 120
atatagagcg agtaaatctg ttacattctc gttcttctcg atgcactcac aagcgggtgaa 180
ctaggtgcaca agaaaacaaa gatcttattc aaaagaggtc ttacagcaac ccaactgtctc 240
atcttcccat agtaaagatg acggcgccct gaggtaaagt acaggcaaca ccaacttcgc 300
gtttctcttg cgcctctgtc caagatggcg gatgaagcca cgcgacgtgt tgtgtctcag 360
atcccggtgc tgaagactaa cgcgcgaccc cgagatctgt agttgtgggt gcagcgactg 420

```

```

aaggagggaat atcagtcctt tatccggtat gtggggaaca acaagaatgc tgacaacgat 480
tggtttccagc tggagtcctt caagggaagga actcgtgtgt ttggaaaaatg ctgggtatct 540
catgacccctc tgaatatatga gtttgacatc gagtttgaca ttccatcact atatcctact 600
actgcccacag aaattgcagtg tcttgagctg gatggaaaga cagcaaatgag gtacagggggt 660
ggcaaaaatat gcttgacgga tcatcttctt cctttgtggg ccaggaaatgt gcccacattt 720
ggatagctctc atctcatggc tctggggctg ggtccatggc ttggcagtga aatccctgat 780
ctgatttcaga agggcgctcat ccaacacaaa tccacctcta gttgttacta agtagctgca 840
ctgaggcagg gcagagggac ctttgatagg ctacgatact attttcctgt gcatcaact 900
taactcatct aactgcttcc cgggacaccc ttccacctta gttgttacta agtagctgca 960
gtaggcatct gctggggaaga acaaacacac caccacacag tactgctact tagtttctaa1020
ggctgcacag ggaagggaaa gactgggctt gacacaatct agaggttaat tatatccggc1080
cccagtgga gcaacatcgc attctggagg caggggggta actgaaagtgt agtaccatata1140
ctctttctgg ttctggaga taacctcatca ataaaagctg ctctctctgg taataaaaaa1200
aaaaaaaaaa aaaaaaaaaa

```

&lt;210&gt; 272

&lt;211&gt; 1303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

```

cgcagtcgagc aggcgtgggg cctctctcctt gtcagtcggc gccgcgtgctg ggctgggtggc 60
tctgtggcagc cggcgccggc aggactccgg cactatgagc ggcttcagca ccggagagcgt 120
cgccgcgtccc tcttccctgg agtaccggag tcttctcctt aatgagaagat gacaataact 180
atctccattt catgatattc caatttatgc agataaggat gtgtttcaca tggtagttga 240
agtaccacgc tgggtctaatg caaaaatgga gattgtctca aaggacctt taacacctat 300
taacaacagat gtgaaaaaag gaaaactctg ctatgttggc aattgttcc cgtataaagg 360
atatactctg aactatctgt ccatccctca gacttgggaa gaccocaggc caaatgataa 420
acatactggc tgtttgtgtg acaatgaccc taatgtatgt tgtgaaattg gaagcaaggt 480
atgtgcaaga ggtgaaataa ttggcggtgaa agttctaggc atattggcta tgattgacga 540
aggggaaacg gactggaaag tcatgtccat taatgtggat gatcctgatg cagccaatta 600
taatgatata aatgatgtca aacggctgaa acctggctac ttagaagcta ctgtggactg 660
gtttagaagg tataaggctt ctgatggaaa accagaaaat gagtttgcgt ttaatgcaga 720
atttaagat aaggactttg ccatgtatat tattaaaagc actcatgacc attggaagc 780
attagtgcact aagaaaaacg atgaaaaagg aatcagttgc atgaatacaa cttgtctga 840
gagccccctc aagtgtgatc ctgatgtctc cagagccatt gtggatgctt taccaccacc 900
ctgtgaatct cctgcacag taccacacga cgtggataag tggttccatc ctagatgtat1020
tagaagtaaa agtagtagct tttcaaagct ttaaattgtt agaactcatc taactaaagt1080
aaattctgct gtgactaatc caatatactc agaattgtat ccatctaaag catttttcat1140
atctcaacta agataacttt tagcacatgc ttaaatatca aagcagttgt catttggaa1200
tcacttgtga atagatgtgc aaggggagca catattggat gtatatgtta ccatatgtta1260
ggaataaaaa ttattttgct gaaacttgga aaaaaaaaaa aaa

```

&lt;210&gt; 273

&lt;211&gt; 1586

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

```

cggctcagagc ggctcgagat tgcaggtcgt ggtggtcttg gaagagcgtc gaggggggccg 60
tggaagtgga atggggccgag gagatggagt tgattctcgt ggcaaacgtg aattgatag 120
gcatagtgga agtgatagat ctggcctgaa ccacaggagc aaacgtggag gtacgggact 180
tcacaactgg ggaactgtca aagacgaatt aacagatgcc cccaaatata actaggaaaa 240
aatctcttat aattcacagt acttgatcca atcaaatgtg actaggaaaa cactgaagg 300
tagaagaact catccagtgg cagacactga aaataaggag aatgaagtgt aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgaatggaa gctatcctaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgtggggc agtggaaaga 480
gggattttgtt cttcataaat caaagagtga agaggtctat gctgaagatt cggttatgga 540
ccatcatttc cgggaagccag caaatgatat aacgtctcag ctggagatca attttggaga 600
ccttggccgc caggagcgtg cggcgagggt aggacaggtt ggaagtgagg gtaggtggcg 660

```



```

ccccaccgt ggcagcagga cgcacaagtc aagtgtctct gctcctgatg tggatgaccc 720
agaggccttc ccagctctgg cttaactgga tgcataaga caaccctggg tcctttgtga 780
accctctctg tcaaaagcttt tgcactgtta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcctac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgtacacag aagtaacaaa tatggtagtc agttttgtat ttagaaaagt 960
attgtgtagca gggatgtttt cataattttc agagattatg cattcttcac gaatactttt1020
gtattgtctg ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac1080
cagtttaaaag ctttcaacttc atttgtgttt ttttaattaag gatttagaag tcccccaatt1140
tacaaaactgg ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac1200
atgggtcaact gggacatgtt aaactttgat ttgtcaaaatt ttatgctgtg tggataatac1260
actatatgta ttttaactta gttttaatat ttccattttt ggggaaaaat cttttttcac1320
ttctcatgat agctgtttata tatatatgct aaactcttat atacagaaat atcagtactt1380
gaacaaatcc aaagcaactt tggtttatta acccgtggct gccctggcag tggggccatt1440
tgggggtccaa attataactg atttacattt tcagcgatat tacttttaaa tgccgtgagt1500
ccattttaaa atctaactag acacctaatt ggggaagtgtt taaccactat gtgggtagcca1560
cgggccag 1568

```

&lt;210&gt; 274

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Val | Lys | Cys | Ala | Lys | Val | Ser | Tyr | Leu | Leu | Phe | Leu | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Cys | Ala | Ile | Asp | Ser | Cys | Ile | Lys | Phe | Trp | Asn | Ala | Gly | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Leu | Ser | Ser | Val | Thr | Leu | Trp | Ser | Met | Ser | Ser | Val | Ser | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ser | Asn | Val | Gly | Arg | Val | Arg | Ile | Lys | Ser | Glu | Gly | Cys | Ser | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Lys | Leu | Ser | Leu | Gly | Val | Pro | Ala | Ser | Lys | Ala | Thr | Glu | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Phe | Arg | Arg | Arg | Ser | Ser | Cys | Ser | Leu | Cys | Cys | Trp | Leu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Ala | Ser | Asp | Phe | Phe | Arg | Arg | Ser | Tyr | Ser | Gly | Arg | Tyr | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Tyr | Ser | Ser | Ala | Ala | Leu | Val | Thr | Cys | Thr | Lys | Ser | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Pro | Val | Pro | Arg | Thr | Ala | Glu | Thr | Pro | Thr | Thr | Leu | Ser | Glu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |

&lt;210&gt; 275

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 275

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Val | Leu | Asp | Glu | Phe | Tyr | Ser | Ser | Leu | Arg | Val | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Ala | Val | Leu | Gly | Thr | Gly | Leu | Asp | Glu | Leu | Phe | Val | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |



180

<210> 277  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 277

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Glu | Leu | Ile | Ile | Trp | Gln | Arg | Val | Leu | Pro | Lys | Cys | Gln | Val | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Glu | Cys | Val | Ala | Asn | Leu | Thr | His | Gln | Pro | Thr | His | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Ser | Ala | Leu | Cys | Ser | Arg | Trp | Leu | Gln | Arg | Cys | Arg | Asp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Cys | Leu | Leu | Gln | Val | Gly | Gln | Gly | Ala | Leu | Arg | Asp | Val | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Phe | Val | Leu | His | Val | Asp | Val | Leu | Gln | His | Leu | Leu | Pro | Met |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Gln | Leu | Cys | Gln | Val | Leu | Leu | Asp |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

<210> 278  
 <211> 401  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 278

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asn | Phe | Cys | Ala | Ala | Pro | Asn | Cys | Thr | Arg | Lys | Ser | Thr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asp | Leu | Ala | Phe | Phe | Arg | Phe | Pro | Arg | Asp | Pro | Ala | Arg | Cys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Trp | Val | Glu | Asn | Cys | Arg | Arg | Ala | Asp | Leu | Glu | Asp | Lys | Thr | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Leu | Asn | Lys | His | Tyr | Arg | Leu | Cys | Ala | Lys | His | Phe | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Met | Ile | Cys | Arg | Thr | Ser | Pro | Tyr | Arg | Thr | Val | Leu | Arg | Asp | Asn |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ile | Pro | Thr | Ile | Phe | Asp | Leu | Thr | Ser | His | Leu | Asn | Asn | Pro | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Arg | His | Arg | Lys | Arg | Ile | Lys | Glu | Leu | Ser | Glu | Asp | Glu | Ile | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Leu | Lys | Gln | Lys | Lys | Ile | Asp | Glu | Thr | Ser | Glu | Gln | Glu | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Lys | Glu | Thr | Asn | Asn | Ser | Asn | Ala | Gln | Asn | Pro | Ser | Glu | Glu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Glu | Gly | Gln | Asp | Glu | Asp | Ile | Leu | Pro | Leu | Thr | Leu | Glu | Glu | Lys |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Glu        | Asn        | Lys        | Glu        | Tyr<br>165 | Leu        | Lys        | Ser        | Leu        | Phe<br>170 | Glu        | Ile        | Leu        | Ile        | Leu<br>175 | Met        |
| Gly        | Lys        | Gln        | Asn<br>180 | Ile        | Pro        | Leu        | Asp        | Gly<br>185 | His        | Glu        | Ala        | Asp        | Glu<br>190 | Ile        | Pro        |
| Glu        | Gly        | Leu<br>195 | Phe        | Thr        | Pro        | Asp        | Asn<br>200 | Phe        | Gln        | Ala        | Leu        | Leu<br>205 | Glu        | Cys        | Arg        |
| Ile        | Asn<br>210 | Ser        | Gly        | Glu        | Glu        | Val<br>215 | Leu        | Arg        | Lys        | Arg        | Phe<br>220 | Glu        | Thr        | Thr        | Ala        |
| Val<br>225 | Asn        | Thr        | Leu        | Phe        | Cys<br>230 | Ser        | Lys        | Thr        | Gln        | Gln<br>235 | Arg        | Gln        | Met        | Leu        | Glu<br>240 |
| Ile        | Cys        | Glu        | Ser        | Cys<br>245 | Ile        | Arg        | Glu        | Glu        | Thr<br>250 | Leu        | Arg        | Glu        | Val        | Arg<br>255 | Asp        |
| Ser        | His        | Phe        | Phe<br>260 | Ser        | Ile        | Ile        | Thr        | Asp<br>265 | Asp        | Val        | Val        | Asp        | Ile<br>270 | Ala        | Gly        |
| Glu        | Glu        | His<br>275 | Leu        | Pro        | Val        | Leu        | Val<br>280 | Arg        | Phe        | Val        | Asp        | Glu<br>285 | Ser        | His        | Asn        |
| Leu        | Arg<br>290 | Glu        | Glu        | Phe        | Ile        | Gly<br>295 | Phe        | Leu        | Pro        | Tyr        | Glu<br>300 | Ala        | Asp        | Ala        | Glu        |
| Ile<br>305 | Leu        | Ala        | Val        | Lys        | Phe<br>310 | His        | Thr        | Met        | Ile        | Thr<br>315 | Glu        | Lys        | Trp        | Gly        | Leu<br>320 |
| Asn        | Met        | Glu        | Tyr        | Cys<br>325 | Arg        | Gly        | Gln        | Ala        | Tyr<br>330 | Ile        | Val        | Ser        | Ser        | Gly<br>335 | Phe        |
| Ser        | Ser        | Lys        | Met<br>340 | Lys        | Val        | Val        | Ala        | Ser<br>345 | Arg        | Leu        | Leu        | Glu        | Lys<br>350 | Tyr        | Pro        |
| Gln        | Ala        | Ile<br>355 | Tyr        | Thr        | Leu        | Cys        | Ser<br>360 | Ser        | Cys        | Ala        | Leu        | Asn<br>365 | Met        | Trp        | Leu        |
| Ala        | Lys<br>370 | Ser        | Val        | Pro        | Val        | Met<br>375 | Gly        | Val        | Ser        | Val        | Ala<br>380 | Leu        | Gly        | Thr        | Ile        |
| Glu<br>385 | Glu        | Val        | Cys        | Ser        | Phe<br>390 | Phe        | His        | Xxx        | Ile        | Thr<br>395 | Thr        | Thr        | Ala        | Phe        | Arg<br>400 |
| Thr        |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |

&lt;210&gt; 279

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 279

|          |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |
|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Met<br>1 | Leu | Ile       | Ser       | Gly<br>5 | Thr | Leu | Ser       | His       | Gly<br>10 | Thr | Thr | Gln       | Ile       | Gln<br>15 | Tyr |
| Xxx      | Xxx | Glu       | Glu<br>20 | His      | His | Ala | Asp       | Met<br>25 | Tyr       | Arg | Ser | Asp       | Leu<br>30 | Pro       | Asn |
| Pro      | Asp | Thr<br>35 | Leu       | Ser      | Ala | Glu | Leu<br>40 | His       | Cys       | Trp | Arg | Ile<br>45 | Lys       | Trp       | Lys |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Arg | Gly | Lys | Asp | Ile | Glu | Leu | Pro | Ser | Thr | Ile | Tyr | Glu | Ala | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Leu | Pro | Asp | Ile | Lys | Phe | Phe | Pro | Asn | Val | Tyr | Ala | Leu | Leu | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | Leu | Cys | Ile | Leu | Pro | Val | Met | Lys | Val | Glu | Asn | Glu | Arg | Tyr | Glu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Gly | Thr | Lys | Ala | Ser | Leu | Lys | His | Ile |     |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

<210> 280  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 280

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Arg | Lys | Cys | Asn | Lys | Phe | Trp | Asp | Asn | Ala | Gln | Thr | Ser | Gly | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Glu | Pro | Ser | Glu | Thr | Lys | Gly | Ser | Met | Gln | Lys | Ser | Lys | Phe | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Lys | Leu | Val | Pro | Glu | Glu | Glu | Thr | Thr | Ala | Ser | Glu | Asn | Thr | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Thr | Ser | Glu | Arg | Gln | Lys | Glu | Gly | Ile | Lys | Leu | Thr | Ile | Arg | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Ser | Arg | Lys | Lys | Lys | Pro | Asp | Ser | Pro | Pro | Lys | Val | Leu | Glu | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Asn | Lys | Gln | Glu | Lys | Thr | Glu | Lys | Glu | Glu | Glu | Lys | Thr | Asn | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Arg | Thr | Leu | Arg | Arg | Ser | Pro | Arg | Ile | Ser | Arg | Pro | Thr | Ala | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Ala | Glu | Ile | Arg | Asp | Gln | Lys | Ala | Asp | Lys | Lys | Arg | Gly | Glu | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Asp | Glu | Val | Glu | Glu | Glu | Ser | Thr | Ala | Leu | Gln | Lys | Thr | Asp | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Glu | Ile | Leu | Lys | Lys | Ser | Glu | Lys | Asp | Thr | Asn | Ser | Lys | Val | Ser |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys | Val | Lys | Pro | Lys | Gly | Lys | Val | Arg | Trp | Thr | Gly | Ser | Arg | Thr | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Arg | Trp | Lys | Tyr | Ser | Ser | Asn | Asp | Glu | Ser | Glu | Gly | Ser | Gly | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Lys | Ser | Ser | Ala | Ala | Ser | Glu | Glu | Glu | Glu | Glu | Lys | Glu | Ser | Glu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Ala | Ile | Leu | Ala | Asp | Asp | Asp | Glu | Pro | Cys | Lys | Lys | Cys | Gly | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Pro | Asn | His | Pro | Glu | Leu | Ile | Leu | Leu | Cys | Asp | Ser | Cys | Asp | Ser | Gly |  |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 225        |            |            |            |            | 230        |            |            |            |            | 235        |            |            |            | 240        |
| Tyr        | His        | Thr        | Ala        | Cys<br>245 | Leu        | Arg        | Pro        | Pro        | Leu<br>250 | Met        | Ile        | Ile        | Pro        | Gly<br>255 |
| Glu        | Trp        | Phe        | Cys<br>260 | Pro        | Pro        | Cys        | Gln        | His<br>265 | Lys        | Leu        | Leu        | Cys        | Glu<br>270 | Leu        |
| Glu        | Glu        | Gln<br>275 | Leu        | Gln        | Asp        | Leu        | Asp<br>280 | Val        | Ala        | Leu        | Lys        | Lys<br>285 | Lys        | Arg        |
| Ala        | Glu<br>290 | Arg        | Arg        | Lys        | Glu        | Arg<br>295 | Leu        | Val        | Tyr        | Val        | Gly<br>300 | Ile        | Ser        | Glu        |
| Asn<br>305 | Ile        | Ile        | Pro        | Pro        | Gln<br>310 | Glu        | Pro        | Asp        | Phe        | Ser<br>315 | Glu        | Asp        | Gln        | Glu<br>320 |
| Lys        | Lys        | Lys        | Asp        | Ser<br>325 | Lys        | Lys        | Ser        | Lys        | Ala<br>330 | Asn        | Leu        | Leu        | Glu        | Arg<br>335 |
| Ser        | Thr        | Arg        | Thr<br>340 | Arg        | Lys        | Cys        | Ile        | Ser<br>345 | Tyr        | Arg        | Phe        | Asp        | Glu<br>350 | Asp        |
| Glu        | Ala        | Ile<br>355 | Asp        | Glu        | Ala        | Ile        | Glu<br>360 | Asp        | Asp        | Ile        | Lys        | Glu<br>365 | Ala        | Gly        |
| Gly        | Gly<br>370 | Val        | Gly        | Arg        | Gly        | Lys<br>375 | Asp        | Ile        | Ser        | Thr        | Ile<br>380 | Thr        | Gly        | Arg        |
| Gly<br>385 | Lys        | Asp        | Ile        | Ser        | Thr<br>390 | Ile        | Leu        | Asp        | Glu        | Lys<br>395 | Ile        | Ile        | Thr        |            |

<210> 281  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens  
 <400> 281

|           |           |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Ser<br>1  | Ser       | Glu        | Lys        | Ser<br>5  | Gly       | Ser       | Cys        | Gly        | Gly<br>10 | Met       | Met       | Phe        | Ser        | Ile<br>15 | Leu       |
| Ile       | Pro       | Thr        | Tyr<br>20  | Thr       | Lys       | Arg       | Ser        | Phe<br>25  | Leu       | Arg       | Ser       | Ala        | Arg<br>30  | Ser       | Phe       |
| Phe       | Phe       | Lys<br>35  | Ala        | Thr       | Ser       | Lys       | Ser<br>40  | Cys        | Asn       | Cys       | Ser       | Ser<br>45  | Asn        | Phe       | Ser       |
| Gln       | Ser<br>50 | Ser        | Leu        | Cys       | Trp       | Gln<br>55 | Gly        | Gly        | Gln       | Asn       | His<br>60 | Ser        | Pro        | Ser       | Gly       |
| Met<br>65 | Ile       | Ile        | Arg        | Gly       | Gly<br>70 | Arg       | Arg        | Gln        | Ala       | Val<br>75 | Trp       | Tyr        | Pro        | Leu       | Ser<br>80 |
| Gln       | Glu       | Ser        | His        | Arg<br>85 | Arg       | Ile       | Ser        | Ser        | Gly<br>90 | Trp       | Phe       | Gly        | Arg        | Pro<br>95 | His       |
| Phe       | Leu       | His        | Gly<br>100 | Ser       | Ser       | Ser       | Ser        | Ala<br>105 | Arg       | Met       | Ala       | Ser        | Ser<br>110 | Leu       | Ser       |
| Phe       | Ser       | Ser<br>115 | Ser        | Ser       | Ser       | Glu       | Ala<br>120 | Ala        | Asp       | Asp       | Phe       | Ser<br>125 | Leu        | Pro       | Asp       |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Leu | Ser | Ser | Leu | Leu | Glu | Tyr | Phe | His | Leu | Pro | Arg | Val | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Pro | Val | His | Arg | Thr | Leu | Pro | Leu | Gly | Phe | Thr | Leu | Leu | Thr | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Phe | Val | Ser | Phe | Ser | Asp | Phe | Phe | Lys | Ile | Ser | Phe | Leu | Ser | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Cys | Lys | Ala | Val | Asp | Ser | Ser | Ser | Thr | Ser | Ser | Ser | Pro | Ser | Pro |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Leu | Phe | Leu | Ser | Ala | Phe |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 282

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Leu | Pro | Phe | Ser | Gly | Arg | Gly | Arg | Gly | Lys | Lys | Val | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Asp | Gly | Val | Ala | Ser | Leu | Pro | Leu | Lys | Leu | Gly | Arg | Leu | Phe | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Val | Thr | Arg | Gly | Phe | Asn | Met | Arg | Ile | Glu | Lys | Cys | Tyr | Phe | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Pro | Ile | Tyr | Pro | Gly | His | Gly | Met | Met | Phe | Val | Arg | Asn | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Lys | Val | Phe | Arg | Phe | Cys | Lys | Ser | Lys | Cys | His | Lys | Asn | Phe | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Arg | Asn | Pro | Arg | Lys | Val | Arg | Trp | Thr | Lys | Ala | Phe | Arg | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Gly | Lys | Glu | Leu | Thr | Val | Asp | Asn | Ser | Phe | Glu | Phe | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Asn | Glu | Pro | Ile | Lys | Tyr | Gln | Arg | Glu | Leu | Trp | Asn | Lys | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Asp | Ala | Met | Lys | Arg | Val | Glu | Glu | Ile | Lys | Gln | Lys | Arg | Gln | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Phe | Ile | Met | Asn | Arg | Leu | Lys | Lys | Asn | Lys | Glu | Leu | Gln | Lys | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Asp | Ile | Lys | Glu | Val | Lys | Gln | Asn | Ile | His | Leu | Ile | Arg | Ala | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Gly | Lys | Gly | Lys | Gln | Leu | Glu | Glu | Lys | Met | Val | Gln | Gln | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Glu | Asp | Val | Asp | Met | Glu | Asp | Ala | Pro |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |

&lt;210&gt; 283

&lt;211&gt; 84

<212> PRT  
 <213> Homo sapiens

<400> 283

|           |           |           |     |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Ile<br>1  | Ile       | His       | Cys | Lys<br>5 | Leu       | Phe       | Thr       | Ser       | Cys<br>10 | Phe       | Pro       | Glu       | Cys       | Phe<br>15 | Gly       |
| Pro       | Pro       | Asn<br>20 | Phe | Ala      | Arg       | Ile       | Ala       | Leu<br>25 | Leu       | Phe       | Lys       | Val       | Phe<br>30 | Met       | Thr       |
| Phe       | Arg       | Phe<br>35 | Ala | Lys      | Ser       | Glu       | His<br>40 | Leu       | Ala       | Ile       | Val       | Ala<br>45 | Asp       | Glu       | His       |
| His       | Ala<br>50 | Val       | Ser | Arg      | Ile       | Asp<br>55 | Gly       | Pro       | Arg       | Thr       | Glu<br>60 | Ile       | Thr       | Leu       | Phe       |
| Asp<br>65 | Thr       | His       | Val | Glu      | Pro<br>70 | Ala       | Cys       | Asn       | Pro       | Thr<br>75 | Lys       | Gln       | Thr       | Pro       | Lys<br>80 |
| Leu       | Glu       | Arg       | Lys |          |           |           |           |           |           |           |           |           |           |           |           |

<210> 284  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 284

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg<br>1   | Leu        | Glu        | Pro        | Arg<br>5   | Ser        | Val        | Thr        | Arg        | Ser<br>10  | Arg        | Arg        | Ala        | Val        | Ser<br>15  | Arg        |
| Leu        | Ser        | Ala        | Arg<br>20  | Pro        | Gly        | Lys        | Val        | Ser<br>25  | Ala        | Val        | Met        | Ala        | Phe<br>30  | Leu        | Ala        |
| Ser        | Gly        | Pro<br>35  | Tyr        | Leu        | Thr        | His        | Gln<br>40  | Gln        | Lys        | Val        | Leu        | Arg<br>45  | Leu        | Tyr        | Lys        |
| Arg        | Ala<br>50  | Leu        | Arg        | His        | Leu        | Glu<br>55  | Ser        | Trp        | Cys        | Val        | Gln<br>60  | Arg        | Asp        | Lys        | Tyr        |
| Arg<br>65  | Tyr        | Phe        | Ala        | Cys        | Leu<br>70  | Met        | Arg        | Ala        | Arg        | Phe<br>75  | Glu        | Glu        | His        | Lys        | Asn<br>80  |
| Glu        | Lys        | Asp        | Met        | Ala<br>85  | Lys        | Ala        | Thr        | Gln        | Leu<br>90  | Leu        | Lys        | Glu        | Ala        | Glu<br>95  | Glu        |
| Glu        | Phe        | Trp        | Tyr<br>100 | Arg        | Gln        | His        | Pro        | Gln<br>105 | Pro        | Tyr        | Ile        | Phe        | Pro<br>110 | Asp        | Ser        |
| Pro        | Gly        | Gly<br>115 | Thr        | Ser        | Tyr        | Glu        | Arg<br>120 | Tyr        | Asp        | Cys        | Tyr        | Lys<br>125 | Val        | Pro        | Glu        |
| Trp        | Cys<br>130 | Leu        | Asp        | Asp        | Trp        | His<br>135 | Pro        | Ser        | Glu        | Lys        | Ala<br>140 | Met        | Tyr        | Pro        | Asp        |
| Tyr<br>145 | Phe        | Ala        | Lys        | Arg        | Glu<br>150 | Gln        | Trp        | Lys        | Lys        | Leu<br>155 | Arg        | Arg        | Glu        | Ser        | Trp<br>160 |
| Glu        | Arg        | Glu        | Val        | Lys<br>165 | Gln        | Leu        | Gln        | Glu        | Glu<br>170 | Thr        | Pro        | Pro        | Gly        | Gly<br>175 | Pro        |
| Leu        | Thr        | Glu        | Ala        | Leu        | Pro        | Pro        | Ala        | Arg        | Lys        | Glu        | Gly        | Asp        | Leu        | Pro        | Pro        |



| 180                |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |  |  |  |  |
|--------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Leu                | Trp | Trp | Tyr | Ile | Val | Thr | Arg | Pro | Arg | Glu | Arg | Pro | Met |     |     |  |  |  |  |
|                    |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| <210> 285          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <211> 139          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <212> PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <213> Homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <400> 285          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| Pro                | Leu | Val | Pro | Ser | Phe | Pro | Ser | Ala | Val | Ser | Ser | Thr | Val | Leu | Ser |  |  |  |  |
| 1                  |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |  |  |
| Trp                | Gln | Ser | Asn | Gln | Asp | Thr | Leu | Pro | Ser | Gln | Lys | Asp | Ala | Ser | His |  |  |  |  |
|                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| Leu                | Ser | Thr | Ile | Leu | Gly | Pro | Cys | Ser | Asn | Arg | Ile | Ser | His | Arg | Arg |  |  |  |  |
|                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Cys                | Pro | Gln | Glu | Ser | Gln | Gly | Arg | Cys | Met | Ala | Val | Asp | Ala | Asp | Gly |  |  |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Thr                | Arg | Ile | Leu | Pro | Arg | Pro | Pro | Ser | Ala | Ala | Gly | Trp | Pro | Ser | Pro |  |  |  |  |
| 65                 |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Tyr                | Pro | Phe | His | Ser | Tyr | Val | Leu | Gln | Thr | Gly | Leu | Ser | Ser | Asn | Lys |  |  |  |  |
|                    |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Gln                | Ser | Ile | Gly | Ile | Cys | Leu | Ser | Gly | Arg | Thr | Thr | Thr | Arg | Gly | Gly |  |  |  |  |
|                    |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Val                | Ala | Pro | Ala | Tyr | Lys | Ala | Ala | Thr | Pro | Phe | Ala | Asp | Gly | Ser | Gly |  |  |  |  |
|                    |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Arg                | Val | Pro | Thr | Pro | Arg | Thr | Pro | Leu | Arg | Arg |     |     |     |     |     |  |  |  |  |
|                    | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <210> 286          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <211> 80           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <212> PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <213> Homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <400> 286          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| Leu                | Met | Met | Thr | Ile | Tyr | Ala | Leu | Ser | Asn | Glu | Phe | Ala | Phe | Lys | Ile |  |  |  |  |
| 1                  |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |
| Asn                | Glu | Glu | Gln | Leu | Ser | Phe | Phe | Pro | Leu | Leu | Ser | Val | Gln | Leu | Trp |  |  |  |  |
|                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |  |
| His                | Ala | Gln | Arg | Phe | Leu | Leu | Asp | Ser | Ser | Trp | Ser | Gly | Val | Ile | Pro |  |  |  |  |
|                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Phe                | Phe | Phe | Ser | Cys | Ser | Cys | Leu | Pro | Phe | Leu | Tyr | Pro | Pro | Arg | Trp |  |  |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Arg                | Gln | Ile | His | Asp | Leu | Lys | Asp | Thr | Gln | Tyr | Leu | Leu | Asn | Ser | Ser |  |  |  |  |
| 65                 |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| <210> 287          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| <211> 80           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

<212> PRT  
 <213> Homo sapiens  
 <400> 287

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Met | Met | Thr | Ile | Tyr | Ala | Leu | Ser | Asn | Glu | Phe | Ala | Phe | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Glu | Glu | Gln | Leu | Ser | Phe | Phe | Pro | Leu | Leu | Ser | Val | Gln | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | Gln | Arg | Phe | Leu | Leu | Asp | Ser | Ser | Trp | Ser | Gly | Val | Ile | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Phe | Phe | Ser | Cys | Ser | Cys | Leu | Pro | Phe | Leu | Tyr | Pro | Pro | Lys | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gln | Ile | His | Asp | Leu | Lys | Asp | Thr | Gln | Tyr | Leu | Leu | Asn | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

<210> 288  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<400> 288

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Ser | Cys | Ala | Gly | Thr | Leu | Ser | Gly | Ser | Gly | Pro | His | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Leu | Thr | Gln | Gly | Arg | Trp | Val | Arg | Lys | Ser | Arg | Val | Ala | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Ile | Pro | Val | Ser | Ala | Phe | Leu | Leu | Leu | Val | Ala | Leu | Ser | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Ala | Arg | Asp | Thr | Thr | Val | Lys | Pro | Gly | Ala | Lys | Lys | Asp | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asp | Ser | Arg | Pro | Lys | Leu | Pro | Gln | Thr | Leu | Ser | Arg | Gly | Trp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gln | Leu | Ile | Trp | Thr | Gln | Thr | Tyr | Glu | Glu | Ala | Leu | Tyr | Lys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Thr | Ser | Asn | Lys | Pro | Leu | Met | Ile | Ile | His | His | Leu | Asp | Glu | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | His | Ser | Gln | Ala | Leu | Lys | Lys | Val | Phe | Ala | Glu | Asn | Lys | Glu | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Lys | Leu | Ala | Glu | Gln | Phe | Val | Leu | Leu | Asn | Leu | Val | Tyr | Glu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asp | Lys | His | Leu | Ser | Pro | Asp | Gly | Gln | Tyr | Val | Pro | Arg | Ile | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Val | Asp | Pro | Ser | Leu | Thr | Val | Arg | Ala | Asp | Ile | Thr | Gly | Arg | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Asn | Arg | Leu | Tyr | Ala | Tyr | Glu | Pro | Ala | Asp | Thr | Ala | Leu | Leu | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

[illegible]

<400> 289

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |     |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| Gly<br>1  | Asn       | Pro       | Glu       | Leu<br>5 | Pro       | Trp       | Arg       | Lys       | Phe<br>10 | Gln       | Cys       | Gln       | His       | Ser<br>15 | Cys |
| Ser       | Leu       | Trp       | Pro<br>20 | Ser      | Pro       | Thr       | Leu       | Trp<br>25 | Pro       | Glu       | Ile       | Pro       | Gln<br>30 | Ser       | Asn |
| Leu       | Glu       | Pro<br>35 | Lys       | Arg      | Thr       | Gln       | Arg<br>40 | Thr       | Leu       | Asp       | Pro       | Asn<br>45 | Cys       | Pro       | Arg |
| Pro       | Ser<br>50 | Pro       | Glu       | Val      | Gly       | Val<br>55 | Thr       | Asn       | Ser       | Ser       | Gly<br>60 | Leu       | Arg       | His       | Met |
| Lys<br>65 | Lys       | Leu       | Tyr       | Ile      | Asn<br>70 | Pro       | Arg       | Gln       | Ala       | Thr<br>75 | Asn       | Pro       |           |           |     |

```
<210> 290
<211> 160
<212> PRT
<213> Homo sapiens
```

<400> 290

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Gly<br>1   | Gly        | Xxx        | Gly        | Xxx<br>5  | Gln        | Leu        | Leu        | Xxx        | Pro<br>10 | Xxx        | Ala        | Xxx        | Gln        | Gly<br>15 | Xxx        |
| Pro        | Ala        | Ala        | Ser<br>20  | Cys       | Xxx        | Xxx        | Gln        | Asp<br>25  | Val       | His        | Leu        | Xxx        | Arg<br>30  | Cys       | Xxx        |
| Thr        | Val        | Val<br>35  | Arg        | Trp       | Tyr        | Gln        | Arg<br>40  | Ile        | Thr       | Gly        | Met        | Pro<br>45  | Xxx        | Xxx       | Ala        |
| Pro        | Thr<br>50  | Arg        | Asn        | Phe       | Ser        | Lys<br>55  | Phe        | Gln        | Arg       | Xxx        | Val<br>60  | Met        | Asp        | Leu       | His        |
| Gly<br>65  | Phe        | Pro        | Lys        | Glu       | Xxx<br>70  | Gly        | Gln        | Xxx        | Glu       | Xxx<br>75  | Gln        | Glu        | Xxx        | Leu       | Gln<br>80  |
| Trp        | Glu        | Gly        | Arg        | Ser<br>85 | Ser        | Ser        | Gly        | Lys        | Cys<br>90 | Arg        | Ile        | Ser        | Xxx        | Ser<br>95 | Xxx        |
| Leu        | Pro        | Xxx        | Ser<br>100 | Thr       | Ile        | Xxx        | Xxx        | Phe<br>105 | Leu       | Lys        | Xxx        | Xxx        | Trp<br>110 | Xxx       | Xxx        |
| Ile        | Arg        | Xxx<br>115 | Gln        | Ser       | Pro        | Xxx        | Thr<br>120 | Trp        | Xxx       | Arg        | Thr        | Tyr<br>125 | Leu        | Arg       | Leu        |
| Gly        | Ser<br>130 | Ile        | Ser        | Glu       | Phe        | Ser<br>135 | Pro        | Gly        | Ser       | Cys        | Leu<br>140 | Pro        | Asn        | Trp       | Leu        |
| Glu<br>145 | Gly        | Lys        | Pro        | Arg       | Met<br>150 | Thr        | Xxx        | Ala        | Lys       | Trp<br>155 | Pro        | Lys        | Phe        | Phe       | Leu<br>160 |

&lt;210&gt; 291

<211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 291

|            |            |            |            |           |            |            |            |            |           |           |            |            |            |           |           |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Arg<br>1   | His        | Xxx        | Pro        | Leu<br>5  | Xxx        | Leu        | Gly        | Xxx        | His<br>10 | Gly       | His        | Arg        | Ala        | His<br>15 | Ser       |
| Cys        | Leu        | Gly        | Trp<br>20  | Ser       | Gln        | Xxx        | Ala        | Leu<br>25  | Trp       | Asp       | Xxx        | Ala        | Trp<br>30  | Gly       | Leu       |
| Xxx        | Xxx        | Xxx<br>35  | Gly        | Ser       | Xxx        | Gln        | Xxx<br>40  | Arg        | Lys       | Lys       | Glu        | Ala<br>45  | Xxx        | Trp       | Cys       |
| Val        | Xxx<br>50  | Val        | Gly        | Xxx       | Val        | Gly<br>55  | Xxx        | Cys        | Xxx       | Xxx       | Pro<br>60  | Xxx        | Glu        | Xxx       | Met       |
| Xxx<br>65  | Xxx        | Gly        | Phe        | Glu       | Gln<br>70  | Asn        | Xxx        | Xxx        | Gly       | Pro<br>75 | Xxx        | Asn        | Xxx        | Xxx       | Val<br>80 |
| Ser        | Xxx        | Leu        | Gly        | Xxx<br>85 | Xxx        | Xxx        | Trp        | Asn        | Arg<br>90 | Xxx       | Ala        | Glu        | Lys        | Asn<br>95 | Met       |
| Xxx        | Gly        | Cys        | Cys<br>100 | Ala       | Lys        | Xxx        | Val        | Asn<br>105 | Xxx       | Xxx       | Met        | Asp        | His<br>110 | Xxx       | Xxx       |
| Gly        | Phe        | Gln<br>115 | Xxx        | Arg       | Gln        | Ile        | Arg<br>120 | Gly        | Leu       | Cys       | Ser        | His<br>125 | Ala        | His       | Thr       |
| Gly        | Xxx<br>130 | Asn        | Cys        | His       | Val        | Ser<br>135 | Xxx        | Ser        | Gly       | Ser       | Asp<br>140 | Thr        | Gln        | Leu       | Cys       |
| Xxx<br>145 | Gly        | Leu        | Ser        | Phe       | Met<br>150 |            |            |            |           |           |            |            |            |           |           |

<210> 292  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 292

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Arg<br>1  | Ala       | Ala       | Lys       | Ile<br>5  | Leu       | Lys       | Gly       | Gly       | Leu<br>10 | Gln       | Glu       | Val       | Ala       | Glu<br>15 | Gln       |
| Leu       | Glu       | Leu       | Glu<br>20 | Arg       | Ile       | Gly       | Pro       | Gln<br>25 | His       | Gln       | Ala       | Gly       | Ser<br>30 | Asp       | Ser       |
| Leu       | Leu       | Thr<br>35 | Gly       | Met       | Ala       | Phe       | Phe<br>40 | Lys       | Met       | Arg       | Glu       | Met<br>45 | Phe       | Phe       | Glu       |
| Asp       | His<br>50 | Ile       | Asp       | Asp       | Ala       | Lys<br>55 | Tyr       | Cys       | Gly       | His       | Leu<br>60 | Tyr       | Gly       | Leu       | Gly       |
| Ser<br>65 | Gly       | Ser       | Ser       | Tyr       | Val<br>70 | Gln       | Asn       | Gly       | Thr       | Gly<br>75 | Asn       | Ala       | Tyr       | Glu       | Glu<br>80 |
| Glu       | Ala       | Asn       | Lys       | Gln<br>85 | Ser       |           |           |           |           |           |           |           |           |           |           |

<210> 293  
 <211> 64

<212> PRT  
 <213> Homo sapiens

<400> 293

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Ala | Lys | Phe | Asn | Leu | Asn | Ala | Phe | Phe | Phe | Phe | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Arg | Ser | Glu | Ile | Gly | Thr | Val | Ile | Leu | Ser | Thr | Glu | Arg | Gln | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Ile |
| Lys | Trp | Ala | Met | Lys | Gly | Gly | Gly | Lys | Val | Leu | Ser | Ile | Val | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     | Gly |
| Ile | Gln | Pro | Glu | Ile | Lys | Pro | Ile | Tyr | Lys | His | Val | Cys | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     | Lys |

<210> 294  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 294

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Thr | Ile | Met | Asp | Leu | Leu | Phe | Gly | Arg | Arg | Lys | Thr | Pro | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Leu | Arg | Gln | Asn | Gln | Arg | Ala | Leu | Asn | Arg | Ala | Met | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Arg | Glu | Arg | Gln | Lys | Leu | Glu | Thr | Gln | Glu | Lys | Lys | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asp | Ile | Lys | Lys | Met | Ala | Lys | Gln | Gly | Gln | Met | Asp | Ala | Val | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Met | Ala | Lys | Asp | Leu | Val | Arg | Thr | Arg | Arg | Tyr | Val | Arg | Lys | Phe |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Leu | Met | Arg | Ala | Asn | Ile | Gln | Ala | Val | Ser | Leu | Lys | Ile | Gln | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Lys | Ser | Asn | Asn | Ser | Met | Ala | Gln | Ala | Met | Lys | Gly | Val | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Met | Gly | Thr | Met | Asn | Arg | Gln | Leu | Lys | Leu | Pro | Gln | Ile | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Met | Met | Glu | Phe | Glu | Arg | Gln | Ala | Glu | Ile | Met | Asp | Met | Lys | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Met | Met | Asn | Asp | Ala | Ile | Asp | Asp | Pro | Met | Gly | Asp | Glu | Glu | Asp |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Glu | Glu | Ser | Asp | Ala | Val | Val | Ser | Gln | Val | Leu | Asp | Glu | Leu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ser | Leu | Thr | Asp | Glu | Leu | Ser | Asn | Leu | Pro | Ser | Thr | Gly | Gly | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ser | Val | Ala | Ala | Gly | Gly | Lys | Lys | Ala | Glu | Ala | Ala | Ala | Ser | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Leu Ala Asp Ala Asp Ala Asp Leu Glu Glu Arg Leu Lys Asn Leu Arg  
 210 215 220  
 Arg Asp  
 225

<210> 295  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 295

Lys Ile Leu Gly Ile His Trp Leu Ser Arg Ser Gly Arg Gly Thr Gln  
 1 5 10 15  
 Ser Leu Arg Arg Phe Leu Ser Arg Ser Arg Ser Ala Ser Ala Ser  
 20 25 30  
 Ala Arg Ala Glu Ala Ala Ala Ser Ala Phe Phe Pro Pro Ala Ala Thr  
 35 40  
 Leu Ser Glu Pro Pro Val Glu Gly Arg Phe Asp Ser Ser Ser Val Arg  
 50 55 60  
 Leu Ser Pro Ser Ser Ser Arg Thr Trp Asp Thr Thr Ala Ser Leu Ser  
 65 70 75  
 Ser Ser Ser Ser Ser Ser Pro Met Gly Ser Ser Met Ala Ser Phe Ile  
 85 90 95  
 Ile Ser Ser Phe Ile Ser Met Ile Ser Ala Cys Arg Ser Asn Ser Ile  
 100 105  
 Met Ile Phe Trp Ile Trp Gly Asn Phe Ser Cys Leu Phe Met Val Pro  
 115 120 125  
 Met Ala Leu Val Thr Pro Phe Met Ala Cys Ala Ile Glu Leu Leu Asp  
 130 135 140  
 Leu Ser Val Trp Ile Leu Arg Asp Thr Ala Trp Met Leu Ala Arg Ile  
 145 150 155 160  
 Asn Thr Asn Leu Arg Thr  
 165

<210> 296  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Lys Pro Glu Gly Ala Arg Arg Val Gln Phe Val Met Gly Leu Phe Gly  
 1 5 10 15  
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu  
 20 25 30  
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile  
 35 40 45  
 Gln Arg Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys

| 50                 |            |            |            |            | 55         |            |            |            |            | 60         |            |            |            |            |            |
|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Lys<br>65          | Gly        | Gln        | Lys        | Asp        | Val<br>70  | Cys        | Ile        | Val        | Leu        | Ala<br>75  | Lys        | Glu        | Met        | Ile        | Arg<br>80  |
| Ser                | Arg        | Lys        | Ala        | Val<br>85  | Ser        | Lys        | Leu        | Tyr        | Ala<br>90  | Ser        | Lys        | Ala        | His        | Met<br>95  | Asn        |
| Ser                | Val        | Leu        | Met<br>100 | Gly        | Met        | Lys        | Asn        | Gln<br>105 | Leu        | Ala        | Val        | Leu        | Arg<br>110 | Val        | Ala        |
| Gly                | Ser        | Leu<br>115 | Gln        | Lys        | Ser        | Thr        | Glu<br>120 | Val        | Met        | Lys        | Ala        | Met<br>125 | Gln        | Ser        | Leu        |
| Val                | Lys<br>130 | Ile        | Pro        | Glu        | Ile        | Gln<br>135 | Ala        | Thr        | Met        | Arg        | Glu<br>140 | Leu        | Ser        | Lys        | Glu        |
| Met<br>145         | Met        | Lys        | Ala        | Gly        | Ile<br>150 | Ile        | Glu        | Glu        | Met        | Leu<br>155 | Glu        | Asp        | Thr        | Phe        | Glu<br>160 |
| Ser                | Met        | Asp        | Asp        | Gln<br>165 | Glu        | Glu        | Met        | Glu        | Glu<br>170 | Glu        | Ala        | Glu        | Met        | Glu<br>175 | Ile        |
| Asp                | Arg        | Ile        | Leu<br>180 | Phe        | Glu        | Ile        | Thr        | Ala<br>185 | Gly        | Ala        | Leu        | Gly        | Lys<br>190 | Ala        | Pro        |
| Ser                | Lys        | Val<br>195 | Thr        | Asp        | Ala        | Leu        | Pro<br>200 | Glu        | Pro        | Glu        | Pro        | Pro<br>205 | Gly        | Ala        | Met        |
| Ala                | Ala<br>210 | Ser        | Glu        | Asp        | Glu        | Gly<br>215 | Glu        | Glu        | Glu        | Glu        | Ala<br>220 | Leu        | Glu        | Ala        | Met        |
| Gln<br>225         | Ser        | Arg        | Leu        | Ala        | Thr<br>230 | Leu        | Arg        | Ser        |            |            |            |            |            |            |            |
| <210> 297          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <211> 129          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <212> PRT          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <213> Homo sapiens |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| <400> 297          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
| Leu<br>1           | Met        | Pro        | Phe        | Gln<br>5   | Ser        | Gln        | Asn        | Leu        | Gln<br>10  | Glu        | Arg        | Trp        | Leu        | Pro<br>15  | Gln        |
| Arg                | Met        | Arg        | Gly<br>20  | Arg        | Arg        | Lys        | Arg        | Leu<br>25  | Trp        | Arg        | Pro        | Cys        | Ser<br>30  | Pro        | Gly        |
| Trp                | Pro        | His<br>35  | Ser        | Ala        | Ala        | Arg        | Gly<br>40  | Cys        | Leu        | Pro        | Arg        | Trp<br>45  | Val        | Cys        | Thr        |
| His                | Ser<br>50  | Ser        | Gln        | Glu        | Leu        | Pro<br>55  | Phe        | Tyr        | Val        | Ser        | Leu<br>60  | Ala        | Leu        | His        | Leu        |
| Cys<br>65          | Cys        | Glu        | Asp        | Tyr        | His<br>70  | Phe        | Gly        | Glu        | Gly        | Ser<br>75  | Val        | Cys        | Leu        | Phe        | Ser<br>80  |
| Phe                | Ser        | Ala        | Gln        | Val<br>85  | Leu        | Gly        | Ser        | Gln        | Arg<br>90  | Asp        | Cys        | Ser        | Tyr        | Lys<br>95  | Ser        |
| Gly                | Ile        | Asn        | Lys<br>100 | Cys        | Ile        | Ile        | Phe        | Arg<br>105 | Ser        | Ile        | Asp        | Arg        | Tyr<br>110 | Ile        | Leu        |

Leu Trp Gly Gly Glu Arg Asn Pro Ser Ala His Glu Ala Leu Leu Lys  
 115 125  
 Ile

<210> 298  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 298

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Trp | Cys | Thr | Thr | Thr | Met | Leu | Ala | Ala | Arg | Leu | Val | Cys | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Pro | Ser | Arg | Val | Phe | His | Pro | Ala | Phe | Thr | Lys | Ala | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Lys | Asn | Ser | Ile | Thr | Lys | Asn | Gln | Trp | Leu | Leu | Thr | Pro | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Tyr | Ala | Thr | Lys | Thr | Arg | Ile | Gly | Ile | Arg | Arg | Gly | Arg | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gln | Glu | Leu | Lys | Glu | Ala | Ala | Leu | Glu | Pro | Ser | Met | Glu | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Lys | Ile | Asp | Gln | Met | Gly | Arg | Trp | Phe | Val | Ala | Gly | Gly | Ala | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gly | Leu | Gly | Ala | Leu | Cys | Tyr | Tyr | Gly | Leu | Gly | Leu | Ser | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ile | Gly | Ala | Ile | Glu | Lys | Ala | Val | Ile | Trp | Pro | Gln | Tyr | Val | Lys | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ile | His | Ser | Thr | Tyr | Met | Tyr | Leu | Ala | Gly | Ser | Ile | Gly | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Leu | Ser | Ala | Ile | Ala | Ile | Ser | Arg | Thr | Pro | Val | Leu | Met | Asn | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Met | Arg | Gly | Ser | Trp | Val | Thr | Ile | Gly | Val | Thr | Phe | Ala | Ala | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Gly | Ala | Gly | Met | Leu | Val | Arg | Ser | Ile | Pro | Tyr | Asp | Gln | Ser | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Pro | Lys | His | Leu | Ala | Trp | Leu | Leu | His | Ser | Gly | Val | Met | Gly | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Val | Ala | Pro | Leu | Thr | Ile | Leu | Gly | Gly | Pro | Leu | Leu | Ile | Arg | Ala |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Trp | Tyr | Thr | Ala | Gly | Ile | Val | Gly | Gly | Leu | Ser | Thr | Val | Ala | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Ala | Pro | Ser | Glu | Lys | Phe | Leu | Asn | Met | Gly | Ala | Pro | Leu | Gly | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Leu | Gly | Leu | Val | Phe | Val | Ser | Ser | Leu | Gly | Ser | Met | Phe | Leu | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Thr | Val | Ala | Gly | Ala | Thr | Leu | Tyr | Ser | Val | Ala | Met | Tyr | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Leu | Val | Leu | Phe | Ser | Met | Phe | Leu | Leu | Tyr | Asp | Thr | Gln | Lys | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Lys | Arg | Ala | Glu | Val | Ser | Pro | Met | Tyr | Gly | Val | Gln | Lys | Tyr | Asp |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Ile | Asn | Ser | Met | Leu | Ser | Ile | Tyr | Met | Asp | Thr | Leu | Asn | Ile | Phe |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Met | Arg | Val | Ala | Thr | Met | Leu | Ala | Thr | Gly | Gly | Asn | Arg | Lys | Lys |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

&lt;210&gt; 299

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Ala | Pro | Ala | Thr | Val | Val | Gly | Gly | Arg | Asn | Ile | Asp | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Thr | Lys | Thr | Arg | Pro | Arg | Pro | Thr | Pro | Arg | Gly | Ala | Pro | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Arg | Asn | Phe | Ser | Leu | Gly | Ala | His | Met | Ala | Thr | Val | Glu | Arg | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Met | Pro | Ala | Val | Tyr | His | Ala | Ala | Leu | Met | Arg | Arg | Gly | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asn | Ile | Val | Arg | Gly | Ala | Thr | Thr | Ala | Pro | Ile | Thr | Pro | Glu | Cys |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Asn | Gln | Ala | Arg | Cys | Phe | Gly | Pro | Gly | Leu | Trp | Ser | Tyr | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Arg | Thr | Ser | Ile | Pro | Ala | Pro | Thr | Met | Ala | Ala | Lys | Val | Thr | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Thr | Gln | Glu | Pro | Leu | Ile | Met | Lys | Phe | Met | Arg | Thr | Gly | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Ile | Ala | Met | Ala | Asp | Lys | Ala | Val | Lys | Pro | Ile | Leu | Pro | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Tyr | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 300

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 300

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Leu | Glu | Val | Ser | Tyr | Arg | Gln | His | His | Phe | Arg | Val | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Trp | Ser | Lys | Met | Ala | Asp | Glu | Ala | Thr | Arg | Arg | Val | Val | Ser |

|                    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|--------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|                    |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |  |  |
| Glu                | Ile | Pro | Val | Leu | Lys | Thr | Asn | Ala | Gly | Pro | Arg | Asp | Arg | Glu | Leu |  |  |
|                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Trp                | Val | Gln | Arg | Leu | Lys | Glu | Glu | Tyr | Gln | Ser | Leu | Ile | Arg | Tyr | Val |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Glu                | Asn | Asn | Lys | Asn | Ala | Asp | Asn | Asp | Trp | Phe | Arg | Leu | Glu | Ser | Asn |  |  |
|                    | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Lys                | Glu | Gly | Thr | Arg | Trp | Phe | Gly | Lys | Cys | Trp | Tyr | Ile | His | Asp | Leu |  |  |
|                    |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu                | Lys | Tyr | Glu | Phe | Asp | Ile | Glu | Phe | Asp | Ile | Pro | Ile | Thr | Tyr | Pro |  |  |
|                    |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Thr                | Thr | Ala | Pro | Glu | Ile | Ala | Val | Pro | Glu | Leu | Asp | Gly | Lys | Thr | Ala |  |  |
|                    |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Lys                | Met | Tyr | Arg | Gly | Gly | Lys | Ile | Cys | Leu | Thr | Asp | His | Phe | Lys | Pro |  |  |
|                    | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Leu                | Trp | Ala | Arg | Asn | Val | Pro | Lys | Phe | Gly | Leu | Ala | His | Leu | Met | Ala |  |  |
|                    | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Leu                | Gly | Leu | Gly | Pro | Trp | Leu | Ala | Val | Glu | Ile | Pro | Asp | Leu | Ile | Gln |  |  |
|                    |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Lys                | Gly | Val | Ile | Gln | His | Lys | Glu | Lys | Cys | Asn | Gln |     |     |     |     |  |  |
|                    |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |  |  |
| <210> 301          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <211> 172          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <212> PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <213> Homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| <400> 301          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Ser                | Lys | Phe | Gly | His | Ile | Pro | Gly | Pro | Gln | Arg | Phe | Glu | Met | Ile | Arg |  |  |
|                    | 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |
| Gln                | Ala | Tyr | Phe | Ala | Thr | Pro | Val | His | Leu | Cys | Cys | Leu | Ser | Ile | Gln |  |  |
|                    |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Leu                | Arg | Asn | Cys | Asn | Phe | Trp | Gly | Ser | Ser | Arg | Ile | Cys | Asp | Arg | Asn |  |  |
|                    |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Val                | Lys | Leu | Asp | Val | Lys | Leu | Ile | Phe | Gln | Glu | Val | Met | Asp | Ile | Pro |  |  |
|                    | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Ala                | Phe | Ser | Lys | Pro | Pro | Ser | Ser | Phe | Leu | Val | Gly | Leu | Gln | Ser | Glu |  |  |
|                    | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Pro                | Ile | Val | Val | Ser | Ile | Leu | Val | Val | Leu |     |     |     |     |     |     |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Phe | Ile | Arg | His | Leu | Gly | Pro | Gly | Arg | Lys | Arg | Asn | Ala | Glu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Pro | Val | Ala | Tyr | Leu | Lys | Ala | Pro | Ser | Ser | Leu | Leu | Trp | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Glu | Thr | Leu | Gly | Cys | Cys | Lys | Thr | Ser | Phe | Glu |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

&lt;210&gt; 302

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Arg | Arg | Arg | Gly | Ala | Leu | Ser | Leu | Ser | Val | Gly | Ala | Ala | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Val | Ala | Leu | Trp | Gln | Arg | Arg | Arg | Gln | Asp | Ser | Gly | Thr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Phe | Ser | Thr | Glu | Glu | Arg | Ala | Ala | Pro | Phe | Ser | Leu | Glu | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Phe | Leu | Lys | Asn | Glu | Lys | Gly | Gln | Tyr | Ile | Ser | Pro | Phe | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Pro | Ile | Tyr | Ala | Asp | Lys | Asp | Val | Phe | His | Met | Val | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Pro | Arg | Trp | Ser | Asn | Ala | Lys | Met | Glu | Ile | Ala | Thr | Lys | Asp | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asn | Pro | Ile | Lys | Gln | Asp | Val | Lys | Lys | Gly | Lys | Leu | Arg | Tyr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asn | Leu | Phe | Pro | Tyr | Lys | Gly | Tyr | Ile | Trp | Asn | Tyr | Gly | Ala | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gln | Thr | Trp | Glu | Asp | Pro | Gly | His | Asn | Asp | Lys | His | Thr | Gly | Cys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Gly | Asp | Asn | Asp | Pro | Ile | Asp | Val | Cys | Glu | Ile | Gly | Ser | Lys | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Ala | Arg | Gly | Glu | Ile | Ile | Gly | Val | Lys | Val | Leu | Gly | Ile | Leu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Ile | Asp | Glu | Gly | Glu | Thr | Asp | Trp | Lys | Val | Ile | Ala | Ile | Asn | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Asp | Pro | Asp | Ala | Ala | Asn | Tyr | Asn | Asp | Ile | Asn | Asp | Val | Lys | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Lys | Pro | Gly | Tyr | Leu | Glu | Ala | Thr | Val | Asp | Trp | Phe | Arg | Arg | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Val | Pro | Asp | Gly | Lys | Pro | Glu | Asn | Glu | Phe | Ala | Phe | Asn | Ala | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Lys | Asp | Lys | Asp | Phe | Ala | Ile | Asp | Ile | Ile | Lys | Ser | Thr | His | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Trp | Lys | Ala | Leu | Val | Thr | Lys | Lys | Thr | Asn | Gly | Lys | Gly | Ile | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Met | Asn | Thr | Thr | Leu | Ser | Glu | Ser | Pro | Phe | Lys | Cys | Asp | Pro | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ala | Arg | Ala | Ile | Val | Asp | Ala | Leu | Pro | Pro | Pro | Cys | Glu | Ser | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Thr | Val | Pro | Thr | Asp | Val | Asp | Lys | Trp | Phe | His | His | Gln | Lys | Asn |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

&lt;210&gt; 303

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Leu | Cys | Ser | Asn | Leu | His | Phe | Cys | Ile | Arg | Pro | Ala | Trp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asn | Tyr | His | Val | Lys | His | Ile | Leu | Ile | Cys | Ile | Asn | Trp | Asn | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Lys | Trp | Arg | Tyr | Ile | Leu | Ser | Phe | Leu | Ile | Phe | Glu | Asp | Ser |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Gln | Gly | Glu | Gly | Arg | Gly | Ala | Leu | Leu | Gly | Ala | Glu | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Ser | Ala | Gly | Val | Leu | Pro | Pro | Pro | Leu | Pro | Gln | Ser | His | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Arg | Gly | Ala | Asp |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 304

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 304

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Ser | Gly | Ser | Arg | Phe | Glu | Val | Val | Val | Val | Leu | Glu | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Gly | Arg | Gly | Arg | Gly | Met | Gly | Arg | Gly | Asp | Gly | Phe | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gly | Lys | Arg | Glu | Phe | Asp | Arg | His | Ser | Gly | Ser | Asp | Arg | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | His | Glu | Asp | Lys | Arg | Gly | Gly | Ser | Gly | Ser | His | Asn | Trp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Val | Lys | Asp | Glu | Leu | Thr | Glu | Ser | Pro | Lys | Tyr | Ile | Gln | Lys | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Tyr | Asn | Tyr | Ser | Asp | Leu | Asp | Gln | Ser | Asn | Val | Thr | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

&lt;400&gt; 305

&lt;400&gt; 306

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Ala<br>1 | Thr | Arg | Gly | Ala<br>5 | Glu | Gln | Asp | Gly | Gly<br>10 | Ala | Ser | Ala | Ala | Arg<br>15 | Pro |
| Arg      | Arg | Arg | Trp | Ala      | Gly | Gly | Leu | Leu | Gln       | Arg | Ala | Ala | Pro | Cys       | Ser |

| 20         |            |            |            |            |            |            | 25         |            |            |            |            | 30         |            |            |            |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Leu        | Leu        | Pro<br>35  | Arg        | Leu        | Arg        | Thr        | Trp<br>40  | Thr        | Ser        | Ser        | Ser        | Asn<br>45  | Arg        | Ser        | Arg        |  |
| Glu        | Asp<br>50  | Ser        | Trp        | Leu        | Lys        | Ser<br>55  | Leu        | Phe        | Val        | Arg        | Lys<br>60  | Val        | Asp        | Pro        | Arg        |  |
| Lys<br>65  | Asp        | Ala        | His        | Ser        | Asn<br>70  | Leu        | Leu        | Ala        | Lys        | Lys<br>75  | Glu        | Thr        | Ser        | Asn        | Leu<br>80  |  |
| Tyr        | Lys        | Leu        | Gln        | Phe<br>85  | His        | Asn        | Val        | Lys        | Pro<br>90  | Glu        | Cys        | Leu        | Glu        | Ala<br>95  | Tyr        |  |
| Asn        | Lys        | Ile        | Cys<br>100 | Gln        | Glu        | Val        | Leu        | Pro<br>105 | Lys        | Ile        | His        | Glu        | Asp<br>110 | Lys        | His        |  |
| Tyr        | Pro        | Cys<br>115 | Thr        | Leu        | Val        | Gly        | Thr<br>120 | Trp        | Asn        | Thr        | Trp        | Tyr<br>125 | Gly        | Glu        | Gln        |  |
| Asp        | Gln<br>130 | Ala        | Val        | His        | Leu        | Trp<br>135 | Arg        | Tyr        | Glu        | Gly        | Gly<br>140 | Tyr        | Pro        | Ala        | Leu        |  |
| Thr<br>145 | Glu        | Val        | Met        | Asn        | Lys<br>150 | Leu        | Arg        | Glu        | Asn        | Lys<br>155 | Glu        | Phe        | Leu        | Glu        | Phe<br>160 |  |
| Arg        | Lys        | Ala        | Arg        | Ser<br>165 | Asp        | Met        | Leu        | Leu        | Ser<br>170 | Arg        | Lys        | Asn        | Gln        | Leu<br>175 | Leu        |  |
| Leu        | Glu        | Phe        | Ser<br>180 | Phe        | Trp        | Asn        | Glu        | Pro<br>185 | Val        | Pro        | Arg        | Ser        | Gly<br>190 | Pro        | Asn        |  |
| Ile        | Tyr        | Glu<br>195 | Leu        | Arg        | Ser        | Tyr        | Gln<br>200 | Leu        | Arg        | Pro        | Gly        | Thr<br>205 | Met        | Ile        | Glu        |  |
| Trp        | Gly<br>210 | Asn        | Tyr        | Trp        | Ala        | Arg<br>215 | Ala        | Ile        | Arg        | Phe        | Arg<br>220 | Gln        | Asp        | Gly        | Asn        |  |
| Glu<br>225 | Ala        | Val        | Gly        | Gly        | Phe<br>230 | Phe        | Ser        | Gln        | Ile        | Gly<br>235 | Gln        | Leu        | Tyr        | Met        | Val<br>240 |  |
| His        | His        | Leu        | Trp        | Ala<br>245 | Tyr        | Arg        | Asp        | Leu        | Gln<br>250 | Thr        | Arg        | Glu        | Asp        | Ile<br>255 | Arg        |  |
| Asn        | Ala        | Ala        | Trp<br>260 | His        | Lys        | His        | Gly        | Trp<br>265 | Glu        | Glu        | Leu        | Val        | Tyr<br>270 | Tyr        | Thr        |  |
| Val        | Pro        | Leu<br>275 | Ile        | Gln        | Glu        | Met        | Glu<br>280 | Ser        | Arg        | Ile        | Met        | Ile<br>285 | Pro        | Leu        | Lys        |  |
| Thr        | Ser<br>290 | Pro        | Leu        | Gln        |            |            |            |            |            |            |            |            |            |            |            |  |

&lt;210&gt; 307

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 307

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Arg | Asn | Ser | Thr | Ala | Leu | Leu | Glu | Gly | Arg | Gly | Leu | Gln | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Asp        | His        | Asp        | Ser<br>20  | Gly        | Phe        | His        | Phe        | Leu<br>25  | Asn        | Lys        | Trp        | Asn        | Cys<br>30  | Val       | Ile        |
| Tyr        | Gln        | Phe<br>35  | Leu        | Pro        | Ala        | Met        | Phe<br>40  | Val        | Pro        | Cys        | Cys        | Ile<br>45  | Pro        | Tyr       | Val        |
| Phe        | Pro<br>50  | Gly        | Leu        | Lys        | Ile        | Pro<br>55  | Val        | Ser        | Pro        | Lys        | Met<br>60  | Val        | His        | His       | Val        |
| Gln<br>65  | Leu        | Pro        | Asn        | Leu        | Arg<br>70  | Glu        | Glu        | Ser        | Ser        | Asp<br>75  | Gly        | Phe        | Val        | Thr       | Ile<br>80  |
| Leu        | Ser        | Glu        | Ala        | Asp<br>85  | Cys        | Thr        | Ser        | Pro        | Val<br>90  | Ile        | Ala        | Pro        | Phe        | Asn<br>95 | His        |
| Gly        | Ser        | Trp        | Ser<br>100 | Glu        | Leu        | Val        | Arg        | Pro<br>105 | Glu        | Phe        | Ile        | Tyr        | Ile<br>110 | Arg       | Ser        |
| Gly        | Ser        | Trp<br>115 | His        | Arg        | Leu        | Ile        | Pro<br>120 | Glu        | Thr        | Glu        | Leu        | Gln<br>125 | Gln        | Glu       | Leu        |
| Ile        | Leu<br>130 | Pro        | Gly        | Glu        | Lys        | His<br>135 | Val        | Thr        | Ser        | Cys        | Leu<br>140 | Thr        | Lys        | Phe       | Gln        |
| Lys<br>145 | Phe        | Leu        | Ile        | Phe        | Ser<br>150 | Glu        | Phe        | Ile        | His        | Asp<br>155 | Phe        | Cys        | Glu        | Gly       | Trp<br>160 |
| Ile        | Ala        | Ser        | Phe        | Ile<br>165 | Pro        | Pro        | Glu        | Val        | Asp<br>170 | Ser        | Leu        | Val        | Leu        | Leu       | Ala<br>175 |
| Ile        | Pro        | Arg        | Val<br>180 | Pro        | Ser        | Pro        | His        | Gln<br>185 | Ser        | Thr        | Arg        | Val        | Val<br>190 | Phe       | Ile        |
| Phe        | Val        | Asn<br>195 | Leu        | Trp        | Gln        | His        | Leu<br>200 | Leu        | Thr        | Asn        | Phe        | Val<br>205 | Val        | Cys       | Phe        |